

Biota 2

The Biodiversity Database Manager



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To tireless visionaries and unsung heroes around the world who work to document, understand, and preserve the biodiversity of the planet.

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Preface

How Biota Began

I originally developed the prototype of Biota to manage biodiversity information for the Arthropods of La Selva (ALAS) project at La Selva Biological Station in Costa Rica (<http://viceroy.eeb.uconn.edu/ALAS/ALAS.html>), which I have co-directed with Jack Longino (The Evergreen State College) for the past decade.

A quantitative, ecologically-structured inventory of rainforest insects and arachnids, Project ALAS is an institutional collaboration between the Organization for Tropical Studies (OTS) and the Costa Rican Instituto Nacional de Biodiversidad (INBio), with nearly a hundred systematist collaborators in Latin America, North America, and Europe.

ALAS began using Biota in early 1992. By mid-1996, the application had been used intensively by ALAS personnel for more than four years, with continual addition of functionality, refinement of structure, and improvement of the user interface in response to the daily needs of the project. During that period, records for nearly 80,000 specimens, with associated collection and taxonomic information, were entered into the database, with no data-entry backlog. Trained local parataxonomists were primarily responsible for data entry.

Biota 1

Based on comments and enthusiasm of visitors to the ALAS laboratory in Costa Rica and from the response of colleagues elsewhere (including NSF program directors), it became apparent that, if Biota could be made sufficiently flexible, it might meet the needs of a wide variety of individual ecologists, systematists, and conservation biologists for an inexpensive but powerful toolkit for managing all kinds of biodiversity information for their own research.

Moreover, many field stations, reserves, museums, and herbaria were (and some still are) relying on either antiquated or “home-made” database systems of limited usability and scalability, but could afford the cost of developing custom software or of licensing existing high-end specimen management systems.

Biota 1 was published by Sinauer Associates at the end of 1996 to help fill these needs. Initially, Biota operated only in the Macintosh operating system, but within a year the first Windows version (Version 1.2) was released, and Biota has been a completely cross-platform application ever since. Compared with the ALAS prototype, Biota 1 was quite general in its design, with many ways to customize entry, archival, and analysis of biodiversity data and images.

Over the following six years, Biota 1 was continually broadened to accommodate the needs of a wide variety of projects in ecology, biogeography, systematics, and collections management. Six major (and several minor) upgrades of Biota 1 were released, all free to registered owners of Biota 1. By the end of 2002, Biota 1 had a thousand or so users, with registrants in more than 40 countries and in 47 U.S. States.

Biota 2

While retaining Biota’s popular and familiar features and basic structure, Biota 2 incorporates a thorough re-design of the input interface, based on tabbed input screens.

Image-handling capability is greatly enhanced and extended to the Specimen, Collection, and Locality tables. Images may now reside in external files in virtually any format, with transparent links to thumbnails inside Biota. Major new features in Biota 2 include a literature Reference system and a Project system to control views of Auxiliary Fields. The most innovative feature is an on-board Web server, which allows any Biota owner to publish a Biota Data File on the internet with no additional software. (Biota 1.x users can review all the changes in “[New Tools and Features in Biota 2](#)” in Chapter 1.)

Development of Biota 2 began in 2000, with the first beta version in testing in March, 2001. By the time of this writing, in September, 2003, Biota 2 has been through 24 beta versions, tested by some 50 beta testers in a wide variety of contexts.

My objective with Biota 2 is unchanged: to provide a low-cost, but highly capable, flexible, and scalable application for managing specimen-based, biodiversity data in virtually all its forms. Biota is my contribution to helping projects around the world (especially low-budget ones) to inventory, catalogue, curate, observe, and carry out experiments on Earth’s biota, with the conviction that we cannot conserve what we do not understand.

Acknowledgments

Although I personally designed every form and wrote every line of code in Biota and every word of this Manual (with the exception of two appendices), my debt of gratitude to many others runs deep.

The launching of Project ALAS and the development of the prototype of Biota 1 would not have been possible without grants from the U.S. National Science Foundation (BSR 90-25024). Through my professorial salary, the University of Connecticut supported me throughout the development of Biota. Although Project ALAS continues to be supported by the U.S. National Science Foundation and the Organization for Tropical Studies, Biota has been completely self-supporting since its publication in 1994. My royalties are ploughed back into software licensing and other development costs.

Several of the Biota’s most innovative and useful features are the direct result of the suggestions and taxonomic experience of Jack Longino. The ALAS parataxonomists—Danilo Brenes, Flor Cascante, Nelci Oconotillo, Maylin Paniagua, and Ronald Vargas, and other members of the ALAS team have put Biota to the acid test of daily use for a decade, and continually contribute ideas for improvement.

Many Biota beta testers in many countries have contributed suggestions, bug reports, enthusiasm, and occasional despair to the development of Biota 2, just as they did with Biota 1. I have never met many of you, in person, but I take this opportunity to offer my heartfelt thanks. I could not have done this without you!

This manual would not be in your hands were it not for Andy Sinauer’s steadfast confidence in the Biota project and his infinite patience with many delays. The Sinauer team has made it possible to produce a truly usable and elegant manual for Biota that stands ready to help you efficiently when you need it. I am particularly grateful to Dean Scudder, Jason Dirks, Sydney Carroll, Mara Silver, and Parker Morse. The cover art is the generous contribution of my dear friend Shahid Naeem.

To all I am thankful, but to no one more than my wife, Robin Chazdon, for her gifts of unwavering support and understanding.

Robert K. Colwell
University of Connecticut, USA

PART
1

Introducing Biota

Chapter 1 Quick Start

NOTE TO BIOTA 1 USERS: If you are updating from Biota 1.x, and already know how to use Biota 1, proceed directly to “[Upgrading from Biota 1.x](#),” later in this chapter.

Quick-Start Strategies

Different people approach the task of learning how to use software in different ways. This section attempts to guide you based on common learning strategies.

- **Regardless of your strategy**, you should read or scan Chapter 2, “[Biodiversity Data and Relational Databases](#),” and Chapter 3, “[Key Concepts](#),” before using Biota. *It will save you time, even if you are a trial-and-error learner.*
- **If you prefer to by learn by trial and error**, with reference to a manual only when necessary:
 - ◊ **Your next step should be a session with the Biota2Demo Data File.** Feel free to add records, delete records...whatever. You can always load another copy of the Biota2Demo Data File if you want a clean copy later. (Starting out with an empty Data File does not make as much sense, since there is nothing to look at until you create it yourself.)
 - ◊ **Take a look at Appendix A,** “[Biota Tables, Fields, and Relational Links](#),” to get an idea of Biota’s design.
 - ◊ **Scan Chapter 4,** “[Biota Menus and Menu Items: An Annotated Guide](#),” to get an idea about Biota’s tools and where to find them. Each menu command description in that section has a hyperlink to the appropriate section of this Manual for further details, if you need them.
 - ◊ **If you are not already burned out on manual reading**, continue by scanning Chapter 5, “[Overview of Biota’s Tools and Features](#).”
- **If you prefer to spend some time with the Manual first**, before trying Biota:
 - ◊ **Read Chapter 2,** “[Biodiversity Data and Relational Databases](#),” **and Chapter 3,** “[Key Concepts](#).”
 - ◊ **Scan Chapter 4,** “[Biota Menus and Menu Items: An Annotated Guide](#),” to get an idea about Biota’s tools and where to find them. Each menu command description in that section has a hyperlink to the appropriate section of this Manual for further details, if you need them.

- ◊ [Read Chapter 5, “Overview of Biota’s Tools and Features”.](#)
- ◊ [Do the Tutorial in Chapter 6, “A Brief Tutorial With the Demo Database.”](#)
- ◊ [Read or scan Part 2, “Entering Data” \(5 chapters\) and Part 3, “Finding and Revising Data” \(2 chapters, especially Chapter 12, “\[Finding and Updating Records\]\(#\)”\).](#)

Special Strategies for Special Uses of Biota

This section attempts to guide you to special tools you may find useful, based on common specialized uses of Biota. It is assumed that you have already mastered the basics, covered in Part 1 (“[Introducing Biota](#)”), Part 2 (“[Entering Data](#)”), and Chapter 12 (“[Finding and Updating Records](#)”).

- **If you need to move data from a Biota 1 Data File, do nothing** until you read “[Upgrading from Biota 1.x](#),” later in this chapter. If you don’t want to read even that, *at least* read Appendix F, “[Updating Biota 1.x Data Files to Biota 2 Format](#).”
- **If you need to populate a Biota Data File by importing data** from another source, see Chapter 28, “[Importing Data](#),” especially the section “[A Strategy for Importing Text Files into Hierarchically Linked Tables](#).”
- **If you are using Biota in a biodiversity survey or inventory** (a particular strength of Biota’s because of its history), you may find the tools described in the following chapters particularly useful:
 - ◊ [Chapter 8, “Record Codes”](#)
 - ◊ [Chapter 13, “Creating, Finding, and Updating Specimen Series”](#)
 - ◊ [Chapter 15, “Printing Labels”](#)
 - ◊ [Chapter 17, “Default Entries and Entry Choice Lists \(Pick Lists\)”](#)
 - ◊ [Chapter 19, “Images”](#)
 - ◊ [Chapter 21, “Specimen Loan System”](#)
 - ◊ [Chapter 22, “Determination Histories”](#)
 - ◊ [Chapter 25, “Temporary Taxa for Approximate Determinations”](#)
 - ◊ [Appendix K, “Barcodes”](#)
- **If you are using Biota in museum or herbarium for historical specimens**, you may find the tools described in the following sections and chapters particularly useful:
 - ◊ “[Specimen and Collection Combined Input](#)” in **Chapter 11** (specifically designed for historical specimens)
 - ◊ [Chapter 8, “Record Codes”](#)
 - ◊ [Chapter 14, “Printing Reports”](#)
 - ◊ [Chapter 15, “Printing Labels”](#)
 - ◊ [Chapter 17, “Default Entries and Entry Choice Lists \(Pick Lists\)”](#)
 - ◊ [Chapter 18, “Renaming Fields”](#)
 - ◊ [Chapter 19, “Images”](#)
 - ◊ [Chapter 21, “Specimen Loan System”](#)
 - ◊ [Chapter 20, “References”](#)

- ◊ [Chapter 22, “Determination Histories”](#)
- ◊ [Chapter 23, “Synonymy System”](#)
- ◊ [Chapter 26, “Security: Passwords and Access Privileges”](#)
- ◊ [Part 8, “Biota and the Internet”](#)
- ◊ [Appendix H, “Using Biota4D with 4D Server or 4th Dimension”](#)
- ◊ [Appendix K, “Barcodes”](#)
- If you are a systematist using Biota for specimens involved in systematic revision, you may find the tools described in the following sections and chapters particularly useful:
 - ◊ “[Specimen and Collection Combined Input](#)” in [Chapter 11](#) (specifically designed for historical specimens)
 - ◊ [Chapter 8, “Record Codes”](#)
 - ◊ [Chapter 16, “User-Defined Auxiliary Fields and the Project System,”](#) for character data, especially the section “[Exporting Auxiliary Fields in the NEXUS Format](#)”
 - ◊ [Chapter 17, “Default Entries and Entry Choice Lists \(Pick Lists\)”](#)
 - ◊ [Chapter 19, “Images”](#)
 - ◊ [Chapter 21, “Specimen Loan System”](#) (to keep track of borrowed material)
 - ◊ [Chapter 20, “References”](#)
 - ◊ [Chapter 22, “Determination Histories”](#)
 - ◊ [Chapter 23, “Synonymy System”](#)
 - ◊ “[Exporting ‘Specimens Examined’ Lists for Publications](#)” in [Chapter 27](#)
- If you are an ecologist or conservation biologist using Biota for data on living organisms or plot-based specimen data, you may find the tools described in the following sections and chapters particularly useful:
 - ◊ [Chapter 8, “Record Codes”](#)
 - ◊ [Chapter 13, “Creating, Finding, and Updating Specimen Series”](#)
 - ◊ [Chapter 16, “User-Defined Auxiliary Fields and the Project System,”](#) to add environmental or morphological data fields
 - ◊ [Chapter 17, “Default Entries and Entry Choice Lists \(Pick Lists\)”](#)
 - ◊ [Chapter 19, “Images”](#)
 - ◊ [Chapter 22, “Determination Histories”](#)
 - ◊ “[Exporting Place- by-Taxon Incidence or Abundance Tables](#)” in [Chapter 27](#), for exporting data from Biota to statistical or spreadsheet applications

- If you manage data for a field station or natural area and use Biota for data on living organisms, you may find the tools described in the following sections and chapters particularly useful:
 - ◊ “[Specimen and Collection Combined Input](#)” in **Chapter 11** (specifically designed for historical specimens)
 - ◊ **Chapter 13**, “[Creating, Finding, and Updating Specimen Series](#)”
 - ◊ **Chapter 14**, “[Printing Reports](#)”
 - ◊ **Chapter 15**, “[Printing Labels](#)”
 - ◊ **Chapter 16**, “[User-Defined Auxiliary Fields and the Project System](#),” to add environmental or morphological data fields
 - ◊ **Chapter 17**, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#)”
 - ◊ **Chapter 18**, “[Renaming Fields](#)”
 - ◊ **Chapter 19**, “[Images](#)”
 - ◊ **Chapter 20**, “[References](#)”
 - ◊ **Chapter 23**, “[Synonymy System](#)”
 - ◊ **Chapter 26**, “[Security: Passwords and Access Privileges](#)”
 - ◊ **Part 8**, “[Biota and the Internet](#)”

Upgrading from Biota 1.x

Updating Biota 1.x Data Files

Biota 1 Data Files are fully compatible with Biota 2. You can update a Data File created under any version of Biota 1, from the first version, 1.0, to the final version, 1.6.1.

Although you could simply open the Biota 1.x Data File with Biota 2, and allow Biota 2 to convert it, this approach is *not recommended*. Instead, *please follow the instructions in Appendix F, “[Updating Biota 1.x Data Files to Biota 2 Format](#).”*

New Tools and Features in Biota 2

There are hundreds of changes in Biota 2, but here are the principal ones. If you are a Biota 1.x user, you should at least scan this list for items of interest to you. Below are links to the paragraphs of this section:

- [Tabbed Input screens](#)
- [Greatly enhanced Image-handling capability](#)
- [Literature Reference system](#)
- [Project System](#)
- [New Entry Choice List \(Pick List\) System](#)
- [Specimen and Collection combined Input screen for historical specimens](#)
- [On-board Web server](#)
- [Opening and creating Biota Data Files from within Biota](#)
- [Table and field lists in the Search and Sort editors](#)
- [Expanded scope of export place-by-taxon tools](#)

- [Enhanced Label tools](#)
- [Expanded keyboard shortcuts](#)
- **Tabbed Input screens.** While retaining Biota's popular and familiar features and basic structure, Biota 2 incorporates a thorough re-design of the input interface, based on tabbed Input screens. Instead of clicking an onscreen button to open a subsidiary screen (e.g. for Determination Histories, Subspecies, Notes, or Auxiliary Fields), as in Biota 1.x, ancillary input screens for each Core table input screen are placed on tabs in Biota 2 (see Chapter 11, "[Input—Table by Table](#)" for illustrations).

The enormous advantage of the tab design is that the Input Screen navigation buttons (as well as Save, Carry, Delete, Print, and Cancel buttons) are accessible from all tabs. So if you want to scan through a series of records to see the Notes, Images, References, or Auxiliary Fields attached to them, just go to the appropriate tab and use the navigation buttons.

Where appropriate, control automatically shifts to the next tab when you complete the last item in a previous tab (e.g. the Preparation tab screen opens automatically when you complete the General tab in the Specimen Input screen). You can switch tabs quickly using keyboard shortcuts (see "[Keyboard Shortcuts for Input Screen Tabs](#)" in Chapter 7).

- **Greatly enhanced Image-handling capability.** Support for images, available only for the Species table in Biota 1, are extended to the Specimen, Collection, and Locality tables in Biota 2. Equally important, images may now reside in external files in virtually any format, with transparent links to corresponding thumbnails inside Biota. New image-comparison screens have been added, and a comprehensive set of image-editing tools is available in the new QPix Image Console, as well as direct TWAIN device capture ability (scanners, digital cameras, etc.). Biota 2 supports batch import (linked thumbnails or full images) as well as batch export of external images files. See Chapter 19, "[Images](#)."

Appendix F, "[Updating Biota 1.x Data Files to Biota 2 Format](#)," explains the tools available for quickly transferring your Biota 1.x Images to the Biota 2 format.

- **Literature Reference system.** In Biota 2, a capable and flexible Reference system has been added. A separate Reference table, designed around a subset of EndNote reference styles and fields, holds Reference records that can be quickly linked (many-to-many) to any record in the Species, Specimen, Collection, or Locality table. References exported from EndNote can be directly imported to the Reference table. Records from other reference management applications can be imported with appropriate preparation of the input file. See Chapter 20, "[References](#)."
- **Project System.** In Biota 2, you can create any number of Projects (in a new Project table). Each Project record can be one-to-one with a Personnel record to allow you to keep track of overlapping sets of participants and contacts for different Projects (because a Personnel Project record can simultaneously be a Personnel Group record).

Projects also allow different views of Auxiliary Fields. In Biota 1.x, all Auxiliary Fields for a parent table (e.g. for the Species table) were visible in each parent record (e.g. all Species records), whether appropriate or not. Thus, if you had a database with moths and host plants, with Species Auxiliary Fields for moth morphometric characters as well as host plant phenology, all were shown at all times. In Biota 2, you could create a Moth Project and a Host Plant Project and choose which Species Auxiliary Fields were associated with each.

When you convert a Biota 1.x Data File to Biota 2 format, all your Auxiliary Fields are initially placed in a “Global Project,” and the Biota 1.x Personnel Project record (if you have one) is converted to a Project table record. See Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”

- **New Entry Choice List (Pick List) System.** A new “List Items” table has been incorporated in Biota 2, replacing the off-the-shelf 4D pick list system in Biota 1. You can easily import and export List Items for any of the fields in Biota that support Entry Choice Lists. A new, drag-and-drop List Editor make it easy to manage List Items for each field. The new Choice List pick screen has a “type-ahead” feature, so you can type in the first letter and letters of the entry you want and Biota automatically scrolls to the corresponding point in the pick list.

When you convert a Biota 1.x Data File to Biota 2 format, your Entry Choice Lists are automatically transferred to the List Items table, and they will continue to function in the same way you set them up. See “[Using Entry Choice Lists](#)” in Chapter 17.

- **Specimen and Collection combined Input screen for historical specimens.** Many Biota 1.x users, especially those cataloging specimen collections in museums and herbaria, complained about the need to create a separate Collection record for each Specimen record when entering data for historic material, for which each specimen generally has distinct collection data. Adding fields to the Specimen table is not a good approach, since Biota must continue to support “inventory-style” data, with many Specimen records linked to each Collection record—a powerful design for inventories and ecological studies.

The solution Biota 2 provides is a single (multi-tab) Input screen (Input menu→Input Specimen and Collection) that offers all the functionality of the Biota 2 Specimen Input screen, with provision to enter key fields from the Collection table on a tab panel. A new Collection record, linked to each new Specimen record is automatically created and linked, to accommodate the collecting-event data while conforming to Biota's data structure. See “[Specimen and Collection Combined Input](#)” in Chapter 11.

- **On-board Web server.** Biota 2 offers a fully-imbedded, on-board Web server that allows any Biota owner to publish a Biota Data File on the internet with no additional software (although for anything but trial use, you must purchase a Web Extension license from Sinauer). You can use any computer to run the Web server. See Chapter 29, “[Internet Strategies](#),” and especially Chapter 30, “[Biota's Onboard Web Server](#).”

You can choose to publish your Biota Data File on the Web in either or both of two modes: (1) *Web Browser Mode* allows you to control exactly which tables and fields are accessible to website visitors, in classic browser mode. (2) *Database Client Mode* emulates Biota's desktop interface, allowing full access to Biota's powerful search tools. See Chapter 31, “[Web Browser Mode and the Web Assistant](#),” and Chapter 32, “[Database Client Mode](#).”

- **Opening and creating Biota Data Files from within Biota.** In Biota 2, two new commands have been added to the File menu: “Open Data File” and “Create New Data File,” solving a long-standing annoyance for Biota 1.x users (thanks to new commands now available in 4D). You may continue to use the traditional Biota 1 methods for opening a different Data File or creating a new one if you prefer. See “[Opening a Biota Data File or Creating a New Biota File from Within Biota](#)” in Chapter 3.
- **Table and field lists in the Search and Sort editors.** In Biota 2, table and field lists appear in alphabetical order in the in Search and Sort Editors (and in other

places, such as in the Quick Report Editor). Even better, field lists in these tools now include any Core Field Aliases you have set up, instead of the corresponding internal field names. The awkward (and ugly) floating “Field Alias” windows of Biota 1.x have been eliminated, thanks to new programming capabilities in 4D. See Chapter 18, “[Renaming Fields](#)” for information on Aliases.

- **Expanded scope of export place-by-taxon tools.** In Biota 2, you can export incidence (presence-absence) or abundance-based place-by-taxon tables, based on either the Locality or Collection table and a taxon table at any level, Species or above. For example, you can export a Localities-by-Families table, based on a variety of different Record Set options. See “[Exporting Place- by-Taxon Incidence or Abundance Tables](#)” in Chapter 27.
- **Enhanced Label tools.** In Biota 2, you can export labels of any kind directly to a tab-delimited text file, adding greater flexibility for external processing or importing to other applications.
- **Expanded keyboard shortcuts.** Biota 2 offers many new keyboard shortcuts for buttons and tabs in Input screens and for records in Record Listing screens, while maintaining those available in Biota 1. This comprehensive set of keyboard shortcuts represents an important new feature for people with disabilities, including mouse-related repetitive motion disorders, and to any user who dislikes using the mouse. Windows users can also tab between buttons and use the menu shortcuts that Windows automatically provides. See “[Keyboard Shortcuts for Input Screen Tabs](#)” and “[Keyboard Shortcuts for Input Screen Buttons](#)” in Chapter 7, and “[Keyboard Shortcuts for Record Listing Screens](#)” in Chapter 10. These sections are summarized in Appendix C, “[Keyboard Shortcuts](#).”

Chapter 2

Biodiversity Data and Relational Databases

Biodiversity Data

Consider an ecologist who needs to record data for a quadrat-based plant survey of a large area being considered for protection as a reserve. Imagine a systematist or a biogeographer who must keep track of the classification and geographical origin of a large number of research specimens. Or, imagine a museum or herbarium with specimens from thousands of taxa, collectors, and localities.

In each of these examples (and many others in ecology, conservation biology, systematics, biogeography, and evolutionary biology), we need to record not only taxonomic information (Species, Genus, Family, and so on) for each specimen or group of specimens, but also collection and location data (collector or observer, collection or observation date, method, site characteristics, map coordinates, and names for localities and political units). This manual will refer to information with these characteristics as *specimen-based biodiversity data*.

Why Use a Relational Database?

Each individual organism in a biodiversity data set has two allegiances. It belongs to a particular species, and it belongs to a particular place and date (a particular observation or collecting event). The organism shares with all other members of its species—wherever they are—precisely the same taxonomic data, all the way up the Linnean hierarchy. At the same time, it shares with all organisms from the same collecting event—whatever their species—the same date and locality data.

Flatfiles

To record all these data for each specimen in a single column-by-row table requires repeating all the taxonomic data for each member of the same species and all the collection data for each specimen from a given collecting event. This kind of table is called a *flatfile* (or a spreadsheet). As anyone who has made a large one knows, flatfiles for floristic, faunistic, and collections data are not only clumsy and error-prone, but highly repetitive and therefore wasteful of skilled human effort—the most precious scientific resource of all.

The Relational Model

A powerful alternative to a flatfile is a *relational database*, a design for storing and retrieving data in *linked tables* that reduces repetitive input and redundant storage of data to an absolute minimum. Each row of a *table* represents a *record* (sometimes called an instance or a case). Each column represents a *field* (or attribute).

For hierarchical data, the familiar format of an indented text table is a good model for a relational database, because both have non-repetitive entries. In the indented taxonomic table below, each taxon name appears only once, regardless of taxonomic rank.

Family	Genus	Specific Name
Campanulaceae	<i>Centropogon</i>	<i>caoutchouc</i> <i>erianthus</i>
	<i>Lobelia</i>	<i>laxiflora</i> <i>salicifolia</i>
	<i>Siphocampylus</i>	<i>ecuadorensis</i> <i>sanguineus</i> <i>scandens</i>
	<i>Anthopterus</i>	<i>verticillatus</i>
	<i>Cavendishia</i>	<i>forreroi</i> <i>gilgiana</i> <i>leucantha</i> <i>lindauiana</i>
	<i>Ceratostema</i>	<i>nodosum</i> <i>peruvianum</i> <i>reginaldi</i>
	<i>Macleania</i>	<i>bullata</i> <i>cf. ericae</i> <i>coccocoloides</i> <i>glabra</i>
Ericaceae		

In fact, translating an indented table, like the one above, to the relational equivalent is straightforward. Each column of the indented table forms the basis for a separate *relational table*. In this example, three separate tables (for Family, Genus, and Specific Name) are required.

Linking Fields

In the indented format, the physical layout of the table indicates the generic membership of each species and the familial membership of each genus. In the separate tables of the relational equivalent, illustrated below, the generic membership of each species is recorded by adding a *linking field*—the Genus column, to the Specific Name table. Likewise, the familial membership of each genus is indicated in a linking field—the Family column in the Genus table. (Relational database jargon for “linking field” is “foreign key.”)

Specific Name Table

Specific Name	Genus
caoutchouc	Centropogon
erianthus	Centropogon
laxiflora	Lobelia
salicifolia	Lobelia
ecuadoriensis	Siphocampylus
sanguineus	Siphocampylus
scandens	Siphocampylus
verticillatus	Anthopterus
forreroi	Cavendishia
gilgiana	Cavendishia
leucantha	Cavendishia
lindauiana	Cavendishia
nodosum	Ceratostema
peruvianum	Ceratostema
reginaldi	Ceratostema
bullata	Macleania
cf. ericae	Macleania
coccoloboides	Macleania
glabra	Macleania

Genus Table

Genus	Family
Centropogon	Campanulaceae
Lobelia	Campanulaceae
Siphocampylus	Campanulaceae
Anthopterus	Ericaceae
Cavendishia	Ericaceae
Ceratostema	Ericaceae
Macleania	Ericaceae

Family Table

Family
Campanulaceae
Ericaceae

Although the taxonomic example above used a familiar hierarchy to illustrate the relational representation of data, the relational model can accommodate any logical structure, not just hierarchies.

Biota's structure, discussed in detail in the Chapter 3, “[Key Concepts](#),” and shown in Appendix A, “[Biota Tables, Fields, and Relational Links](#),” takes advantage of the relational model to represent and manage data for a variety of non-hierarchical logical relationships, as well as for the taxonomic and geographic hierarchies.

Efficiency of Data Input and Updating

Biota organizes biodiversity information according to the relational data model. For each class of information, such as the names and other attributes of species, genera, localities, or personnel connected with a data set, Biota records information in a separate relational table, with just one record for each genus, locality, or person.

Because of the repeated values in linking fields, it might appear that the relational design is not much of an improvement over a flatfile, in terms of avoiding data entry error and the burden of updating records. In fact, an efficient interface for a relational design allows one-time entry for each distinct value and automatic updating for linking fields, if necessary.

In a new Species record in Biota, for example, the specific name and author of a species need be entered exactly once. If a correction or update is required later, the correction is made in just one record.

Using Biota's Lookup and wildcard entry tools, you can quickly enter the linking field values for new records (for example, new Species records), when the related parent record (a Genus record, in this example) is already in your database (Chapter 11,

“[Input—Table by Table](#)”). In short, none of the repetitive data that are characteristic of flatfiles ever need be entered more than once.

Efficiency of Relational Searches

Relational databases are much more quickly searched and sorted than equivalent large flatfiles, especially for complex queries. Suppose you want a list of the Collection records for all 14,000 individual ant specimens in a Biota Data File of 150,000 records. Using Biota’s “Lower Taxa for Higher Taxa” tool (see “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12), the ant Specimen records can be found and displayed in about 2 seconds, simply by constructing the query: “Find all Specimens of the Family Formicidae.” A second query, “Find all Collections for the Specimen Record Set” using the “Places for Specimens or Species” tool (see “[Finding Specimen or Species Records for Places \(Collections or Localities\)](#)” in Chapter 12) then displays the desired Collection records in another 2 seconds.

The speed of the search is entirely a result of the relational structure of the data and the use of powerful relational commands in the programming language (4th Dimension, in the case of Biota). In contrast, a flatfile search tool would have to look at the Family column of each of the 150,000 specimen records to find those listed as Formicidae (ants). Once the ant records were found, you would need to eliminate—manually—all redundant collection data for specimens derived from the same collecting events, or work out a spreadsheet macro to do the job.

Chapter 3

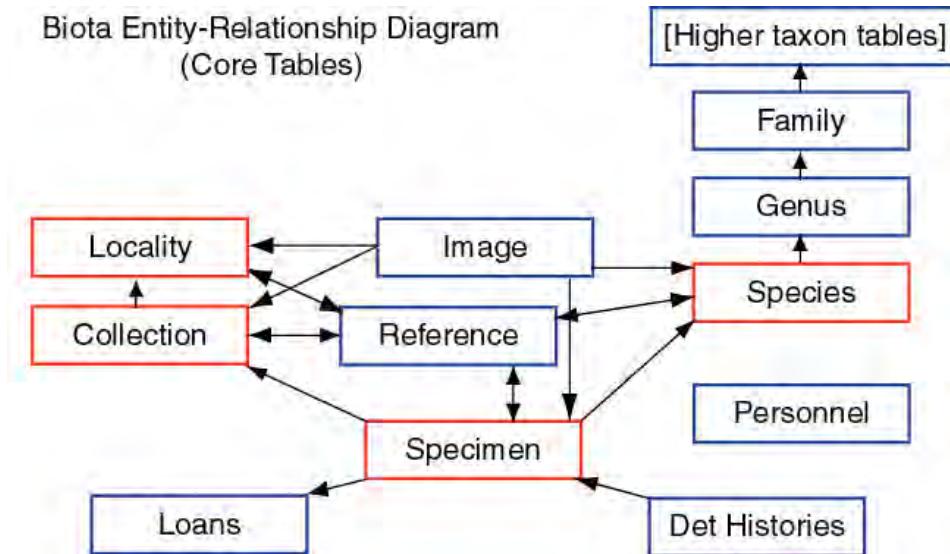
Key Concepts

Tables

As explained in Chapter 2 (“[Biodiversity Data and Relational Databases](#)”), a relational database embodies the structure of data by means of linked tables. This section introduces Biota’s data tables. For details, see Appendix A, “[Biota Tables, Fields, and Relational Links](#).” Biota’s tables are internal components of the database and thus do not appear as ordinary files on your hard disk.

Core Tables

Biota is structured around 14 *Core Tables* of data. You need to understand what each Core Table is used for, since all Biota records are entered and displayed through the Core Tables. The diagram below (in database jargon, an “entity-relationship” diagram), shows most of the links between Core Tables in Biota.



- **The taxonomic hierarchy** includes the *Specimen* table and a table for each of the seven obligatory levels of the Linnean classification system: *Species*, *Genus*, *Family*, *Order*, *Class*, *Phylum*, and *Kingdom* (see Chapter 11, “[Input—Table by Table](#)”).
- **The place hierarchy** has two levels. The *Collection* table records data for collecting events (including collector and collection date), whereas each record in the *Locality* table keeps track of the geographical site of one or more collecting events (see “[Collection Input](#)” and “[Locality Input](#)” in Chapter 11).

- **Literature references** are recorded in the *References* table. Reference records can be linked to records in the Species, Specimen, Collection, and Locality tables (see Chapter 20, “[References](#)”).
- **Names and contact data** for collectors, preparators, borrowers, Project participants, and authors of Notes are recorded in the *Personnel* table (see “[Personnel Input](#)” in Chapter 11).
- **To allow several projects to share the same Data File**, the *Project* table keeps track of project names and descriptions, and provides project-specific views of Auxiliary Fields (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).
- **To keep track of specimen loans**, the *Loans* table records which specimens have been loaned, borrowed, and returned (see Chapter 21, “[Specimen Loan System](#)”).

Peripheral Tables

In addition to the 14 Core Tables, Biota’s relational structure encompasses an additional 20 *Peripheral Tables* (see Appendix A, “[Biota Tables, Fields, and Relational Links](#).”).

Peripheral Tables keep track of supporting or ancillary data related to Core Table records.

For data entry, you will generally not need to think about what data the Peripheral Tables record, or how they are linked to each other or to the Core Tables. But you will need to understand them fully if you wish to import data into Peripheral Tables or export data directly from them.

- **Images** are saved in the *Image Archive* table, which is linked with the Species, Specimen, Collection, and Locality tables (see Chapter 19, “[Images](#)”).
- **Notes** are saved in the *Specimen Notes*, *Species Notes*, *Collection Notes*, *Locality Notes* and *Loan Notes* tables (see “[Notes Input](#)” in [Chapter 11](#)).
- **User-Defined Auxiliary Field Names and Auxiliary Field Values** for the Species, Specimen, Collection, and Locality tables are recorded in four *Field Name* and four *Field Value* tables (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).
- **Entry choice lists (pick lists)** are enabled by settings in the *Lists* table. The list values themselves are saved in the *List Items* table (see Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#)”).
- **Field name aliases** for re-namable fields are also saved in the *Lists* table (see Chapter 18, “[Renaming Fields](#)”).
- **Specimen determination histories** are kept in the *Det History* table (see Chapter 22, “[Determination Histories](#)”).
- **Personnel groups are defined** by records in the *Group* table (see “[Entering Personnel Data: the ‘Group’ Tab](#)” in Chapter 11).
- **References are linked to Species, Specimen, Collection, or Locality records** through entries in the *Reference Links* table (see Chapter 20, “[References](#)”).
- **Projects are linked to Auxiliary Field names** by means of records in the *Aux Index* table (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).

Fields and Records

Each Biota table consists of a unique set of *fields* that represent data elements (attributes) appropriate to that table. These fields are listed for each table in Appendix A, “[Biota Tables, Fields, and Relational Links](#).”

Most of Biota’s input (detail) screens, record listing screens, and printed reports and labels combine fields from several tables at once. The Specimens Report, for example, lists specimens organized by the taxonomic hierarchy, with collection and locality data for each specimen—it thus includes fields from 10 different tables.

The information in each table is organized by *records*. Each record in a table may include entries for each field in that table. For example, in the Specimen table, each record represents an individual specimen (or a group of specimens that share the same data), with entries for that specimen’s unique Specimen Code, the Collection Code for the sample or collection site from which the specimen came, the Species Code for the species to which the specimen has been assigned or determined, the name of the person who made that assignment (Determined By), and so on through the fields listed for the Specimen table in Appendix A, “[Biota Tables, Fields, and Relational Links](#).”

You can think of an individual database table as a spreadsheet, with fields as columns and records as rows—indeed, records and fields appear in this format in most Biota record listing screens.

Key Fields

In most relational database tables (including all of Biota’s Core Tables) each record must be uniquely identifiable and retrievable. For this reason, one field (in some tables a pair of fields) in each such table is designated as the *Key field*—or simply the *Key*. Every record in such a table must have a unique alphanumeric value for the Key field (or a unique combination of values for a two-valued or *composite key*). In Biota, the Key field for the Locality, Collection, Specimen, Species, and Loans tables is a unique alphanumeric *Record Code* for each record. (You can define Record Codes yourself, or ask Biota to supply them automatically). Chapter 8, “[Record Codes](#),” discusses these codes in depth.

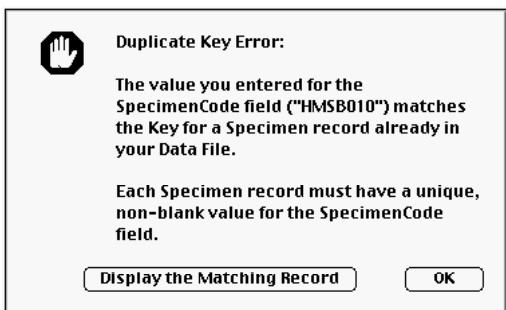
For taxon tables above the species level, the taxon name itself is the Key field, relying on the uniqueness criterion of the Rules of Nomenclature. Names of genera, however, may sometimes be ambiguous. If you need to record generic junior synonyms, or in the rare cases in which genera in two or more Kingdoms share the same genus name and are listed in the same database, you will need to add a distinguishing suffix to generic names.) This approach and Biota’s ability to exclude special characters appended to generic names on labels are discussed in the section “[A Special Problem for Genera: Legitimate Duplicate Generic Names](#)” in Chapter 11.

The Key field for the Personnel table is a user-defined, unique “Short Name” (initials and last name for a person, for example, or an acronym for an institution). The uses of Short Names are discussed in the section “[Entering Personnel Data: The ‘General’ Tab](#)” in Chapter 11.

Duplicate Key Errors

If you enter a value in a Key field that duplicates the Key field entry for any existing record in the same table in your database, Biota will post an error message like the one shown on the next page. You will have to choose a different value for the Key, or change

the Key in the existing record, which you can display for comparison using the “Display the Matching Record” button.



Linking Fields: Parent and Child Records

Relational links (or relationships) join tables through *linking fields* (see Chapter 2, “[Biodiversity Data and Relational Databases](#)”). These links give a relational database its power and efficiency. Appendix A, “[Biota Tables, Fields, and Relational Links](#),” shows the relational links between Biota’s data tables.

The Specimen table lies at the base of two hierarchies of *many-to-one* relationships.

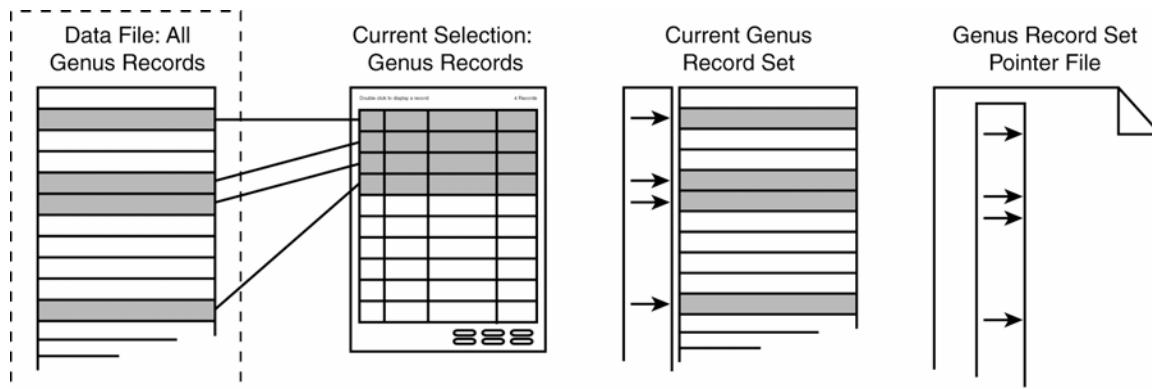
- **In the place hierarchy**, the Specimen table is linked to the Collection table through the Collection Code linking field. (There may be *many* specimens in *one* collection.) In turn, the Collection table is linked to the Locality table through the Locality Code linking field. (There may be *many* collections from *one* locality.)
- **In the taxonomic hierarchy**, the Specimen table is linked to the Species table through the Species Code linking field. (There may be *many* specimens of *one* species). The Species table, in turn, is linked to the Genus table (there may be *many* species in *one* genus), and so on up the Linnean hierarchy.

In menus, screens, and dialogs and in most contexts in this manual, Biota does not use the formal “many-to-one” or “one-to-many” terminology. Instead, a “parent-child” metaphor is used. For example, a particular Family record is the *parent* record for all the Genus records for all genera in that family—the *child* records. Of course, in many cases a particular record is both parent and child; a Genus may be the child record of a Family record, and at the same time parent record to one or more Species (child) records. (The parent-child metaphor works well here, since each of us may be both child and parent, as our own parents undeniably were.)

The metaphor is carried further in the concepts of *orphan* records (those that are not linked to any record in the parent table) and *childless* records (those not linked to any record in the child table, for a particular database relation). For example, a Genus record not linked to any Family record is an orphan record. A Genus record not linked to any Species record is a childless record. Orphan records, especially, and childless records, to a lesser extent, tend to be “invisible” in relational searches. (In relational database terminology, orphan records compromise the *referential integrity* of the database.) Biota offers optimized search tools for finding and displaying orphan and childless records (see “[Finding Childless and Orphan Records](#)” in Chapter 12).

Data Files

To use Biota effectively, it is essential to understand the distinction between four representations of Biota data records, discussed and contrasted in this section and the three that follow. The figure below shows graphically some of the important distinctions among the four ways Biota handles groups of records.



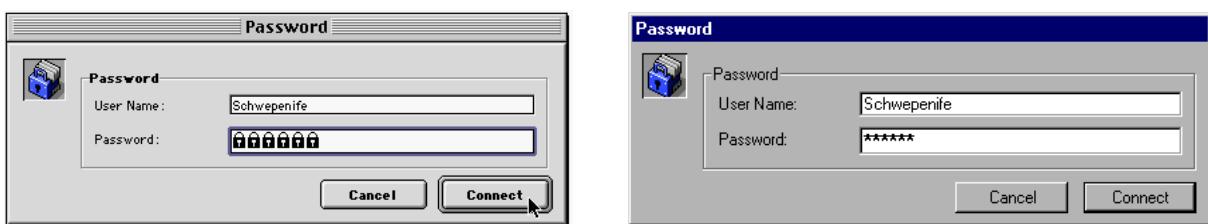
The actual records for a table are recorded in a Biota *Data File*, in a special format that can be opened only by Biota. The figure above illustrates a Biota Data File in the dashed rectangle, with the Genus table as an example. Biota Data Files are separate from the application file itself (BiotaApp or Biota4D).

Opening a Biota Data File When Launching Biota

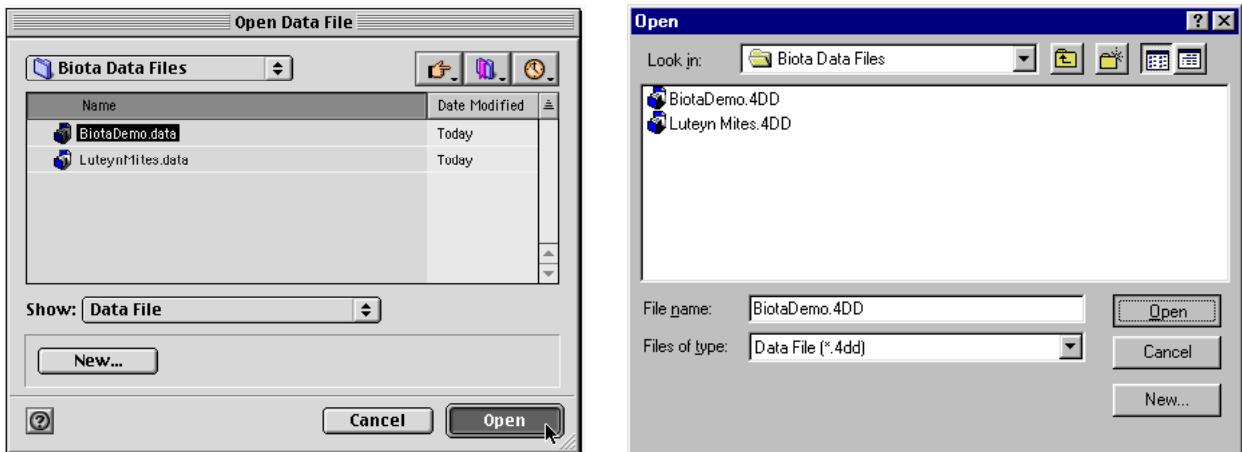
To choose among existing Biota Data Files when you launch Biota, follow these steps.

1. Launch Biota.

- **If you have not enabled the user password system** (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), immediately press and hold the OPTION key (Mac OS) or ALT key (Windows).
- **If you have enabled the password system**, the Password request screen appears. Enter your password, then press and hold the OPTION key (Mac OS) or ALT key (Windows) while clicking the “Connect” button. (In the illustrations below, the Mac OS screen is illustrated on the left, the Windows screen on the right).



The Open Data File (Mac OS) or Open (Windows) screen for your operating system appears.



2. Find the Data File you want to open, select it, then click the “Open” button.

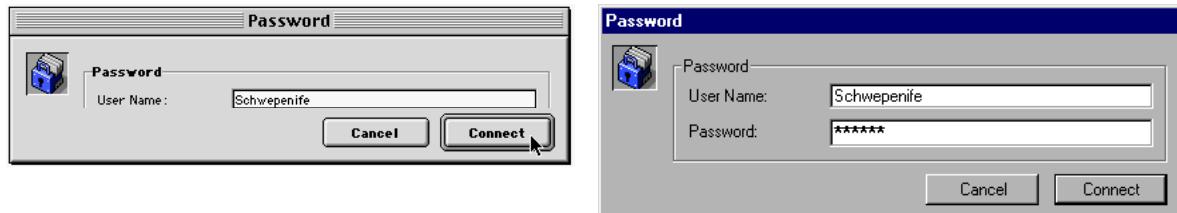
Creating an Empty Biota Data File While Launching Biota

NOTE TO WINDOWS USERS: Due to a 4D bug, BiotaAppWin does not perform consistently using this method for creating a new Data File. (Biota may freeze.) Until the problem is resolved, please use the method in the next section instead ("[Opening a Biota Data File for Creating a New Biota Data File from Within Biota](#)"). This limitation does not apply to Biota4DWin.

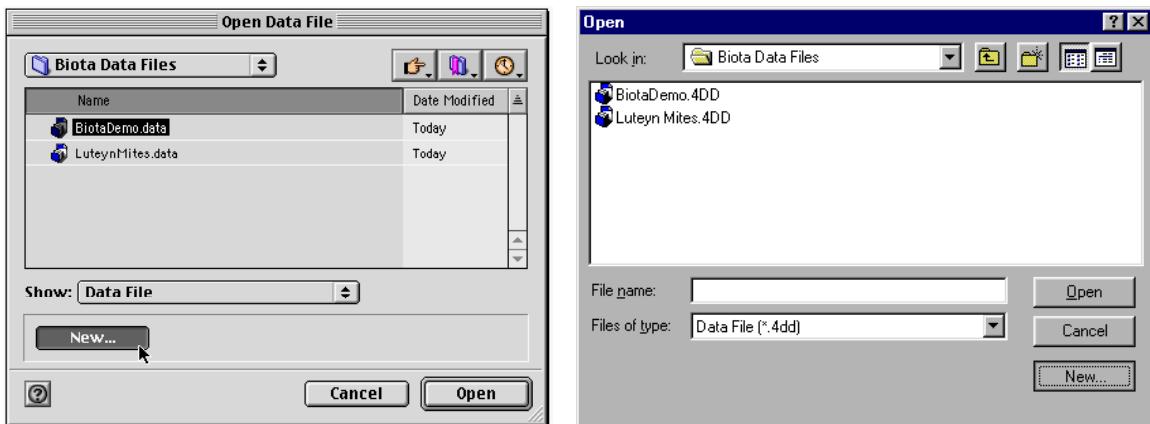
To create a new, empty Biota Data File while launching Biota, follow these steps.

1. Launch Biota.

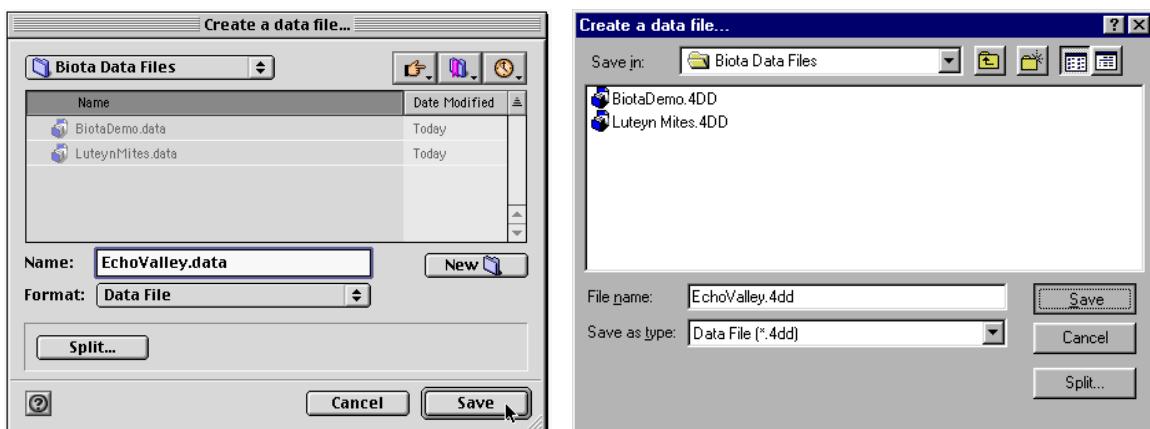
- If you have not enabled the user password system (see Chapter 26, "[Security: Passwords and Access Privileges](#)"), immediately press and hold the OPTION key (Mac OS) or ALT key (Windows).
- If you have enabled the password system, the Password request screen appears. Enter your password, then press and hold the OPTION key (Mac OS) or ALT key (Windows) while clicking the “Connect” button. (In the illustrations below, the Mac OS screen is illustrated on the left, the Windows screen on the right).



The Open Data File (Mac OS) or Open (Windows) screen for your operating system appears.



2. Click the “New” button (not the “Open” button), shown above. A Save File window for your operating system appears, with the instruction “Create a data file.”



3. Name and place the file then click the “Save” button. Biota will take a few moments to create the Data File, so be patient.

Opening a Biota Data File or Creating a New Biota File from Within Biota

While you are working with Biota, you can switch to a different, existing Biota Data File or create a new, blank Biota Data File without quitting Biota. Because you cannot have two Data Files open at once under the same copy of Biota, the Data File you currently have open will first be closed, after automatically saving any recent changes.

- **To switch to a different Biota Data File**, choose “Open Data File” from the File menu and follow the onscreen instructions.
- **To create a new, blank Biota Data File**, choose “Create New Data File” from the File menu and follow the onscreen instructions, which allow you to create a new folder for the blank Data File if you wish.

NOTES:

- (a) **If you have enabled the User Password System** (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), only the Administrator can use these menu items to open or create Biota Data Files. This precaution is intended to prevent accidental change to a different Biota Data File by data entry personnel.
- (b) **These menu items cannot be used from 4D Server or 4D Client.** Under 4D Server, you must change to a different Data File or create a new one using the methods in the previous sections, “[Opening a Biota Data File When Launching Biota](#)” and “[Creating an Empty Biota Data File While Launching Biota](#).”

Saving Changes in a Biota Data File

Biota uses temporary buffers in RAM to keep track of any changes you make in the active Data File. Every three minutes, Biota automatically saves these changes to disk and clears the buffers.

There is one exception: Each group of new records you create or modify using commands from the Series menu is saved immediately.

If you want to force Biota to save changes immediately, press the keys COMMAND+W (Mac OS) or CTRL+W (Windows) at any time.

When you quit Biota, any changes made since the last automatic save are recorded in the Data File.

The small window shown here appears in the corner of the screen during a save operation. Other ongoing operations may be momentarily slowed, but are not halted.

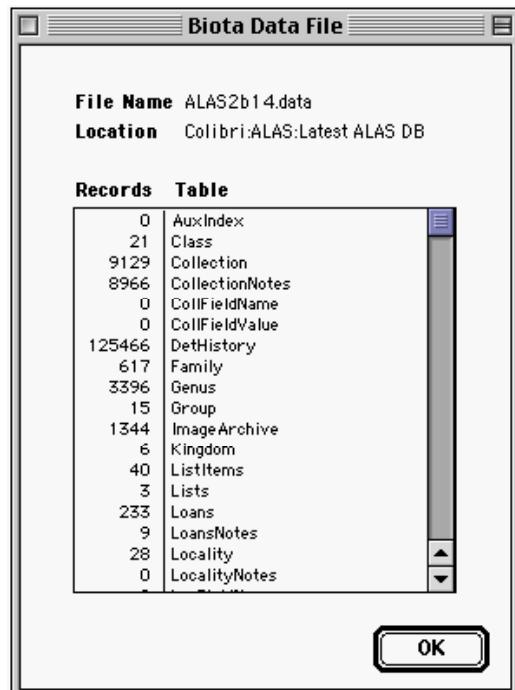


NOTE TO MAC OS USERS: The key combination COMMAND+W, normally used for closing windows in Macintosh applications, is reserved by 4th Dimension for saving data to disk from the buffers. To close a Biota window from the keyboard, press OPTION+W instead. The same shortcut also works in the Windows versions of Biota.

To Find Out Which Data File Is Currently Open

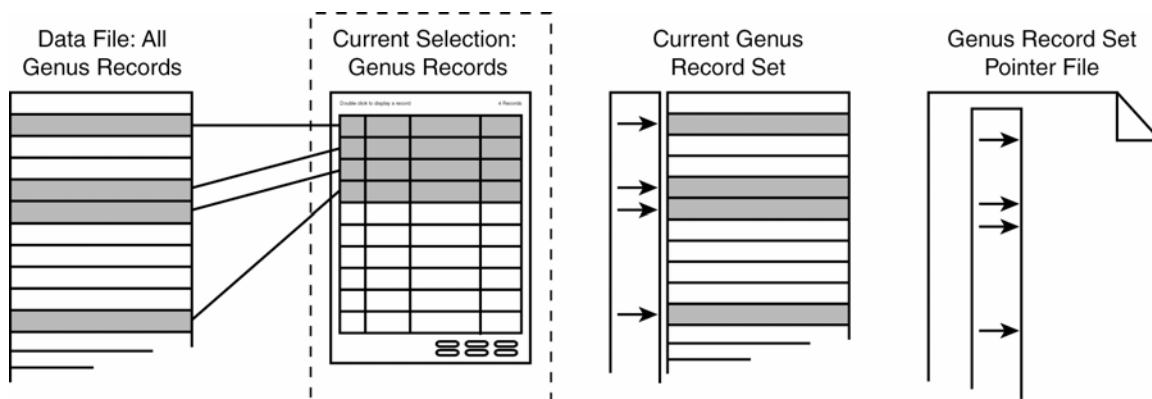
Biota can open only one Data File at a time. If you have enough memory available, however, you can launch two or more copies of Biota simultaneously on the same computer, each with a different Data File. (It is acceptable under the License Agreement to make copies for this purpose, as long all copies are in use by a single user.)

You can find out which Data File is open by selecting “About the Current Data File” from the File menu. The information window that appears also tells you how many records there are in each Biota table in the current Data File.



Selections and Processes

Because a database may become very large, displaying *all* the records in a table every time you want to look up a record, correct mistakes, or view a set of recent entries after entering them would soon become extremely cumbersome and time-consuming. To solve this problem, Biota displays in a window (or prints) only those records in a *Selection* for a particular table. Selections of records are the second way Biota handles records (illustrated below in the dashed rectangle).



A Selection can include all of the records for a table or any subset of them. If you use Biota's search tools to find all records in the Species table for the Family Ericaceae, for example, all the Species records for ericads will become the current Selection for the Species table, and Biota will display them in the record listing screen for the Species table. If a Selection is empty, which will happen, for example, if a search fails to find a match for your query, no records are displayed.

In short, a Selection is simply a “list” of selected records from a particular table in the database. The records in the Selection may be sorted, displayed on the screen, opened one at a time to view or edit, or printed.

Note: Placing records in a Selection or removing records from a Selection has absolutely no effect on their presence in the Data File itself.

During data entry, as each record is accepted, it is added to the Data File itself. Once entered, each record remains in the Data File until and unless it is specifically deleted, regardless of how often it is included in or removed from a Selection.

Biota is based on a *multi-process* or *multi-tasking* architecture. Each time you choose an item from one of Biota's menus, an independent *process* is launched, rather like a mini-application within Biota. You can launch as many independent processes as memory permits. (New processes are also launched by certain buttons on Biota screens.)

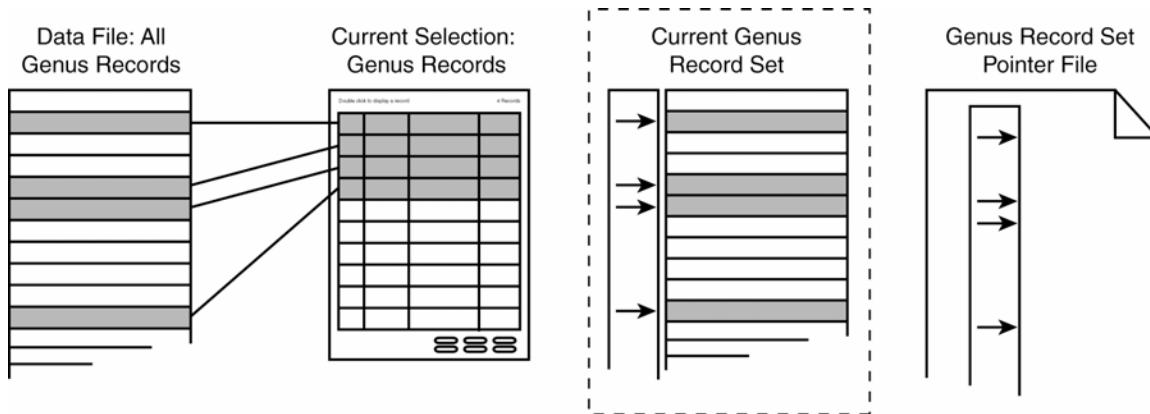
Each process maintains its own Selection for every Biota table, although most Selections will be empty at any given moment. Thus, you can retrieve and display several Selections for the same table simultaneously in different windows. Because simultaneous Selections are entirely independent of one another, they can include distinct, overlapping, or even identical sets of records.

NOTE: To maintain record integrity, however, you may edit an individual record in only one input (detail) screen at a time. You can read about *record locking* in Appendix L, “[Troubleshooting and Support](#).”

Record Sets

The third way you can represent and work with records is by using *Record Sets*. You can tell Biota to “remember” a Selection of records from a particular table and process by establishing it as a Record Set for the table (illustrated below in the dashed rectangle).

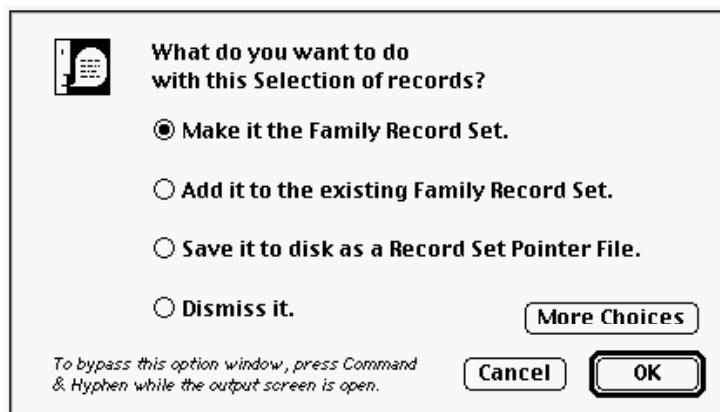
Each of Biota’s 14 Core Tables (see [Core Tables](#), earlier in this chapter), plus the Determination History table (see Chapter 22, “[Determination Histories](#)”), has its own current Record Set, at all times.



Unlike Selections for a particular table, of which many can exist simultaneously in different processes (see “[Selections and Processes](#),” earlier in this chapter), there is always only *one* current Record Set per table. (You can save and retrieve as many Record Sets per table as you wish, however. See “[Record Set Pointer Files](#),” later in this chapter.) When you launch Biota, all Record Sets are empty and remain empty until you retrieve or create Selections of records to place in them.

The Record Set Options Screen

Understanding the Record Set options screen is the key to working effectively with Record Sets in Biota. The options screen (illustrated below) appears whenever you click the “Done” button in a record listing screen.



The Record Set options screen offers the following primary alternatives:

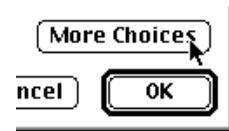
- **Make it the [table name] Record Set.** If you choose this option, the current Selection of records is declared the current Record Set for the table.
- **Add it to the existing [table name] Record Set.** This option allows you to combine the current Selection with the current Record Set for the table. If the current Record Set is empty, this option and the “More Choices” button are disabled (dimmed) and a message appears reading: “The [table name] Record Set is empty,” as illustrated below.

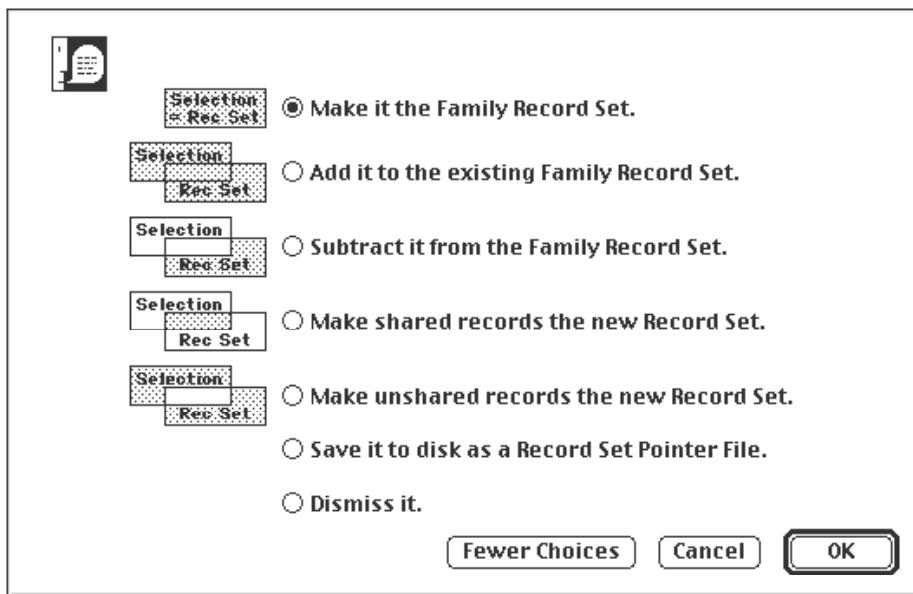


- **Save it to disk as a Record Set Pointer File.** This option saves a disk file that allows you to reload the Selection quickly at a later time. See “[Saving a Record Set Pointer File: First Method](#),” later in this chapter.
- **Dismiss it.** Choosing this option dismisses the Selection of records without affecting the current Record Set for the table.

NOTE: You can achieve the same result as the “Dismiss it” option by bypassing the Record Set options screen entirely. To do so, simultaneously press the COMMAND key plus the HYPHEN key (Mac OS) or the CTRL key plus the HYPHEN key (Windows), to dismiss any record listing screen, instead of clicking the “OK” button. (You can also use this keyboard shortcut to dismiss most input screens, instead of clicking the “Cancel” button.) The HYPHEN key is the key next to the ZERO key; do not confuse it with the MINUS key on the numeric keypad, if you have one.

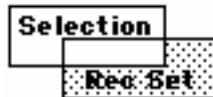
- **The “More Choices” button.** If the current Record Set for the table is not empty, the “More Choices” button in the Record Set options screen is enabled. (If the current Record Set is empty, the button is dimmed.) If you click the “More Choices” button when it is enabled, the Record Set options screen expands to include not only the four original options (illustrated above) but three additional options that allow other operations (“set mathematics”) on Record Sets in relation to the current Selection. (See the next page.)





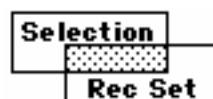
You will probably use the additional options infrequently, but when you need them, they offer powerful and unique solutions to handling Selections and Record Sets. The Venn diagrams show each set operation graphically, on the left side of the screen.

- **Make it the [table name] Record Set.** The Selection *itself* becomes the new current Record Set for the table (the *assignment* set operation). This option is the same as the first of the options offered in the principal Record Set options screen.
- **Add it to the existing [table name] Record Set.** The *union* of the Selection and the Record Set becomes the new current Record Set for the table. This option is the same as the second of the options offered in the principal Record Set options screen.
- **Subtract it from the existing [table name] Record Set.** The set of all records in the current Record Set that are *not* in the Selection (the *difference* between the Record Set and Selection) becomes the new current Record Set for the table.



NOTE: To subtract the current Record set from the Selection, instead, save the current Record Set as a Record Set Pointer File (see “[Saving a Record Set Pointer File: Second Method](#),” later in this chapter), make the Selection the new current Record Set, then load the saved Record Set Pointer File (see “[Loading a Record Set Pointer File](#),” later in this chapter) and use the subtract operation.

- **Make shared records the new Record Set.** The *intersection* of the Selection and the Record Set becomes the new current Record Set for the table.
- **Make unshared records the new Record Set.** The set of all records in *either* the Selection or the current Record Set, *but not both*, becomes the new current Record Set for the table.



- **Save it to disk as a Record Set Pointer File.** This option saves a disk file that allows you to reload the Selection quickly at a later time. See “[Saving a Record Set Pointer File: First Method](#),” later in this chapter. This option is the same as the third of the options offered in the principal Record Set options screen.
- **Dismiss it.** Choosing this option dismisses the Selection of records without affecting the current Record Set for the table. This option is the same as the fourth of the options offered in the principal Record Set options screen.

How Biota Uses Record Sets

Biota uses Record Sets to define groups of records for several kinds of special tasks. For example, the Query Editor can, as an option, search within a Record Set instead of searching through all records in a table (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#),” in Chapter 12).

Four search tools find records in one table based on the current Record Set for another table: Lower Taxa for Higher Taxa, Higher Taxa for Lower Taxa, Places for Specimens Or Species, and Specimens or Species for Places (see “[Special Tools for Finding Records in One Table Based on a Set of Records in Another Table](#)” in Chapter 12).

All of Biota’s Export tools can (some of them must) use the appropriate Record Set as the basis for export (see Chapter 27, “[Exporting Data](#),” and “[Exporting and Importing Images](#)” in Chapter 19). All Labels tools print labels for a Record Set (see Chapter 15, “[Printing Labels](#)”).

A new Specimen Loan can be made for the current Specimen Record Set, or the current Specimen Record Set can be recorded as a returned loan (see Chapter 21, “[Specimen Loan System](#)”).

The Find and Replace tool can be used on Record Sets, as an option (see “[Updating Records Using the Find and Replace Tool](#)” in Chapter 12).

To Display a Record Set

As their only function, commands in the Display menu display the current Record Set for each of the Core Tables. These records are presented in the standard record listing screen for each table, with all the usual tools for output and input screens available (see Chapter 10, “[Working with Records in Record Listing and Input Screens](#)”). If the current Record Set is empty, Biota informs you that the Record Set you asked to display is currently empty, and nothing is displayed.

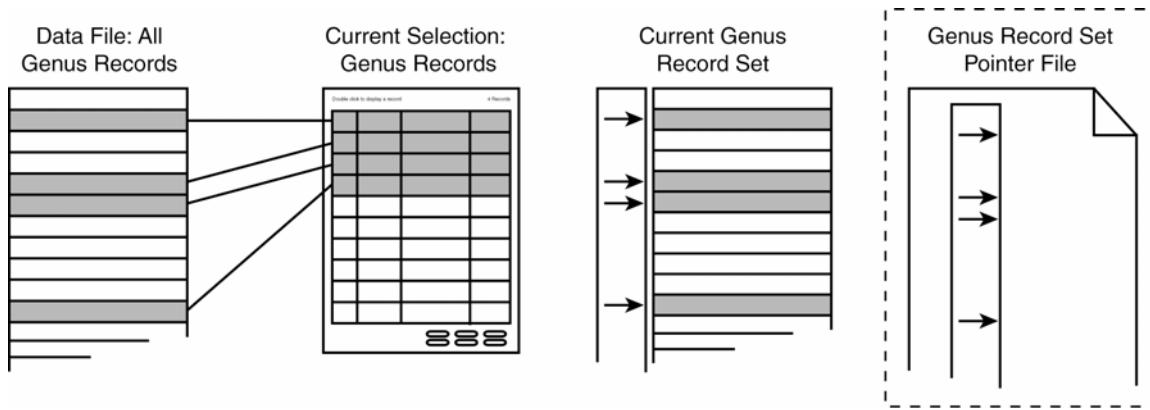
NOTE: The command for displaying the current Record Set for the Det History (Specimen Determination History) table is in the Special menu (see Chapter 22, “[Determination Histories](#)”). If you have activated the user password system, only a user with Administration access privileges can use this command (see Chapter 26, “[Security: Passwords and Access Privileges](#)”).

To Empty All Record Sets

You can empty all current Record Sets by selecting “Empty Record Sets” from the Special menu. Record Sets always start out empty each time you launch Biota.

Record Set Pointer Files

Record Set Pointer Files, the fourth way to represent Biota records, allow you to save the results of searches, input sessions, or import operations for later use, even between Biota sessions. A Record Set Pointer File is illustrated below in the dashed rectangle.



Internally, Record Sets themselves are simply lists of “pointers” to records, not the records themselves. (Record pointers are a very compact and efficient way to keep track of Selections of records.) A Record Set Pointer File is simply a disk file (which you name as you wish) containing a set of record pointers, which can later be loaded from disk to recover a Selection of records for a particular table.

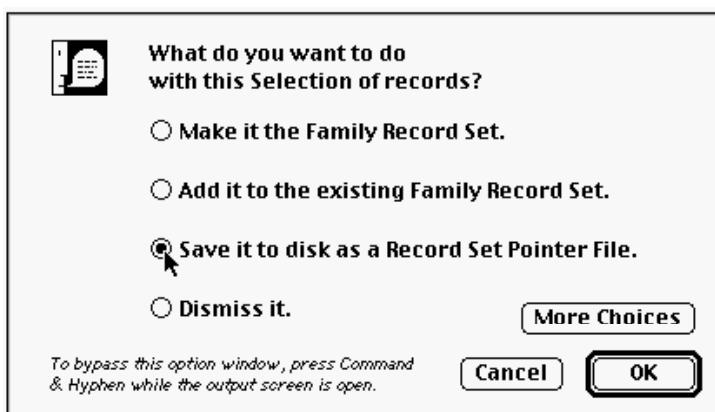
You can create as many Record Set Pointer Files as you wish for each Core Table. They take up virtually no disk space, and they are saved or loaded instantaneously.

Record Set Pointer Files are not readable or useable with other applications. If you want to create a text file from a set of records, use one of the export tools described in Chapter 27, “[Exporting Data](#).”

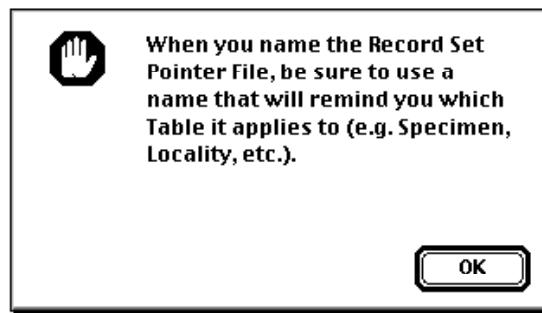
Saving a Record Set Pointer File: First Method

You use this method to create a Record Set Pointer File for a Selection of records when you close a record listing screen with the “Done” button. If a Record Set representing a different group of records already exists for the table, creating a Record Set Pointer File with this method leaves the existing Record Set unchanged.

1. Choose “Save it to disk as a Record Set Pointer File” in the Record Set option window that appears when you close a record listing screen (see “[The Record Set Options Screen](#),” earlier in this chapter).



2. Click the “OK” button in the option window. A message appears reminding you to name the disk file appropriately.
3. Click the “OK” button in the reminder message. The Save File window for your operating system appears.
4. Name and place the Record Set Pointer File.
5. Click the “Save” button (Mac OS) or the “OK” button (Windows) in the Save File window.



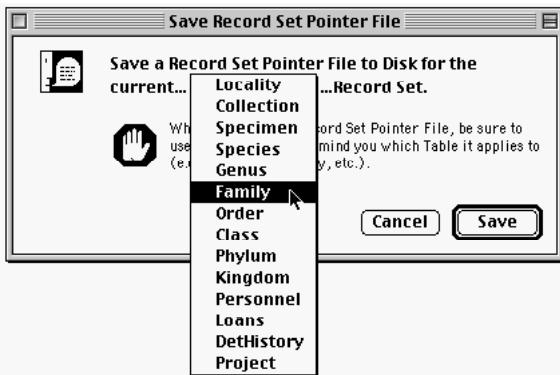
Saving a Record Set Pointer File: Second Method

You can use this method at any time to create a Record Set Pointer File for the current Record Set of a particular table. No records need be displayed.

1. Choose Save Record Set Pointer File from the File menu. A table selection window appears.



2. Choose the table name from the popup list in the table selection window.



The Save File window for your operating system appears.

3. **Name and place the Record Set Pointer File.** Be sure to name the Record Set Pointer File appropriately.
4. **Click the “Save” button (Mac OS) or the “OK” button (Windows)** in the Save File window.

Loading a Record Set Pointer File

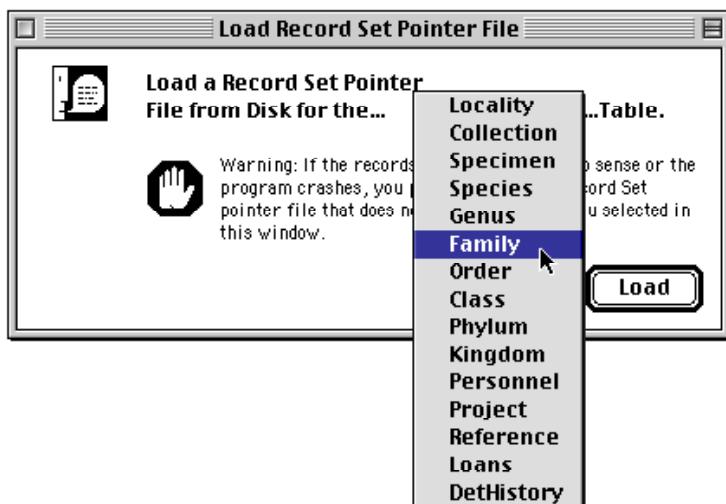
To load a Selection of records using a saved Record Set Pointer File, follow these steps.

1. **From the File menu, choose Load Record Set Pointer File.**

A table selection window appears.



2. **From the popup list in the table selection window (above), select the Biota table for which you intend to retrieve records.**



3. **Click the “Load” button when ready (above).** The file navigation window appears.
4. **Find the Record Set Pointer File** in your folder or directory structure and open it.

WARNING: Be certain that the file you choose applies to the Biota table you have selected in [Step 2](#). If not, you will have unpredictable results—or no results. If you have added or deleted records in the table since saving the Record Set Pointer File, the Selection may not be accurate when you load the Record Set Pointer File.

The records representing the saved Record Set Pointer File you loaded are displayed as a Selection in the record listing screen for the appropriate table.

The Selection displayed is not automatically made the current Record Set for the table. See “[Loaded Record Set Pointer Files and the Current Record Set](#),” below.

5. **If you wish to make the displayed Selection the current Record Set**, click the “Done” button in the listing screen and use the Record Set Options screen to designate the Selection as the current Record Set for the table.

Loaded Record Set Pointer Files and the Current Record Set

The Selection of records retrieved and displayed using a saved Record Set Pointer File is not automatically designated the current Record Set for the appropriate table. If you want to make this Selection the current Record Set or add it to the current Record Set for the table, you must do so in the usual way, using the Record Set Option screen that is displayed when you click the “Done” button in the record listing screen (see “[The Record Set Options Screen](#),” earlier in this chapter).

Why does Biota not declare a retrieved Selection to be the current Record Set automatically? Were that the case, you would be unable to use the “set mathematics” tools in the Record Set Options screen to work with selections saved as separate Record Set Pointer Files, nor could you use these operations on a Selection from a new search and a saved Record Set.

Chapter 4

Biota Menus and Menu Items: An Annotated Guide

Biota Menus: Quick Reference

This section briefly describes the function of each item in the Biota menus and directs you to the appropriate pages of this Manual for full details. The menus and their items (commands) are listed in the order they appear on the screen.

NOTE: The notation used for each item is “**Menu Name → Menu Item.**”

Access Privileges for Menu Items

If the User Password system has been activated, each user is assigned an access privilege level. Depending on the privileges you have been assigned, certain menu commands may be unavailable to you. If so, Biota posts an explanatory message when you select the item. A complete tabulation of commands and the privilege level required to use them appears in the section “[Users, User Names, Passwords, Access Levels, and Privileges](#)” in Chapter 26.

The Menu Bar

Because Biota supports simultaneous procedures (multitasking), the menu bar does not change. All menus are present and active at all times.

File Edit Input Series Find Display Labels Im/Export Loans Special Help

The File Menu

- **File → Open Data File.** Presents a file navigation screen to allow you to close the present Biota Data File and open a different one. See “[Opening a Biota Data File or Creating a New Biota File from Within Biota](#)” in Chapter 3.
- **File → Create Data File.** Presents a file navigation screen to allow you to close the present Biota Data File and create a new, empty one. See “[Opening a Biota Data File or Creating a New Biota File from Within Biota](#)” in Chapter 3.

File	Edit	Input	Series	Find
Open Data File...				
Create New Data File...				
Save Record Set Pointer File...				
Load Record Set Pointer File...				
Print...				⌘P
About Biota...				
About the Current Data File...				
Quit Biota				⌘Q

- **File → Save Record Set Pointer File.** Creates a disk file with pointers to the records in the current Record Set for any Core Table or for the Determination History table. See “[Saving a Record Set Pointer File: Second Method](#)” in Chapter 3.
- **File → Load Record Set Pointer File.** Loads the Selection of records indicated by the record pointers in a saved Record Set Pointer File. See “[Loading a Record Set Pointer File](#)” in Chapter 3.
- **File → Print.** Prints (see “[Printing a Report Based on a Selection of Records](#)” in Chapter 14) or exports to disk file (see “[Printing Reports or Creating Text Files Based on Records in a Record Listing Screen](#)” in Chapter 10) a report for the current Selection of records displayed in an Record Listing screen. (This command is disabled if no records are displayed.)
- **File → About Biota.** Displays the copyright notice, version, and release date for your copy of Biota, as well as the website and support e-mail address for Biota.
- **File → About the Current Data File.** Displays the name and location (path) of the Data File that is currently open, plus a scrolling list of the number of records in each Biota table in the Data File. See “[To Find Out Which Data File Is Currently Open](#)” in Chapter 3.
- **File → Quit Biota.** Choose this command to shut down Biota. See “[Saving Changes in a Biota Data File](#)” in Chapter 3.

The Edit Menu

The Edit Menu contains the standard text editing commands for your operating system. See your operating system manual.

The Input Menu

- **Input → Specimen.** Presents the Specimen Input screen. See “[Specimen Input](#)” in Chapter 11.
- **Input → Specimen & Collection.** Presents the Specimen Input screen. See “[Specimen and Collection Combined Input](#)” in Chapter 11.
- **Input → Collection.** Presents the Collection Input screen. See “[Collection Input](#)” in Chapter 11.
- **Input → Locality.** Presents the Locality Input screen. See “[Locality Input](#)” in Chapter 11.
- **Input → Species.** Presents the Species Input screen. See “[Species Input](#)” in Chapter 11.
- **Input → Genus, Family, Order, Class, Phylum or Division, or Kingdom.** Presents the Input screen for the corresponding table. See “[Genus, Family, Order, Class, Phylum, and Kingdom Input](#)” in Chapter 11.
- **Input → Personnel.** Presents the Personnel Input screen. See “[Personnel Input](#)” in Chapter 11.
- **Input → Project.** Presents the Project Input screen. See “[Project Input](#)” in Chapter 16.
- **Input → Reference.** Presents the Reference Input screen. See “[Reference Input](#)” in Chapter 20.

Input	Series	Find	Disp
Specimen			
Specimen & Collection			
Collection			
Locality			
Species			
Genus			
Family			
Order			
Class			
Phylum or Division			
Kingdom			
Personnel			
Project			
Reference			

The Series Menu

- **Series → Input Specimen Series.** Presents an Input screen for the efficient creation of sets of Specimen records that share Collection data. See “[Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series Tools’](#)” in Chapter 13.
- **Series → Input & Identify Spcm Series.** Presents an Input screen for the efficient creation of sets of Specimen records that share Collection and determination (identification) data. See “[Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series Tools’](#)” in Chapter 13.
- **Series → Find Specimen Series.** Presents a query tool for finding Specimen records efficiently by Specimen Code. The Specimen Codes may be either sequential or non-sequential. (The same command appears in the Find menu.) See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series Tools’](#)” in Chapter 13.
- **Series → Find & Identify Specimen Series.** Presents a query and record update tool for finding Specimen records efficiently by Specimen Code, and for adding determination (identification) data and/or certain other fields in the Specimen table. The Specimen Codes may be either sequential or non-sequential. See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series Tools’](#)” in Chapter 13.

Series	Find	Display	Labels
Input Specimen Series			
Input & Identify Spcm Series			

Find	Display	Labels	Im/Export
Using the Query Editor...			
Lower Taxa for Higher Taxa...			
Higher Taxa for Lower Taxa...			
Places for Spcms or Species...			
Spcms or Species for Places...			
By Specimen Code			
By Specimen Code Series			
By Collection Code			
By Locality Code			
By Species Code			
All Specimens			
All Collections			
All Localities			
All Species			
All Genera			
All Families			
All Orders			
All Classes			
All Phyla or Divisions			
All Kingdoms			
All Personnel			
All Projects			
All References			
Valid Species			
Species With Junior Synonyms			
Junior Synonyms			
Host Specimens & Collections			
Guest Specimens & Collections			
Host Spcms for Guest Spcms			
Guest Spcms for Host Spcms			
Childless Records...			
Orphan Records...			

The Find Menu

- **Find → Using the Query Editor.** Presents the Query Editor, a general purpose query tool for finding records in a particular table based on the content of fields in those records or the content of fields in linked records of other tables. See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12.
- **Find → Lower Taxa for Higher Taxa.** Presents a query tool for finding all records in the Specimen table or a taxon table that are linked to a single record or a Record Set in a higher taxon table (e.g., all Specimens of a Species or a Genus, all Genera for a set of Orders). (The same command appears in the Tree menu.) See “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12.
- **Find → Higher Taxa for Lower Taxa.** Presents a query tool for finding all records in the Species table or a higher taxon table that are linked to a Record Set for the Specimen table or any lower taxon table (e.g., all Species for the Specimen Record Set; all Orders for the Genus Record Set). (The same command appears in the Tree menu.) See “[Finding Records for Higher Taxa Based on Lower Taxa](#)” in Chapter 12.
- **Find → Places for Spcms or Species.** Presents a query tool for finding all records in the Collection table or Locality table that are linked to a Record Set for the Specimen table

or the Species table (e.g., all Localities for the Specimen Record Set; all Collections for the Species Record Set). See “[Finding Place Records \(Collection or Locality\) for Specimens or Species](#)” in Chapter 12.

- **Find → Spcms or Species for Places.** Presents a query tool for finding all records in the Specimen table or Species table that are linked to a Record Set for the Collection table or the Locality table (e.g., all Species for the Locality Record Set; all Specimens for the Collection Record Set). See “[Finding Specimen or Species Records for Places \(Collections or Localities\)](#)” in Chapter 12.
- **Find → By Specimen Code.** Finds and displays a Specimen record based on single Specimen Code. See “[Finding Records by Record Codes](#)” in Chapter 12.
- **Find → By Specimen Code Series.** Presents a query tool for finding groups of Specimen records efficiently by Specimen Code. The Specimen Codes may be either sequential or nonsequential. (The same command appears in the Series menu.) See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13.
- **Find → By Collection Code.** Finds and displays a Collection record based on single Collection Code. See “[Finding Records by Record Codes](#)” in Chapter 12.
- **Find → By Locality Code.** Finds and displays a Specimen record based on single Locality Code. See “[Finding Records by Record Codes](#)” in Chapter 12.
- **Find → By Species Code.** Finds and displays a Species record based on single Species Code. See “[Finding Records by Record Codes](#)” in Chapter 12.
- **Find → All Specimens, All Collections, All Localities, All Species, All Genera, All Families, All Orders, All Classes, All Phyla or Divisions, All Kingdoms, or All Personnel.** Finds and displays all records for the specified table. See “[Finding and Displaying All Records for a Table](#)” in Chapter 12.
- **Find → All Valid Species.** Finds and displays all Species records that are not junior synonyms (i.e., all Species records for which the Species Code equals the Valid Species Code). See “[Finding Valid Species, Species With Synonyms, or Junior Synonym Records](#)” in Chapter 23.
- **Find → Species With Junior Synonyms.** Finds and displays all Species records for which the Species Code is identical to Valid Sp Code that have at least one Junior Synonym. See “[Finding Valid Species, Species With Synonyms, or Junior Synonym Records](#)” in Chapter 23.
- **Find → Junior Synonyms.** Finds and displays all Species records for which the Species Code differs from the Valid Sp Code, whether or not the Valid Sp Code matches the Species Code of a valid Species (senior synonym). See “[Finding Valid Species, Species With Synonyms, or Junior Synonym Records](#)” in Chapter 23.
- **Find → Host Specimens and Collections.** Finds and displays host Specimen records and linked host Collection records based on a search of all Specimen records or a search of the Specimen Record Set. See “[Finding Host Specimens and Host Collections](#)” in Chapter 24.
- **Find → Guest Specimens and Collections.** Finds and displays guest Specimen records and linked guest Collection records based on a search of all Specimen records or a search of the Specimen Record Set. See “[Finding Guest Specimens and Guest Collections](#)” in Chapter 24.
- **Find → Guest Spcms for Host Spcms.** Finds and displays all guest Specimen records that are linked to host Specimen records in the Specimen Record Set. See “[Finding Host Specimens for Guest Specimens](#)” in Chapter 24.

- **Find → Host Spcms for Guest Spcms.** Finds and displays all host Specimen records that are linked to guest Specimen records in the Specimen Record Set. See “[Finding Guest Specimens for Host Specimens](#)” in Chapter 24.
- **Find → Childless Records.** For a specified parent table, finds all records that are not linked to any child record in a Core table. (For example, you could find all Species records that are not linked to any Specimen records.) See “[Finding Childless Records](#)” in Chapter 12.
- **Find → Orphan Records.** For a specified child table, finds all records that are not linked to any parent record in a Core table. (For example, you could find all Specimen records that are not linked to any Species record.) See “[Finding Orphan Records](#)” in Chapter 12.

The Display Menu

- **Display → [Table Name] Set.** Displays the current Record Set for the specified table. See “[To Display a Record Set](#)” in Chapter 3.

Display	Labels	Im/Export
Specimen Set		
Collection Set		
Locality Set		
Species Set		
Genus Set		
Family Set		
Order Set		
Class Set		
Phylum or Division Set		
Kingdom Set		
Personnel Set		
Project Set		
Reference Set		
Loan Set		

The Labels Menu

- **Labels → Collection Labels.** For each record in the current Collection Record Set, prints or exports (to a text file) a label that includes most fields from the Collection record and its linked Locality record. See “[Collection Labels](#)” in Chapter 15.
- **Labels → Pin Labels: Locality.** For each record in the current Specimen Record Set, prints a standard entomological locality label for a pinned specimen, including appropriate fields from linked Collection and Locality records and (optionally) the Specimen Code. See “[Pin and Vial Specimen Locality Labels](#)” in Chapter 15.
- **Labels → Pin Labels: Determination.** For each record in the current Specimen Record Set, prints a standard entomological determination label for a pinned specimen, including appropriate fields from the Specimen record and from linked Species and Genus records. See “[Pin and Vial Specimen Determination Labels](#)” in Chapter 15.
- **Labels → Slide Labels: Locality.** For each record in the current Specimen Record Set, prints a standard locality label for a slide mounted specimen, including appropriate fields from linked Collection and Locality records and (optionally) the Specimen Code. See “[Slide Specimen Labels](#)” in Chapter 15.
- **Labels → Slide Labels: Determination.** For each record in the current Specimen Record Set, prints a standard determination label for a slide mounted specimen, including appropriate fields from the Specimen record and from linked Species, Genus, and Family records. See “[Slide Specimen Labels](#)” in Chapter 15.
- **Labels → Vial Labels: Locality.** For each record in the current Specimen Record Set, prints a standard locality label for a fluid preserved specimen, including appropriate fields from linked Collection and Locality records and (optionally) the Specimen Code. See “[Pin and Vial Specimen Locality Labels](#)” in Chapter 15.
- **Labels → Vial Labels: Determination.** For each record in the current Specimen Record Set, prints a standard determination label for a fluid-preserved specimen,

Labels	Im/Export	Loans	Special
Collection Labels...			
Pin Labels: Locality...			
Pin Labels: Determination...			
Slide Labels: Locality...			
Slide Labels: Determination...			
Vial Labels: Locality...			
Vial Labels: Determination...			
Herbarium Labels...			
Species Labels...			
Design & Print Custom Labels...			

including appropriate fields from the Specimen record and from linked Species, Genus, and Family records. See “[Pin and Vial Specimen Determination Labels](#)” in Chapter 15.

- **Labels → Herbarium Labels.** For each record in the current Specimen Record Set, prints one or more standard herbarium labels, including appropriate fields from the Specimen record and from linked Collection, Locality, Species, Genus, and Family records. See “[Herbarium Specimen Labels](#)” in Chapter 15.
- **Labels → Species Labels.** For each record in the current Species Record Set and/or for Species records found using the Species Labels screen search tools, prints a label including appropriate fields from the Species record and from the linked Genus record, plus (optionally) the determiner’s name. See “[Species Labels](#)” in Chapter 15.
- **Labels → Design & Print Custom Labels.** For each record in the current Record Set for any Core table, prints a label that you design using the 4D Label Wizard, using fields from the selected table and linked records in parent tables. See “[Designing and Printing Custom Labels](#)” in Chapter 15.

The Import/Export (Im/Export) Menu

- **Im/Export → Import by Tables and Fields.** Presents the Import Editor, which imports delimited, column-by-row text files into the fields you specify for any table in Biota’s structure. See Chapter 28, “[Importing Data](#).”
- **Im/Export → Export by Tables and Fields.** Presents the Export Editor, which exports delimited, column-by-row text files based on the fields you specify for any table in Biota’s structure. See “[Exporting Data by Tables and Fields](#)” in Chapter 27.
- **Im/Export → Import Image Files.** Based on an Image File List, imports and links thumbnails from groups of external image files, or imports the full image. See “[Importing Groups of Images](#)” in Chapter 19.
- **Im/Export → Export Image Files.** For each record in the current Species, Specimen, Collection, or Locality Record Set, exports either the first linked image or all linked images, creating a separate disk file for each image exported and an Image File List that can be used to import the images to another Biota Data File, using the “Import Image Files” command. See “[Exporting Groups of Images](#)” in Chapter 19.
- **Im/Export → Export Notes.** For the current Species, Specimen, Collection, Locality, or Loans Record Set, exports (to a text file in report format, or to a records-by-fields text file) the full record for each attached Note, certain fields from each parent record in the Record Set, and appropriate fields from other linked Core tables. See “[Exporting Notes Records Using the Export Notes Tool](#)” in Chapter 27.
- **Im/Export → Export Auxiliary Fields.** For the current Species, Specimen, Collection, or Locality Record Set, exports (to a tab-delimited text file) Auxiliary Field values in matrix format (standard or transposed) or NEXUS format. See “[Exporting Auxiliary Field Values](#)” in Chapter 16.

Im/Export	Loans	Special	Help
Import by Tables and Fields...			
Export by Tables and Fields...			
Import Image Files...			
Export Image Files...			
Export Notes...			
Export Auxiliary Fields...			
Export References...			
Export Taxonomic Flatfile...			
Export Specimen Flatfile...			
Export Custom Flatfile...			
Export Specimens Examined List			
Export Colls x Taxon Table...			
Export Locs x Taxon Table...			
Create Web Pages...			

- **Im/Export → Export References.** Exports all records for the current Reference Record Set, in *American Naturalist* format, to a text file. See “[Exporting References](#)” in Chapter 20.
- **Im/Export → Export Taxonomic Flatfile.** Exports a tab-delimited text file table with the Record Set for a lower taxonomic level as rows and information on the higher classification of those taxa as columns, based on the range of taxonomic levels you specify. See “[Exporting Taxonomic Flatfiles](#)” in Chapter 27.
- **Im/Export → Export Specimen Flatfile.** Exports a tab-delimited text file table with the current Specimen Record Set as rows and fields from any linked Core table as columns. See “[Exporting Specimen Flatfiles](#)” in Chapter 27.
- **Im/Export → Export Custom Flatfile.** For any Core table, exports a text file based on the current Record Set with selected fields from the focal table and related tables, using a custom format that you design using the Quick Report Editor. See “[Exporting Custom Flatfiles](#)” in Chapter 27.
- **Im/Export → Export Specimens Examined List.** For the current Species Record Set, exports (to a text file) draft text for a Specimens Examined section of a taxonomic monograph, based on linked Specimen records. See “[Exporting ‘Specimens Examined’ Lists for Publications](#)” in Chapter 27.
- **Im/Export → Colls x Taxon Table.** Based on the Collection, Specimen, or Taxon (Species or higher rank) Record Set, exports a tab-delimited text file table, with Collections as rows and Taxa as columns, specifying the incidence (presence/absence) or abundance of Specimens of each Taxon in each Collection. See “[Exporting Place- by-Taxon Incidence or Abundance Tables](#)” in Chapter 27.
- **Im/Export → Locs x Taxon Table.** Based on the Locality, Collection, Specimen, or Taxon (Species or higher rank) Record Set, exports a tab-delimited text file table, with Localities as rows and Taxa as columns, specifying the incidence (presence/absence) or abundance of Specimens of each Taxon in each Locality. See “[Exporting Place- by-Taxon Incidence or Abundance Tables](#)” in Chapter 27.
- **Im/Export → Create Web Pages.** Exports hierarchically linked Web pages, ready for posting on a Web server, for any range of taxonomic levels, based on Record Sets that you define. You can include any fields from the Specimen, Collection, or Locality tables, as well as images and host information. See Chapter 33, “[Exporting Static Web Pages](#).”

The Loans Menu

- **Loans → New Loan.** Creates a new Loan record, marks Specimen records and produces documents and text files for a new Specimen loan, based on the current Specimen Record Set and/or on ad hoc entry of Specimen Codes. See “[Recording a New Loan](#)” in Chapter 21.
- **Loans → Record Returns.** Updates an existing Loan record and marks Specimen records to record the return of loaned specimens, based on the current Specimen Record Set, the Specimens in the Loan, and/or on ad hoc entry of Specimen Codes. See “[Recording Specimen Returns](#)” in Chapter 21.
- **Loans → Display All Loans.** Finds and displays all records for the Loans table. See “[Displaying and Editing an Existing Loan](#)” in Chapter 21.

Loans	Special	Help
New Loan		
Record Returns		
Display All Loans		
Display Loan Record Set		
Print List of All Loans		

- **Loans → Display Loan Record Set.** Displays the current Record Set for the Loans table. See “[Displaying and Editing an Existing Loan](#)” in Chapter 21.
- **Loans → Print List of All Loans.** Prints a list of all records for the Loans table, with pertinent information from other tables. See “[Displaying and Editing an Existing Loan](#)” in Chapter 21.

The Special Menu

- **Special → Preferences.** Presents the Preferences screen. See Appendix B, “[Setting Preferences](#),” for a guide to page references for each option in the Preferences screen.
- **Special → Web Server.** Presents the Web Server control and options screen. See Chapter 30, “[Biota's Onboard Web Server](#).”
- **Special → Empty Record Sets.** Empties the Record Set for each Core table and for the Determination History table. See “[To Empty All Record Sets](#)” in Chapter 3.
- **Special → Find and Replace.** Presents the Find and Replace tool, which allows you to replace a specified text string with a new string in a specified field in a specified Biota table, for all records or for selected records. See “[Updating Records Using the Find and Replace Tool](#)” in Chapter 12.
- **Special → Change User Password.** Changes a validated current User Password to a new password that you choose. See “[Changing Your User Password](#)” in Chapter 26. The Administrator can enable or disable the User Password system using this command. See “[Activating the User Password system](#)” and “[Deactivating the User Password system](#)” in Chapter 26.
- **Special → Edit User Password System.** Presents the Password Editor, which the Administrator can use to assign or change user names, User Passwords, access privilege levels, and default language settings for users. See “[Using the Password Editor](#)” in Chapter 26.
- **Special → Edit Data File Password Link.** Enables or disables the Data File Password Link or changes a validated current Data File Password Link to a new one. See “[Using the Data File Password Link](#)” in Chapter 26.
- **Special → Field Value Defaults.** Allows you to set default values for data entry in many fields. See “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17.
- **Special → Entry Choice Lists.** Allows you to enable or disable an Entry Choice List for rapid entry of repetitive data in many fields. See “[Using Entry Choice Lists](#)” in Chapter 17.
- **Special → Core Field Aliases.** Allows you to rename many Core fields. An Alias appears on all input and Record Listing screens and in certain reports instead of the corresponding Internal Field Name. See Chapter 18, “[Re-naming Fields](#).”

Special	Help
Preferences...	
Web Server...	
Empty Record Sets	
Find and Replace...	
Change User Password...	
Edit User Password System...	
Edit Data File Password Link	
Field Value Defaults...	
Entry Choice Lists...	
Core Field Aliases...	
Record Code Settings...	
Maintenance Utilities...	
Make Guest Collection Records	
Specimen Count by Taxon	
Clear All Synonyms	
Delete Images by Record Set	
All Determination Histories	
Display Determination Hists	
Det Hists for the Spcm Rec Set	
Spcms for the Det Hist Rec Set	
Display Active Project Window	
Show Shortcut Screen	
Add Data Segment...	
Biota License Code...	

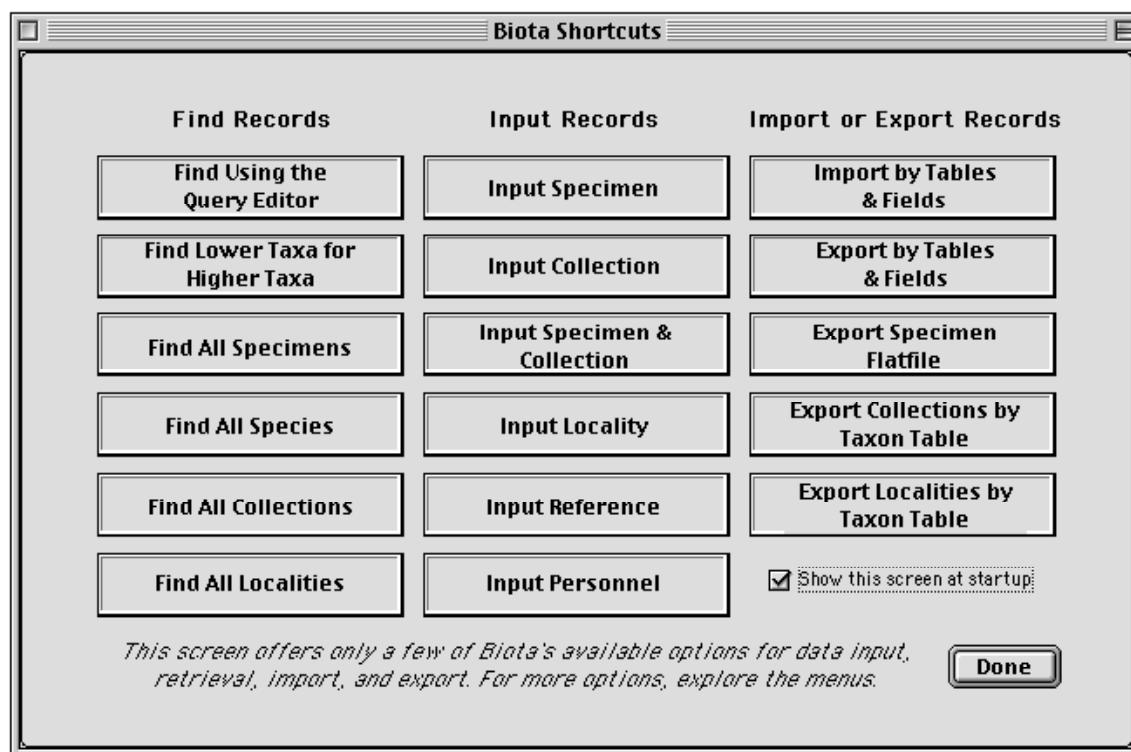
- **Special → Record Code Settings.** Allows you to specify default prefixes for Specimen, Species, Collection, or Locality Record Codes and to set parameters for using barcodes. See “[Assigning New Record Codes Automatically During Data Entry](#)” and “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” in Chapter 8.
- **Special → Maintenance Utilities.** Presents an options screen with tools for maintaining and repairing several table linking systems in Biota. See “[Maintaining and Repairing the Auxiliary Fields and Project Systems](#)” in Chapter 16, “[Maintaining and Repairing Image Links](#)” in Chapter 19, or “[Maintaining and Repairing Reference Links](#)” in Chapter 20.
- **Special → Make Guest Collection Records.** Automatically creates a new Collection record for the “guests” of each Specimen in the current Specimen (host) Record Set. See “[Creating Guest Collection Records Automatically](#)” in Chapter 24.
- **Special → Specimen Count by Taxon.** Prints a report, organized by the taxonomic hierarchy, showing the number of Specimens for each Species and for each higher taxon in the Specimen Record Set. See “[Printing a Specimen Count by Taxon Report](#)” in Chapter 14.
- **Special → Clear All Synonyms.** Sets the Valid Species Code equal to the Species Code for all Species records. See “[Clearing All Synonyms](#)” in Chapter 23.
- **Special → Delete Images by Record Set.** Deletes all the Image Archive records linked to particular group of parent records in the Species, Specimen, Collection, or Locality table. See “[Deleting Images for a Species, Specimen, Collection, or Locality Record Set](#)” in Chapter 19.
- **Special → All Determination Histories.** Finds and displays all records for the Determination History table. See “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22.
- **Special → Display Determination Histories.** Displays the current Record Set for the Determination History table. See “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22.
- **Special → Det Hists for the Spcm Rec Set.** Displays all Determination History records for the current Specimen Record Set. See “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22.
- **Special → Spcms for the Det Hist Rec Set.** Displays all Determination History records for the current Specimen Record Set. See “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22.
- **Special → Display Active Project Window.** Displays the Active Project floating window, which allows you to switch between Projects quickly. See “[To Display the Active Project Floating Window](#)” in Chapter 16.
- **Special → Show Shortcut Screen.** Displays the Shortcut screen, which offers buttons for several common Biota menu commands. See “[The Shortcut Screen](#)” later in this chapter.
- **Special → Add Data Segment.** Presents the 4D “Segments” screen. See “[Segmenting Data Files](#)” in Appendix I.
- **Special → Biota License Code.** Displays the installed Biota License Code, if any. If no Biota License Code has been installed, the License installation dialog appears.

The Help Menu

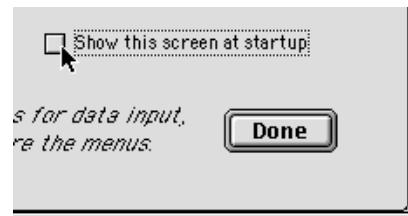
The Help menu in Biota is not functional. Unfortunately, there is no way to eliminate it from the program. This Manual and the (onscreen “Help” buttons that appear in some Biota windows) are your source of information.

The Shortcut Screen

The Shortcut Screen is simply a set a of buttons that execute a small subset of the most frequently used commands from Biota’s menus. It is intended for users just getting started with Biota, but some experienced users may find it useful as well.



- **New, empty Biota Data Files, and the Biota2Demo Data File**, initially display the Biota Shortcuts screen.
- **The Shortcuts screen reappears** each time Biota is launched, unless you turn it off by un-checking the “Show this screen at startup” checkbox on the Shortcut screen.
- **To re-display the Shortcuts screen**, choose “Show Shortcut Screen” from the Special menu, and check the “Show this screen at startup” checkbox.



Chapter 5

Overview of Biota's Tools and Features

This chapter briefly scans the tools and features that Biota offers. Often, there are several different ways to accomplish the same task with Biota. General-purpose tools (like the Query Editor, see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12) are included to cover all possible cases, but for many purposes Biota offers special tools that have been optimized to do a specific task.

Reading through this chapter now (or at least scanning the titles) will save you time later when you need to accomplish tasks for which special tools exist. Active links lead you to a more detailed presentation elsewhere in the Manual, if you need help.

Architectural Features

Multitasking

Each Biota tool or screen that you use runs in an independent *process* that automatically shares microprocessor time with all concurrent Biota processes, independent of the operating system. This means you can open as many windows and carry out as many tasks simultaneously as your hardware will allow. For example, in a large database you could launch a time-consuming search (e.g., for all records for specimens of Verbenaceae collected between 1989 and 1991 in Heredia Province, Costa Rica, by a particular collector) and, while it is running, print herbarium labels for a different set of specimens, while entering data for a third set.

Single-user vs. Client/Server Versions

BiotaApp is the stand-alone, single-user version of Biota. The vast majority of Biota users rely solely on BiotaApp. *Biota4D* is intended primarily for multi-user, client/server use, running under 4D Server, but can also run in single-user mode under 4th Dimension. See Appendix H, “[Using Biota4D with 4D Server or 4th Dimension](#)” for information on Biota4D. Data Files and all tools and features (except for multi-user capability) are identical with BiotaApp and Biota4D, including the ability to run Biota’s onboard Web server to publish your database (see Chapter 30, “[Biota’s Onboard Web Server](#)”).

Biodiversity Information Types

Specimen-Based Data

Because Biota was originally designed for a quantitative, specimen-based, geographically referenced biotic inventory (see the [Preface](#)), its data-input and analysis tools have been crafted for maximum efficiency in dealing with individual specimens from new collections. But many of the same tools have proven themselves worthy in

facilitating specimen-based work in systematics and collections management for historical collections, and many special tools for museum and herbarium needs are included.

Living Organisms

Although Biota was designed to handle specimen-based data from inventories or collections, it is easy to use for surveys of living individual organisms (for example, forest stands or bird sightings).

“Lot”-Based Data

In “lot”-based collections, groups of specimens share site (collection) data, but specimens are simply enumerated by species within each lot, without giving each specimen a separate identifier. (In some disciplines, a lot is a set of specimens from a single species from a single collecting event.) Lot systems are easily handled by Biota’s “voucher” system, by creating just one voucher Specimen record for each species in each lot, with the number of specimens in the lot entered in the [Specimens]Abundance field (see “[Specimen Input](#)” in Chapter 11). If you later need to create individual specimen records for certain specimens (e.g., a mounted series, or types), Biota lets you use the original voucher Specimen record as a template for the new records, using the Carry button (see “[Using an Existing Record as a Template for a New Record](#)” in Chapter 10).

Site-Based Species Lists With No Specimens

By creating one “pseudospecimen” record for each species/site combination, Biota can accommodate species-based data (faunal or floral lists) for which no specific specimens are entered in the database. In this case, the pseudospecimens link taxonomic information with site information. (In technical terms, the pseudospecimens serve as a “relating record” for the many-to-many relation between Species and Collections or Localities; see Chapter 3, “[Key Concepts](#)”). This technique also allows records for actual specimens of parasites, commensals, herbivores, etc., to be linked with host species records for which no specific specimen exists (see Chapter 24, “[Host-Guest Relations](#)”).

Plot-Based Data

Biota has been quite successfully used for plot-based vegetation data, using the “place hierarchy” (Locality and Collection records) to reference stands and plots within stands. For further levels, systems of hierarchical Record Codes have been successfully used. See “[Unified Record Code Systems: Specimen, Collection, and Locality Codes](#)” in Chapter 8. Biota’s Export Place-by-Taxon matrix tools (see “[Exporting Place- by-Taxon Incidence or Abundance Tables](#)” in Chapter 27) make preparing data for statistical analysis of plot-based data a breeze.

Special Data Types

Images

For each Species, Specimen, Collection, and Locality table record, you can link any number of digitized images, in virtually any image format. Images may reside in external files in virtually any format, with transparent links to corresponding thumbnails inside

Biota, or the image itself can be stored in the Biota Data File. Image-comparison screens help you compare images within and among parent records, and a comprehensive set of image-editing tools is available within Biota, as well as direct TWAIN device capture ability (scanners, digital cameras, etc.). Biota supports batch import (linked thumbnails or full images) as well as batch export of external images files. See Chapter 19, “[Images](#).”

Literature Reference System

Biota offers a capable and flexible literature Reference system. A separate Reference table, designed around a subset of EndNote reference styles and fields, holds Reference records that can be quickly linked (many-to-many) to any record in the Species, Specimen, Collection, or Locality table. References exported from EndNote can be directly imported to the Reference table. Records from other reference management applications can be imported with appropriate preparation of the input file. See Chapter 20, “[References](#).”

Recursive Specimen Relations (“Host-Guest” Links)

Biota handles recursive relations between specimens—“host-guest” relationships—by including the “host” specimen as one of the attributes of the Collection record of the “guest” specimen. For example, a DNA sample taken from the tissue of a wasp reared from a caterpillar, found feeding on the leaves of an epiphyte that was growing on a tree, would produce a five-level host-guest recursive chain. Host data are included as an option on locality labels. See Chapter 24, “[Host-Guest Relations](#).”

Tools for Customizing Biota

Field Aliases

For many Core fields distributed among Biota’s 14 Core tables, you can assign a *Field Alias* (using the Core Field Alias tool from the Special menu; see Chapter 18, “[Renaming Fields](#)”). Assigning an Alias changes the field name that is displayed in the Query Editor, the Sort Editor, and the Quick Report Editor, as well as the entry area for the field on input screens, for column headers on output (record listing) screens, in exported files (see Chapter 27, “[Exporting Data](#)”) and printed reports (see Chapter 14, “[Printing Reports](#)”). For example, a marine biologist might re-name the Elevation field in the Collection table *Depth*. A botanist might re-name the [Specimen]Stage/Sex field “Life Form.” In some groups of arthropods, the rank of Cohort is interposed between Suborder and Superfamily. The Biota field Family Custom 1 could be given the Field Alias *Cohort* to accommodate this requirement.

Auxiliary Fields and Projects

For the Species, Specimen, Collection, and Locality tables, you can define any number of *Auxiliary Fields*, named as you wish, and assign values to them for each record in the related Core Table. Auxiliary Fields and their values are part of your Data File, not the Biota application itself, so you must redefine them for each new database you create. The number of Auxiliary Fields you define is unlimited.

You can define any number of Projects for a single Biota Data File. For each Project, you can specify which Auxiliary Fields should be displayed in Input and Record Listing screens. You can quickly switch between Projects using the Active Project floating window.

If you intend to use Auxiliary Fields, be sure to read about how they are created and be aware of their limitations. *Using Core fields is always preferable*, if feasible for your needs. See Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”

Date Formats

Biota automatically complies with the Date Format setting in your operating system: International (dd/mm/yyyy) or U. S. (mm/dd/yyyy). For importing and exporting data, you are automatically offered a choice of International, U.S., or ANSI (yyyy/mm/dd) format, regardless of the current setting in your operating system.

For collection dates, Biota supports full dates, month-year dates, and year-only dates, as well as date ranges based on any mixture of these formats. See “[Dates](#)” in Chapter 9.

Spatial Reference (Georeference) Formats

Biota offers a comprehensive set of options for recording spatial reference data, including decimal degrees (Biota’s internal representation for latitude/longitude), degrees-minutes-seconds, integer degrees-decimal minutes, and fields for alternate coordinate systems (UTM, Lambert, etc.) See “[Spatial Coordinates](#)” in Chapter 9.

Spanish Dialog Screens

Biota is partially bilingual. Spanish language versions are available for all “dialog screens” (instructions, options, warnings, error messages, result reports, and the Preferences screen itself) that are accessible to users with “Read Write Export,” “Read Export,” or “Read Only” access privileges.

Biota tools and screens accessible only to users with “Administration” access privileges are available in English only. The justification for this design is that the Administrator needs to be able to read this manual, to use Biota’s most powerful tools safely. All menu bars and menus are in English for all users.

You can enable or disable the Spanish version of the dialog screens in the “Language” tab of the “Preferences screen (Special menu) or by means of the Startup Procedure assigned to a particular User in the User Password system. See “[The ‘Language’ Tab](#)” in Appendix B, “Setting Preferences.”

Table Colors for Input and Record Listing Screens

Biota uses a set of default colors, one for each Core table, to help you tell which table you are using. If you want a different color scheme, or you prefer the “Microsoft-gray” look, you can change the scheme using the Colors tab of the Preferences screen (Special menu). See “[To Change the Screen Color Scheme](#)” in Chapter 7.

Information Input

Record Sets

A Record Set is a temporary selection of records from among those permanently stored in the database. For each Biota Core table (Specimen, Collection, Species, etc.), you can define any number of Record Sets and save them to disk as Record Set Pointer Files for later rapid recall. Only one Record Set per table can be active (current) at a given time, however. During data entry, you can elect to add new records to the current Record Set or start a new Record Set. Record Sets are also used in printing reports, labels, making or returning loans, and for export options. You can display the current Record Set for a table at any time using commands from the Display menu. See “[Record Sets](#)” in Chapter 3.

Automatic Prompting for Parent Record Entry

Although you can enter data table by table (enter all Genera, then all Species, then all Specimens, etc.), you may also work directly from records lower in a hierarchy—for example, directly from Species entry. With the latter approach, Biota queries you automatically when new entries are required in a related (*parent*) table (e.g., the Genus table, if you enter a new Genus name in a Species record), then returns you automatically to the lower-level (e.g., Species) entry screen. See “[Entering Data in Linking Fields](#)” in Chapter 7.

Wildcard Entry for Linking Fields

During data entry, when the appropriate record already exists in a related table (e.g., the Genus record already exists for a Species record currently being entered), the linking field is automatically looked up and entered, based on the first letter or first few letters you enter. (Press TAB to launch the search.) If more than one related record matches the entry, Biota presents you with an alphabetic list to choose from, including an additional, “helper” field from the related table. For example, if you are entering Genus as a relating field in a new Species record, and you enter the letter P, every Genus that starts with P will appear in a scrollable list along with its Family. You can sort the list by either Family or Genus by clicking the correct record to enter it in the new Species record. This *wildcard entry* feature minimizes not only input effort, but spelling errors. See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.

Lookup Tool for Entering Record Codes in Linking Fields

Each record in the Specimen, Species, Collection, and Locality tables must have a unique Record Code (see Chapter 8, “[Record Codes](#)”). Although you can use any name or mnemonic you like for these codes, they can be hard to remember when you need to enter them in relating fields during data entry. Although wildcard entry is the fastest way to enter data for these relating fields, Biota also provides “Look Up” buttons that open windows with scrollable lists of existing records in the related table, based on criteria you specify, and sorted at your option by one of several criteria. See “[Entering Specimen Data: The ‘General’ Tab](#)” in Chapter 11 for an example.

Default Entries and Entry Choice Lists (Pick Lists)

Some fields in your database will probably have a limited number of repetitive entries—a field for sex or life stage, for example. For many non-linking fields in Biota, you can activate an *Entry Choice List* that presents entry options in a floating window whenever the entry area for the field is accessed during input, and you have activated the Choice List for that field. When the window appears, you simply click an item on the list to enter it, then type in the first letter or first few letters of the entry to find it in the list. You construct each list by entering items with the List Editor or importing to the List Items table. Biota saves the lists you have created as part of your Data File, whether activated or not, until you change or erase them. Since Choice lists eliminate misspellings, they are especially useful when someone else enters data for you. See Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#).”

Field Value Defaults

If you repeatedly enter a single value for a field, or one value is used in a large proportion of your records, you may want to assign a *Field Value Default* for that field (Special menu). The default will be automatically entered in the field as soon as a new record is initiated on an input screen. Biota supports Field Value Defaults for 16 Core Fields in the Specimen, Collection, and Locality tables. See Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#).”

Using an Existing Record as a Template for a New One

Every input screen includes a *Carry* button, which allows you to make a new record using the current record as a template. (If it is a new or edited record, the template record is saved first, automatically, when you click Carry.) Since, in many cases, only one or two fields need changing between a template record and a new one, this capability saves a great deal of effort. A saved, existing record can also be used as a template. Display it in the input screen, click Carry, and a new record will appear, repeating all but the Key field of the template record. (Auxiliary Fields and Notes can be carried or not, according to a setting in the Preferences screen, from the Special menu.) See “[Using an Existing Record as a Template for a New Record](#)” in Chapter 10.

Automated Entry of Specimen Record Series

Extending the Carry concept, two powerful input options (from the Series menu) speed the entry of sets of Specimen records that share either the same Collection data (Input Specimen Series) or both Collection and taxonomic data (Input and Identify Specimen Series). These options require entry of only the first and last Specimen Code numbers (with or without prefixes) and one-time data entry for the other fields for each set of specimens. All records in the specified range are then generated automatically, with sequential Specimen Codes. See Chapter 13, “[Creating, Finding, and Updating Specimen Series](#).”

Automatic Record Code Assignment

Record Codes for Specimen, Species, Collection, and Locality records may be any arbitrary, unique (within tables) alphanumeric code you choose. Alternatively, sequential codes can be automatically assigned with either a default alphanumeric prefix (which you define with the Record Code Prefixes utility in the Special menu) for each table, an ad hoc prefix you assign during record input, or no prefix. See “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8.

Barcode Entry of Record Codes

All Record Code entry areas (including Specimen Code fields for specimen Loans and returns) automatically accommodate barcode entry. All record entry and record retrieval areas for Specimen and Species Codes also provide for barcode prefix recognition and optional substitution of an abbreviated or different code prefix in the database. Barcode entry can be freely mixed with manual entry in the same Data File. See “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” in Chapter 8, and Appendix K, “[Barcodes](#).”

Record Retrieval and Manipulation: General Tools

Multifunction Record Listing Screens

A uniform interface for displaying records allows you to carry out ad hoc sorts, select consecutive or nonconsecutive records to redefine a current selection of records (using the Subselection button), delete records, modify existing records (double-click and modify the record in the input screen, add new records, or use an existing record as a template for a new one that shares information with the template. In each case, Biota immediately displays the result using the same uniform interface, ready for the next action. See Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

Simultaneous Display of Records from Any Number of Tables

The number of open windows Biota can display simultaneously is limited only by the memory allocated to Biota. In fact, you can display different groups of records (or saved Record Sets) in different windows for the same Core table, simultaneously.

Displaying Record Sets

The active Record Set (if any) for each Core table can be displayed and manipulated using commands from the Display menu.

Ad Hoc Queries for All Tables

A general-purpose query construction tool (the Query Editor) allows you to use the content of records, including values in related fields of other tables, to find records. You can choose to search among all records in a table or only among those in a Record Set. If your query can be accommodated by using one or more of the special tools described in “[Special Tools for Finding Records in One Table Based on a Set of Records in Another Table](#)” (in Chapter 12), the search will invariably be much faster than building the query in the Query Editor. See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12.

Special Tools for Finding Records in One Table Based on a Set of Records in Another Table

Biota offers four special tools, with a common interface, for the frequent task of finding related records up, down, and across the taxonomic and place hierarchies. As an option, Biota will keep the linking records for all intermediate tables as Record Sets for those tables. These tools support rapid and intuitive query construction and optimized,

extremely fast search and display. They can also be used sequentially for complex searches. For many users, they are among the most frequently used features of Biota.

Finding Records for Lower Taxa Based on Higher Taxa

The Lower Taxa for Higher Taxa (“top-down”) search tool finds all records for a lower taxonomic level that belong to a higher taxon or a selection of higher taxa. It does not matter whether the two levels are adjacent in the taxonomic hierarchy or not. For example, you could find all Specimens of a Family, or all Genera of three Orders (nonadjacent levels), or all Specimens for a selection of Species or all Classes for a Phylum (adjacent levels). For nonadjacent levels, you can tell Biota to keep all related taxa at intermediate levels as Records Sets. See “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12.

Finding Records for Higher Taxa Based on Lower Taxa

The Higher Taxa for Lower Taxa (“bottom-up”) search tool finds all records for a higher taxonomic level that belong to the active Record Set for a lower taxonomic level. For example, you could find all Orders for the Specimen Record Set (nonadjacent levels) or all Families for the Genus Record Set (adjacent levels). For nonadjacent levels, you can tell Biota to keep all related taxa at intermediate levels as Records Sets. See “[Finding Records for Higher Taxa Based on Lower Taxa](#)” in Chapter 12.

Finding Place Records (Collection or Locality) for Specimens or Species

The Places for Specimens or Species search tool finds all Locality or Collection records for the active Specimen or Species Record Set, according to your query. For example, you could find all Locality records for a set of Species (a cross-hierarchy query). You can tell Biota to keep the related Specimen and Collection records (intermediate tables in the search) as Record Sets. See “[Finding Place Records \(Collection or Locality\) for Specimens or Species](#)” in Chapter 12.

Finding Specimen or Species Records for Places (Collections or Localities)

The Spcms or Species for Places search tool finds all Specimen or Species records for the active Collection or Locality Record Set, as you request. For example, you could find all Species records for a Locality (a cross-hierarchy query). You can tell Biota to keep the related Collection and Specimen records (intermediate tables in the search) as Record Sets. See “[Finding Specimen or Species Records for Places \(Collections or Localities\)](#)” in Chapter 12.

Sequential, Cross-Hierarchy Searches

If you want to find Collections or Localities for taxa above the level of Species, or higher taxa represented in Collections or Localities, you can use the appropriate pair of the above tools sequentially. For example, to find all the Localities for an Order, first find all Species for the Order (using the first tool), declare the result to be the Species Record Set, then find all Localities for the Species Record Set (using the third tool). See “[Sequential, Cross-Hierarchy Searches](#)” in Chapter 12.

Finding Records by Record Code

Single Records

You can quickly find an individual Species, Specimen, Collection, or Locality record by entering its Record Code manually or with a barcode reader. See “[Finding Records by Record Codes](#)” in Chapter 12.

Unordered Specimen Series

The Find Specimen Series tool (Series menu) accepts two kinds of entries. In the “Unordered Series” mode (click “In any order”), you simply enter any Specimen Code, press TAB, then toggle on the “Auto Accept” button. For all subsequent records, just enter the next code, press TAB, and repeat, as Biota retrieves and collects the records. With a barcode reader set to enter carriage returns automatically, this is a completely hands-off operation (neither keyboard nor mouse is needed). When you are done, the records are displayed for examination, modification, or saving as a Specimen Record Set for other operations. See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13.

Ordered Specimen Series

In “Ordered Series” mode (click “In consecutive order”), the Find Specimen Series tool lets you find, in a single action, any series of records that have numerically sequential Specimen Codes. When the search is complete, the records are displayed for examination, modification, or saving as a Specimen Record Set for other operations. See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13.

Special Tools for Updating Records

Updating Specimen Determinations and Other Specimen Information: Unordered Specimen Series

Two tools for rapid updating of data in existing Specimen records share the Identify or Store Specimen Series screen (Series menu). In “Unordered Series” (Auto Carry) mode (click “In any order”), you enter a Specimen Code (manually or with a barcode reader), then enter the Species Code for a new determination or other new information (Determined By, Date Determined, Stage/Sex, Storage, Type Status). Then click the Auto Carry button. Press TAB, enter the next code, press TAB, and so on, as Biota retrieves and updates the records with the same new information. With a barcode reader set to enter carriage returns automatically, updating is a completely hands-off operation (neither keyboard nor mouse is needed). When updating is complete, the records are displayed for examination, further modification, or designation as a Specimen Record Set for other operations. See “[Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series’ Tools](#)” in Chapter 13.

Updating Specimen Determinations and Other Specimen Information: Ordered Specimen Series

In Ordered Series mode (click “In consecutive order”), the Identify or Store Specimen Series screen (Series menu) lets you update, in a single action, any series of records that have numerically sequential Specimen Codes. When the updating is complete, the records are displayed for examination, modification, or designation as a Specimen Record Set for other operations. See “[Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series’ Tools](#)” in Chapter 13.

Updating Records (Any Table) by Importing Information from Text Files

The Import by Tables and Fields tool (Im/Export menu) includes an Update Records option for updating existing records in any table. Biota matches up the imported data with the existing record based on the Key Field for each record. See Chapter 28, “[Importing Data](#).”

The Find and Replace Tool

The Find and Replace tool (Special menu) is a powerful (and therefore dangerous!) utility for correcting errors or updating records in any table in the Biota structure. Not only Core tables but Peripheral tables can be accessed. Changes can be made either in records of a current Record Set (for tables that have them) or for all records in a table. Be sure you know what you are doing before using this tool, and always be sure you have a backup copy of your Data File first! *Changes made cannot be undone*. If the User Password system has been enabled, only a user with Administration access privileges can use this tool. See “[Updating Records Using the Find and Replace Tool](#)” in Chapter 12.

Keeping Track of Synonyms

A species Synonymy system (based on the Valid Species Code field of the Species table) allows you to keep track of historical or new synonymies among Species records. (In inventory work, this system can be used to document the “synonymies” that often arise in pooling several temporarily determined sets of Specimens.) The Synonymy button in the Species input screen finds and displays either the senior synonym for a Species, or a scrollable list of its junior synonyms, if any. A species “Look up” button speeds the recording of new synonymies, and special query tools are available for finding various kinds of synonyms. See Chapter 23, “[Synonymy System](#).”

Tools for Maintaining Database Security and Integrity

User Password System

Biota provides a comprehensive User Password system that you can enable and configure to your needs. To activate the system, you give the Administrator a nonblank password. The Database Administrator can use the Password Editor to set up a system of passwords for other users. A selection of generic user names (e.g., Collaborator, Browser, etc.) with different access levels (see next paragraph) have been preset, but may be changed as you wish. Any user can change his or her password using the Change Password item in the Special menu.

User Access (Privilege) Levels

The Password Editor allows the Administrator to assign each user to one of four *access levels*: (1) Super User (set User Passwords, assign access levels, set the Data File password link (see below), plus all privileges of the Administration access level; (2) Administration (create, delete, display, modify, print, export, or import records; change master settings); (3) ReadWriteExport (create, delete, display, modify, print, or export records); (4) ReadExport (display, print, or export records); or (5) ReadOnly (display records only). See Chapter 26, “[Security: Passwords and Access Privileges](#).”

Data File Password Link

The User Password system protects your copy of the Biota application from unauthorized use but does not in itself protect Biota *Data Files* from unintended or unauthorized access. You can create a secure link between a particular copy of Biota and a particular Data File (or Files) using a *Data File password link*. You need not activate the User Password system in order to activate the Data File password link, although it usually makes sense to activate the User Password system if the Data File link is used. (The two systems are technically independent.) See “[Using the Data File Password Link](#)” in Chapter 26.

Automatic Updating of Linking Fields in Child Records

If you need to change the name of a higher taxon (Genus, Family, Order, etc.), or the Record Code for a Species, Specimen, Collection, or Locality in the parent (one-table) record, Biota will ask if you want to update the linking field in all linked child (many-table) records automatically. For example, suppose you misspelled the genus *Excelsotarsonemus* in the parent (Genus table) record and used the same misspelling in the Genus linking field of the Species records for all species of the genus. You can correct the name in the Genus record and in all linked Species records with one entry (or change only the Genus record, if you choose). See “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12.

Finding Orphan and Childless Records

An *orphan* record is one that is not linked to any record in the next higher table in a hierarchy—for example, a Specimen record that either has no Species Code recorded, or has a Species Code that does not correspond to any Species record. A *childless* record is one that has linked records in the next lower table in a hierarchy—for example, a Genus record that has no linked Species records. Using commands from the Find menu (Find Orphan Records and Find Childless Records) you can find, display, and, if you wish, modify such records easily. See “[Finding Orphan Records](#)” and “[Finding Childless Records](#)” in Chapter 12.

Record Deletion Control

Biota will not allow you to orphan records inadvertently. In other words, if you attempt to delete a record that is linked to records at the next lower table in a hierarchy, Biota warns you that you are about to orphan certain records. You then have the option of doing so, in spite of the warning, or simply canceling the action. See “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12.

Record Creation Control

Whenever you enter a value in the parent linking field of a child record (e.g., when you enter a family name in the [Genus] Family field while creating a new Genus record), Biota checks automatically to see if the record already exists in the parent table (the Family table, in this example). If no parent record exists, Biota prompts you to create one “on the fly,” then returns you to the child record in progress. (If you wish, you can go ahead and create an orphan record, as an option. This option is especially useful for the [Collection] CollectedBy field, linked to the Personnel table, for historical specimens when the collector’s personal data are either unknown or of no interest. See “[“On-the-Fly’ Creation of Linked Records”](#) in Chapter 7.

Automatic Recording of Specimen Determination Histories

If you enable the Determination History system, whenever the identification (determination) of a Specimen is changed, all pertinent information for the old determination (Genus, Species, Author, Determined By, Date Determined) is recorded in a new record in the Determination History table, along with a record of where the determination was changed (in the Specimen record, the Specimen Series tool, the linked Species record, the Synonymy system, or the linked Genus record), when it was changed (current date), and by whom (based on password sign-on). You can view the determination history for a Specimen record on the Determination tab of the Specimen Input screen. See Chapter 22, “[Determination Histories](#).”

Duplicate Species Checking

Although the Key field of the Species table is Species Code, not Species Name (specific epithet), Biota checks for uniqueness each time you enter a new Species Name value, if you enable this feature. (You cannot enter two records with the same Species Code). Of course, more than one record for *sativum* may legitimately exist, in different genera, but you would not want to create two species records for *Pisum sativum* L. Thus, Biota warns you if one or more Species records exist with the same specific epithet (Species Name), and offers to display any such records. You must then decide how to proceed. (Exceptions include “sp.”, “sp. nov.”, and related abbreviations.) See [Step 3 in “Entering Species Data: The ‘Classification’ Tab.”](#) in Chapter 11.

Automatic Record Dating

For Specimen, Species, Collection, Locality, Personnel, Loans, References, and Project records, Biota automatically registers the date each record was created and the most recent date it was changed. (The identity of the user making the most recent change is also recorded, if this option is enabled in the “Admin Settings” tab of the Preferences screen. See Appendix B, “[Setting Preferences](#)”).

If the Determination History option has been activated, the current date is recorded any time the determination of a specimen is updated, directly or indirectly (see [Chapter 22, “Determination Histories”](#)).

Maintenance and Repair Tools

Under normal operations, Biota correctly maintains links between parent records in the Specimen, Species, Collection, and Locality tables and records in the tables that contain information on Auxiliary Fields (the FieldValue and FieldName tables), References, and Images. Power failures, system crashes, and incorrectly imported data, however, can

produce anomalies (orphan or duplicate links). You can correct all these problems, without in any way affecting legitimate records, by running Biota's Maintenance Utilities (Special menu). See “[Maintaining and Repairing the Auxiliary Fields and Project Systems](#)” in Chapter 16, “[Maintaining and Repairing Image Links](#)” in Chapter 19, or “[Maintaining and Repairing Reference Links](#)” in Chapter 20.

More serious problems with Biota Data Files can often be repaired with 4D Tools, a general-purpose checking and repair application. See “[Checking and Repairing a Data File](#)” in Appendix I.

Reports and Labels

Printed Reports

Biota offers a variety of printed reports designed for biodiversity information, as well as user-designed, ad hoc reports (using the built-in Quick Report Editor). See Chapter 14, “[Printing Reports](#).”

Labels for Fluid-Preserved, Pinned, Slide-Mounted, or Herbarium Specimens

Biota prints locality and determination specimen labels for fluid-preserved, pinned entomological, or slide-mounted specimens. Herbarium labels are printed in customary format, including (optionally) both locality and determination data, as well as an option to include a descriptive field note. Numerous other options allow control over the information included on labels. Data for all label types can optionally be exported to a delimited text file, for further processing in other applications. See Chapter 15, “[Printing Labels](#).”

Custom Label Printing

Using the Label Wizard (a built-in 4D tool), you can design your own labels in any size or format for the current Record Set of any Biota Core table and save the template to disk, if you wish. See “[Designing and Printing Custom Labels](#)” in Chapter 15.

Species Labels

Species labels (for entomological unit trays or herbarium folders, for example) can be printed from the Species Record Set or from any arbitrary set of Species Codes entered in a special input screen. See “[Species Labels](#)” in Chapter 15.

Specimen Loan System

Lending Specimens

Biota provides a simple bookkeeping system for specimen Loans. Groups of specimens to be loaned can be selected using any of Biota's usual selection tools, or one-by-one by entering each Specimen Code (with barcodes supported). The Deposited field of the Specimen table is used for recording the Specimen Loan Code in each Specimen record. See Chapter 21, “[The Specimen Loan System](#).”

Recording Returns

Specimen returns can be recorded by selecting records on-screen from the list of those in the original loan, by recording the current Specimen Record Set as returned, or by entering Specimen Codes one-by-one. The Unordered option of the Find Specimen Series tool (Series menu) is particularly useful for gathering records from several loans that have been returned together. See “[Recording Specimen Returns](#)” in Chapter 21.

Loan Forms

For each new loan, Biota generates a standard loan agreement form, with the name of your project, museum, or herbarium if you wish, with complete lender and borrower information. As an option, the Loan system produces a full, taxonomically organized, printed listing of all specimens loaned. See “[Previewing, Printing, and Exporting Loan Records](#)” in Chapter 21.

Text Flatfile Export of Specimens Loaned

As an additional option, Biota will export a text file listing the specimens in any loan, including, for each specimen, all fields from the database that you designate, with blank or partially completed species identification fields. The text file can be opened and modified using any spreadsheet program. Identification fields can then be filled in by the borrower as the specimens are determined and the determinations returned to the lender in the updated flatfile, which can be used to update records in the Biota Data File. See “[Previewing, Printing, and Exporting Loan Records](#)” in Chapter 21.

Importing Data

The Import Editor

New records can be directly imported into Biota tables, one table at a time, from plain-text flatfiles using Biota’s Import Editor (Import by Tables and Fields, Im/Export menu). You can specify the order of fields to match your flatfile, skip fields in the flatfile, specify field and record delimiters, and account for a column header in the flatfile.

The Import Editor supports three modes: Import new records, Update existing records, and Merge imported records. The Update option matches Record Code in the input file to Record Codes in the Data File, and updates any other fields specified. The Merge option ignores duplicated Record Codes, and imports only records with unique Record Codes.

Biota does extensive error checking (validation for correct field types, field lengths, duplicated Key fields, nonexistent dates, etc.) with informative error dialogs. If an error is found, the guilty record is displayed, and you are offered the option of keeping any records already imported successfully, or deleting them and starting “clean” after fixing the problem in the text file. See Chapter 28, “[Importing Data](#).”

Importing Images

Based on an Image File List, Biota can import and link thumbnail images from groups of external image files. Alternatively, you can specify to import the full image. See “[Importing Groups of Images](#)” in Chapter 19.

Exporting Data

The Export Editor

Any field of any Biota record or set of records can be exported, one table at a time, to a plain-text flatfile (readable by spreadsheet, word processing, or other database applications) using Biota's Export Editor (Export by Tables and Fields, Im/Export menu). For a given table, you can specify any order for the exported fields, specify field and record delimiters, and export a column header in the flatfile. Plain-text flatfiles are the *lingua franca* of data exchange among databases, spreadsheets, and statistical applications. When something you like better than Biota comes along, or you need to send data somewhere in electronic form, you can always get your data out of Biota Data Files. See “[Exporting Data by Tables and Fields](#)” in Chapter 27.

Exporting Images

For each record in the current Species, Specimen, Collection, or Locality Record Set, Biota can export either the first linked image or all linked images, creating a separate disk file for each image exported and an Image File List that can be used to import the images to another Biota Data File, using the “Import Image Files” command. See “[Exporting Groups of Images](#)” in Chapter 19.

Exporting Specimen Flatfiles

For any Specimen Record Set, you can export a flatfile, with specimens as rows, that includes columns for any set of fields from Biota Core tables. You choose the export fields simply by clicking checkboxes on a selection screen. See “[Exporting Specimen Flatfiles](#)” in Chapter 27.

Exporting Taxonomic Flatfiles

A taxonomic flatfile is a list of taxa at a particular level (the *base level*), displaying, for each taxon, its membership in one or more higher taxa (for example, a list of species that includes the genus and family of each, or a list of genera that includes the family, suborder, and order for each genus). Biota can export such files based on any taxonomic base level, with additional higher levels (columns) that you specify by clicking checkboxes. See “[Exporting Taxonomic Flatfiles](#)” in Chapter 27.

Exporting Notes

You can export plain-text reports or delimited text files of Notes for Record Sets from the Species, Specimen, Collection, Locality, and Loans tables. See “[Exporting Notes Records Using the Export Notes Tool](#)” in Chapter 27.

Exporting Auxiliary Field Values

If you have defined Auxiliary Fields and entered values for them, you can export matrix with records as rows and Auxiliary Fields as columns directly to a plain-text file, for a Record Set in the Specimen, Species, Collection, or Locality tables. Exported Auxiliary Field data can then be printed, or joined with Core Field data for the same set of records using a spreadsheet application. See “[Exporting Auxiliary Field Values](#)” in Chapter 16.

Exporting Character Matrices in the NEXUS Format

If you have defined Auxiliary Species Fields and have entered single-digit or single-letter values in them, you can export a complete, PAUP- or MacClade-ready NEXUS file, using an option in the Export Auxiliary Fields dialog. Biota also supports this option for Auxiliary Fields of the Specimen, Collection, and Locality tables. See “[Exporting Auxiliary Field Values](#)” in Chapter 16.

Exporting Place- by-Taxon Incidence or Abundance Tables

Based on the Locality, Collection, Specimen, or Taxon (Species or higher rank) Record Set, Biota can export a tab-delimited text file table, with Localities or Collections as rows and Taxa as columns, specifying the incidence (presence/absence) or abundance of Specimens of each Taxon in each Locality or Collection. These data are the raw material for graphical and statistical estimation of species richness from samples, and for ordination, sample classification, and other statistical techniques. See “[Exporting Place-by-Taxon Incidence or Abundance Tables](#)” in Chapter 27.

Exporting “Specimens Examined” Lists

For any Species Record Set, Biota can export a draft text file of Specimens Examined (Exsiccatae) for a taxonomic monograph, organized within species by Locality and Collection, then by Stage/Sex and host (if any), based on linked Specimen records. See “[Exporting ‘Specimens Examined’ Lists for Publications](#)” in Chapter 27.

Custom Export

The Quick Report Editor (a 4D utility) is a powerful and flexible tool for exporting text files to disk, as well as for printing reports. Quick Report formats are easily created and can, themselves, be stored on disk for repeated use. For any Core table, the Quick Report Editor in Biota exports a text file based on the current Record Set, with selected fields from the focal table and related tables, using a custom format that you design using the Quick Report Editor. See “[Exporting Custom Flatfiles](#)” in Chapter 27.

Internet Publishing Tools

On-board Web Server: Dynamic Access

Biota 2 offers a fully-imbedded, on-board Web server that allows any Biota owner to publish a Biota Data File on the internet with no additional software (although for anything but trial use, you must purchase a Web Extension License). You can use any computer to run the Web server. See Chapter 29, “[Internet Strategies](#),” especially Chapter 30, “[Biota’s Onboard Web Server](#).”

You can choose to publish your Biota Data File on the Web in either or both of two modes: (1) *Web Browser Mode* allows you to control exactly which tables and fields are accessible to website visitors, in classic browser mode. (2) *Database Client Mode* emulates Biota’s desktop interface, allowing full access to Biota’s powerful search tools. See Chapter 31, “[Web Browser Mode and the Web Assistant](#),” and Chapter 32, “[Database Client Mode](#).”

Exporting Static Web Pages

If you prefer, or are restricted by your Internet Service Provider or institution to publishing static Web pages, Biota will guide you through the setup for completely automated export of hyperlinked Web pages, ready to post on any Web server. (These are “static” pages, not “dynamic,” on-line access to your Data File from the Internet.) You can export hierarchically linked pages for any range of taxonomic levels (including intermediate levels such as Subfamily), for Record Sets that you define with either a top-down or bottom-up search.

If you include Specimen records, you can select any set of fields in the Specimen, Collection, or Locality tables for inclusion as Specimen data. You can include images for Species records. Other options include custom page footnotes, hyperlinking of host and “guest” Specimen records, and non-ASCII character translation to HTML character codes. See Chapter 33, “[Exporting Static Web Pages](#).”

Accessibility Features

Keyboard Shortcuts

Biota offers many keyboard shortcuts for buttons and tabs in Input screens, and for records in Record Listing screens. This comprehensive set of keyboard shortcuts represents an important feature for people with disabilities, including mouse-related repetitive motion disorders, and to any user who dislikes using the mouse. Windows users can also tab between buttons and use the menu shortcuts that Windows automatically provides. See “[Keyboard Shortcuts for Input Screen Tabs](#)” and “[Keyboard Shortcuts for Input Screen Buttons](#)” in Chapter 7, and “[Keyboard Shortcuts for Record Listing Screens](#)” in Chapter 10.

Chapter 6

A Brief Tutorial

With the Demo Database

It is difficult to see Biota in action with a new, empty Data File. This chapter takes you on a quick tour of Biota's basic capabilities using the "Biota2Demo" Data File that you received on the distribution CD or downloaded from the Biota website at <http://viceroy.eeb.uconn.edu/biota>. More advanced and less frequently used features are covered in the chapters that follow.

Don't be intimidated by the number of pages in this chapter. They go by very quickly, and the chapter is broken up into separate lessons so that you need not do the entire tutorial at one sitting. Although each lesson stands alone, later lessons assume you have done the earlier ones first.

Before starting the tutorial tour, please read Chapter 2, "[Biodiversity Data and Relational Databases](#)," and Chapter 3, "[Key Concepts](#)."

Installing Biota and Opening the Demo Data File

If you have not yet installed Biota, please install it, following the instructions in the "Installing Biota" file on the Biota CD or in the materials you downloaded from the Biota website.

1. **Launch Biota in "Data File finding mode,"** by immediately pressing and holding ALT key (Windows) or the OPTION key (Mac OS) after launching Biota to force the file navigation window to open.
 - **BiotaApp in Windows.** Select the icon for BiotaApp.exe then choose "Open" from the Windows File menu while depressing the OPTION key. Or launch BiotaApp from the Windows "Programs" menu, then immediately press the OPTION key. (You can also launch Biota by double-clicking its icon, then immediately depressing the OPTION key, but if you get the timing wrong, you get the Properties window instead.)
 - **BiotaApp in Mac OS.** Select the icon for BiotaApp, then choose "Open" from the File menu in the Mac OS Finder, while depressing the OPTION key. Or, double-click the BiotaApp icon while depressing the OPTION key.
 - **Biota4D in Windows or Mac OS.** See Appendix H, "[Using Biota4D with 4D Server or 4th Dimension](#)."

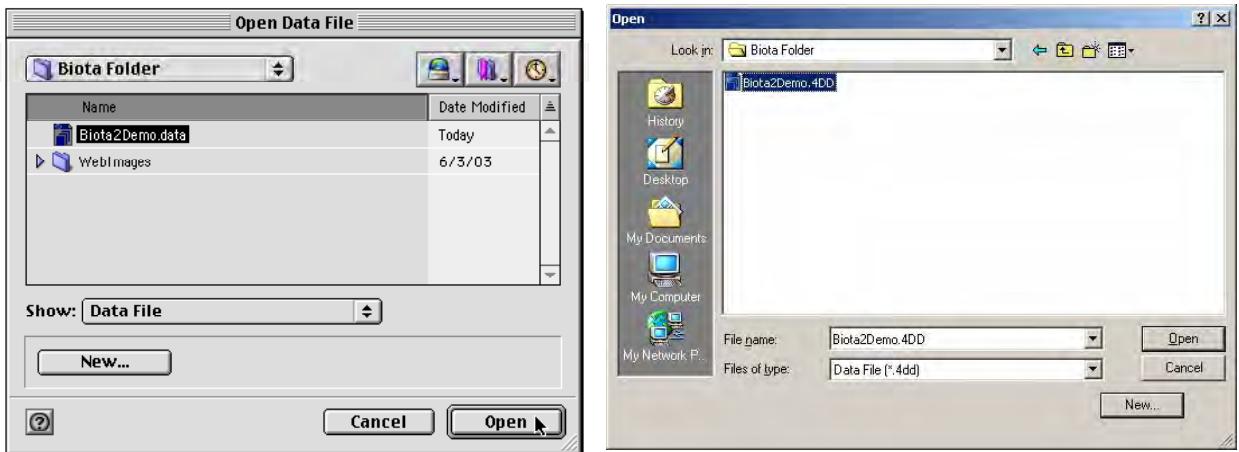
Note: If the password system has been enabled (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), the Password request screen appears at this point.



Enter your password, then press and hold the OPTION key (Mac OS) or ALT key (Windows) while clicking the “Connect” button. (In the illustrations above, the Mac OS screen is illustrated on the left, the Windows screen on the right).

2. When the file navigation window appears, find and open the Biota2Demo Data File.

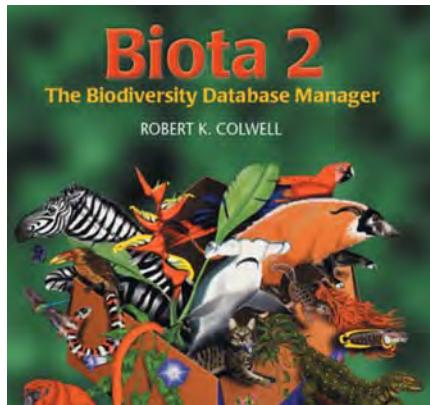
- **Macintosh:** The file is named “Biota2Demo.data.” Find it and open it when the “Open a data file” window appears.
- **Windows:** The Demo Data File is named “Biota2Demo.4DD.” (The extension may not be visible.) Find it in the “Open which data file” window and open it.



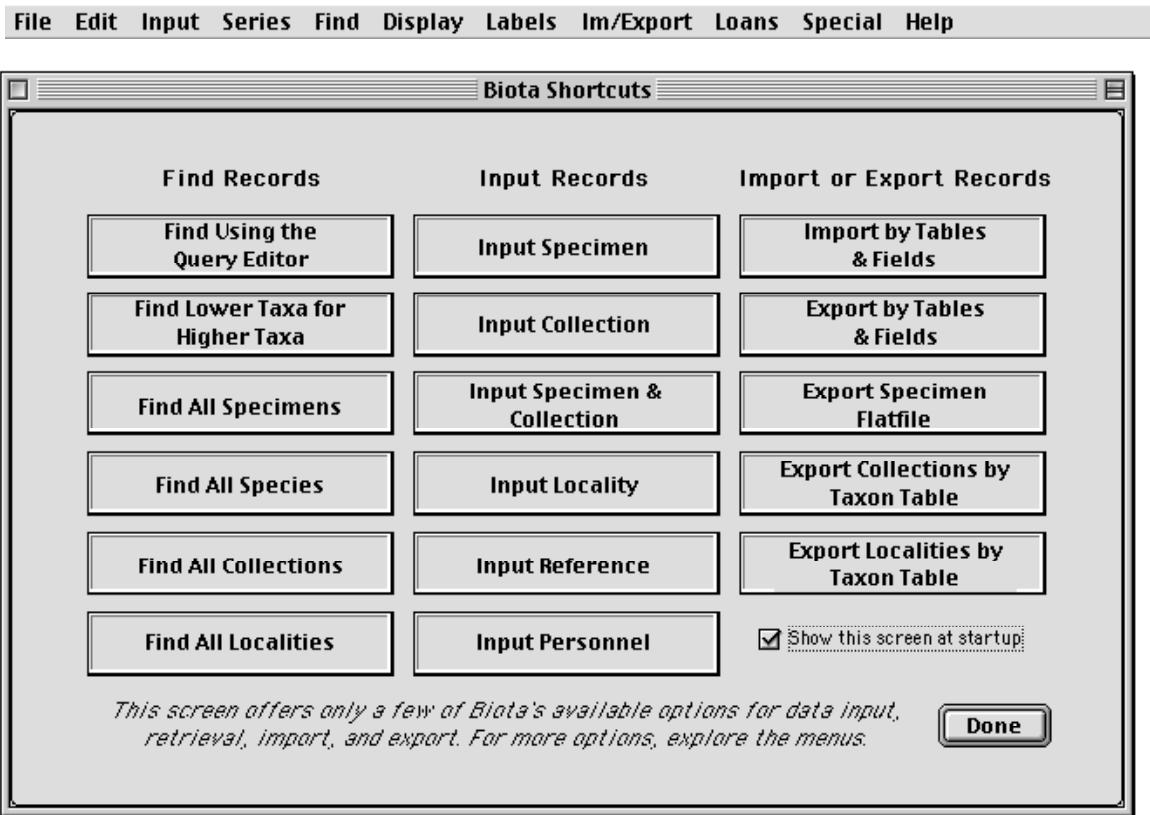
(The folder containing the Biota2Demo file will be different than the one illustrated above.)

Once you have opened a particular Biota Data File using this method, the same Data File will be opened automatically next time you launch Biota—*without* having to use the OPTION/ALT key technique.

The Biota startup screen appears briefly while the program sets up.



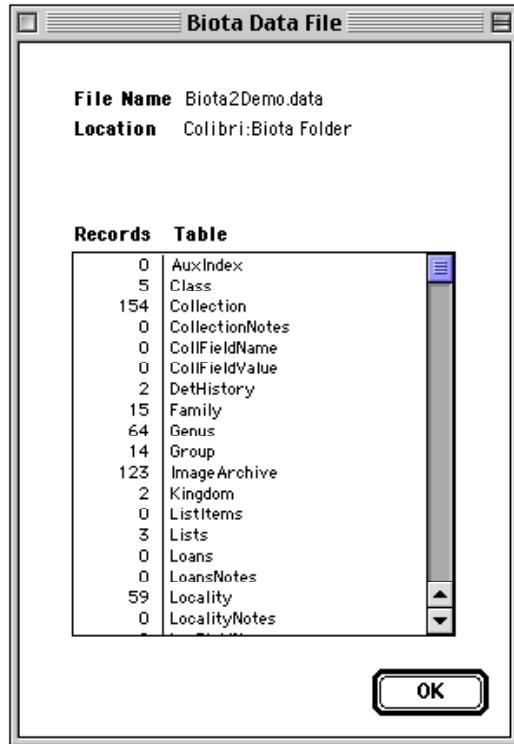
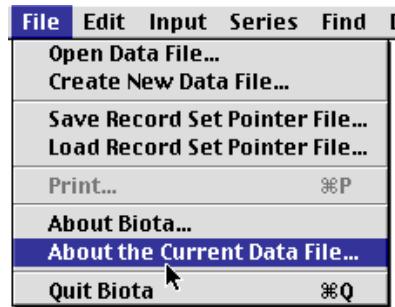
Then you will see the “Shortcut Screen” and menu bar for Biota. (The Macintosh menu bar is shown, but the Windows one is functionally identical.)



The Shortcut screen displays buttons for a few of the most frequently used commands from Biota's menus. You can dismiss it at any time if you prefer to use the menu commands. (To re-display the Shortcut screen, choose “Show Shortcut Screen” from the Special menu.)

3. From the File menu, choose “About the Current Data File” to confirm that the Demo Data File has been loaded.

A screen identifying the Data File appears, specifying its location on your hard disk, and listing the number of records it currently contains for each Biota table. (You will have to scroll the list to see all tables.)



What's in the Demo Data File?

The Demo Data File began life as an actual research dataset from a project on the hummingbird flower mites associated with tropical plants of the families Ericaceae and Campanulaceae. The mites were collected from host flowers preserved in fluid, collected by James Luteyn of the New York Botanical Garden. (You will see Luteyn's name in many places in the file.)

The file thus includes records for both plant and mite taxa and specimens, and demonstrates the “host–guest” capability of Biota (see Chapter 24, “[Host-Guest Relations](#)”).

For this tutorial, in the hope of creating some simple examples using species familiar to all biologists, a small set of fictitious Specimen records for Darwin’s finches was added, along with appropriate higher taxon, Collection, and Locality records.

In addition to mites, their host plants, and fictitious finch specimens, a few records of insects from the Project ALAS database at La Selva Biological Station in Costa Rica (for which Biota was originally developed, see the “[Preface](#)”) have been added to demonstrate Biota’s image capability.

Lesson 1. Displaying and Editing Existing Records

Biota displays groups of records in *Record Listing screens*. In a Record Listing screen, you can sort the records displayed, print a list of them, select some of them to delete from the Data File, or select some of them to retain as a Sub-selection and dismiss the rest from the display. When you leave a Record Listing screen, you can declare the Selection of records last displayed in the Record Listing screen to be a *Record Set*.

An individual record can be displayed and edited in an *Input screen*. In an Input screen, you can change the content of the record, attach Notes, References, Images, or Auxiliary Field Values, use the record as a template for a new record, or delete the record. The Input screen, as the name suggests, is also used when you create new records from scratch, as you will do in a later lesson of the tutorial.

Step by Step

- Click the “Find All Species” button in the Shortcut Screen, or select “All Species” from the Find menu.**



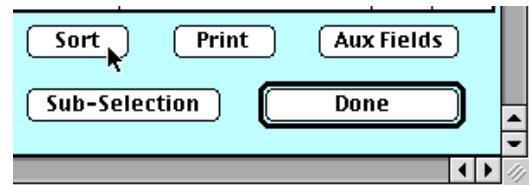
All Species records in the Demo Data File appear in the Species Record Listing screen.

Double click a Species to view or modify record				Var Field 2		
Species Code	Family	Genus	Specific Name, Subsp., Variety	Subgenus	Images	Aux
AL1246157	Chrysomelidae	Alurnus	ornatus		1	0
AL1246154	Chrysomelidae	Alurnus	salvinii		1	0
antvert	Ericaceae	Anthopterus	verticillatus		0	0
AL015248	Formicidae	Aphaenogaster	araneoides		5	0
AL1237844	Formicidae	Azteca	alfari		7	0
AL1238326	Formicidae	Azteca	pittieri		7	0
AL1237841	Formicidae	Azteca	xanthochroa		5	0
AL1238658	Formicidae	Basidioros	manni		0	0
bursp	Campanulaceae	Burmeistera	sp.		0	0
caetheli	Fringillidae	Cactospiza	heliosobates		0	0
caetpall	Fringillidae	Cactospiza	pallida		0	0
camapary	Fringillidae	Camarhynchus	parvulus		0	0
camapaup	Fringillidae	Camarhynchus	pauper		0	0
camapsit	Fringillidae	Camarhynchus	psittacula		0	0
cavcomp	Ericaceae	Cavendishia	complectens subsp. striata		0	0
cavcouat	Ericaceae	Cavendishia	ouatreocasasi?		0	0
cavforn	Ericaceae	Cavendishia	forneral		0	0
cavido	Ericaceae	Cavendishia	oiloiana		0	0

(The Record Listing screen expands vertically to fit your monitor, although you can adjust the size of the window manually. The Tutorial illustrations use a window that has been adjusted in size vertically to save space on the page.)

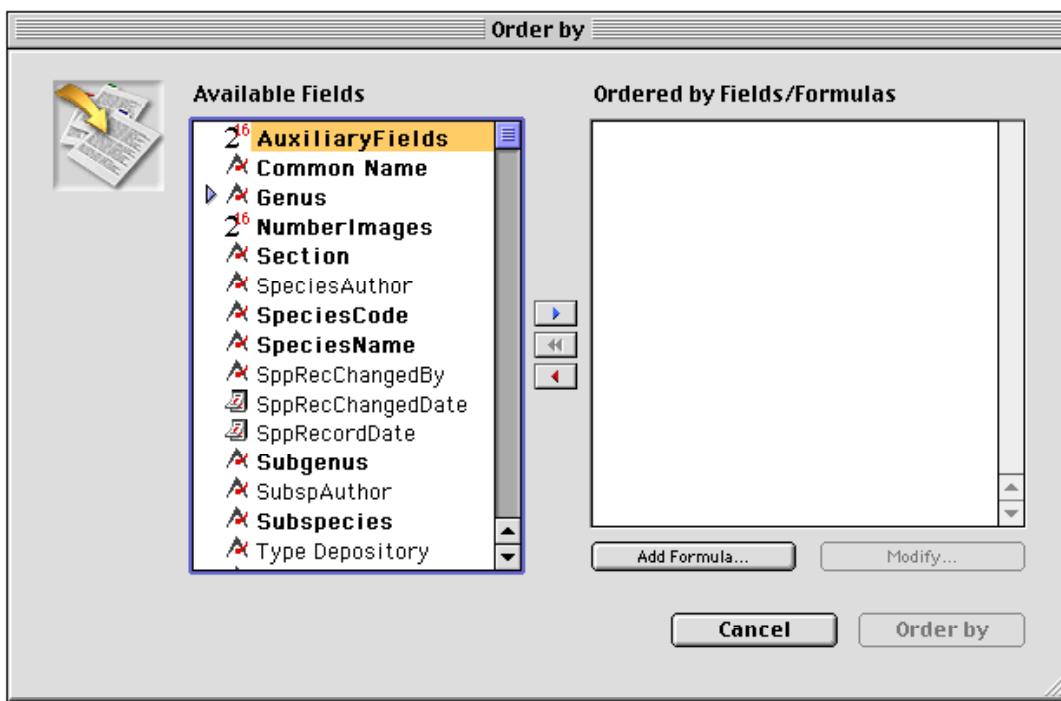
Notice that the Species records are sorted, by default, by Genus and Specific Name (you can change the default in the Preferences screen). See “[Sorting Records by Record Codes](#)” in Chapter 8.

- To sort the records on a different field in the Record Listing screen, click the “Sort” button at the bottom of the display.**

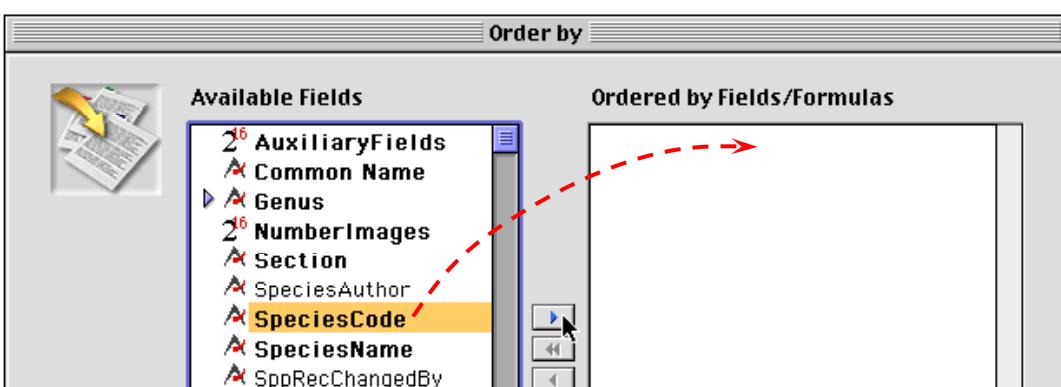


The Sort Editor appears, with the title “Order by.”

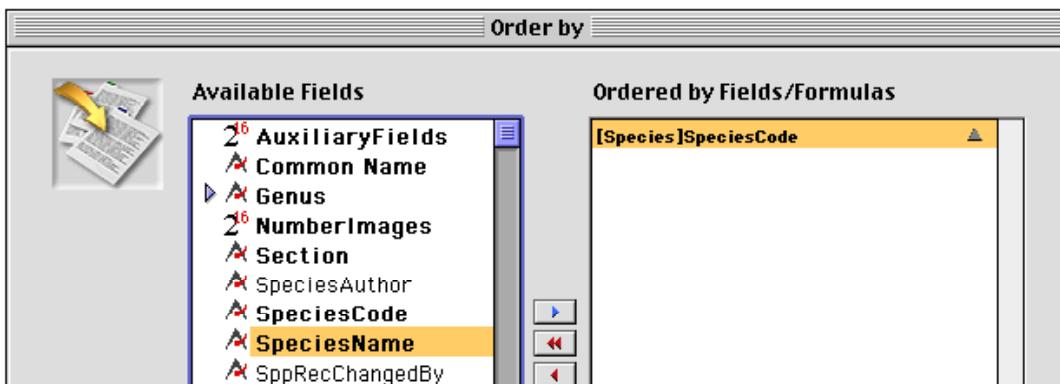
3. Select “Species Code” in the “Available Fields” panel on the left, then click the



“add to list” button to enter “Species Code in the sort criteria panel on the right.



Species Code is the Key field for the Species table, with a unique value for each record. Species Code is added to the sort criteria.



You can add additional criteria—including fields from related tables—or change the direction of the sort; see “[Sorting Records in Record Listing Screens](#)” in Chapter 10.

4. In the “Order by” window, click the “Order by” button.

The Record Listing screen reappears, with the records sorted by Species Code (the left-most column).



The screenshot shows the 'Species Records' window with a table of 108 records. The columns are labeled: Species Code, Family, Genus, Specific Name, Subsp., Variety, Subgenus, Images, and Aux. A specific row for 'Azteca xanthocroa' is highlighted with a red box and a cursor is positioned over the 'xanthocroa' entry in the 'Specific Name' column. The top of the window displays 'Double click a Species to view or modify record' and 'Var Field 1 Var Field 2'. The bottom features various buttons: Change Var Fields, Add Species, Sort, Print, Aux Fields, Display Images (with Scroll, Page, Delete Selection, Sub-Selection, and Done buttons), and a status bar with navigation icons.

Species Code	Family	Genus	Specific Name, Subsp., Variety	Subgenus	Images	Aux
AL013240	Formicidae	Aphaenogaster	araneoides		5	0
AL1237372	Formicidae	Rogeria	inermis		4	0
AL1237430	Formicidae	Pheidole	celaena		4	0
AL1237431	Formicidae	Pheidole	arietans		5	0
AL1237443	Formicidae	Pheidole	boruca		4	0
AL1237521	Formicidae	Pheidole	simonsi		6	0
AL1237841	Formicidae	Azteca	xanthocroa		5	0
AL1237844	Formicidae	Azteca	alfari		7	0
AL1238326	Formicidae	Azteca	pittieri		7	0
AL1238377	Formicidae	Pheidole	cramptoni		4	0
AL1238429	Formicidae	Procryptocerus	pictipes		7	0
AL1238655	Formicidae	Pheidole	JTL-048		4	0
AL1238656	Formicidae	Pheidole	fimbriata		4	0
AL1238657	Formicidae	Procryptocerus	impressus		0	0
AL1238658	Formicidae	Basiberos	manni		0	0
AL1238659	Formicidae	Stromigenys	godmani		0	0
AL1246151	Chrysomelidae	Ischnocodia	annulus		1	0

5. To display an individual Species record, double-click its record in the Record Listing screen. Try it with the record for the tropical ant *Azteca xanthocroa*, as shown above. The full record appears in the Species Input screen (next page).

Species Records

Classification | Subsp/Names | **Synonymy** | Dist/Types | Images (5) | Aux Fields | Notes (3) | Refs (3)

AL1237841
Azteca xanthochroa (Roger 1863)

Species Code AL1237841 **Assign**

Genus Azteca

Specific Name (Specific Epithet) xanthochroa

Species Author (& Date) (Roger 1863)

Subgenus

Section

Synonymy
Valid Species Code AL1237841
A valid Species name with no synonyms in the database

Record
Number 16 of 108
Created May 14, 2003
Last changed Jun 29, 2003
Changed By Administrator

Classification
Family Formicidae
Order Hymenoptera

Show Genus Record **Show Specimens (1)**

This Species record

Navigate records

The Species Input screen is organized by tabs:

Species Records

Classification | Subsp/Names | **Synonymy** | Dist/Types | Images (5) | Aux Fields | Notes (3) | Refs (3)

AL1237841

Record

Notice that the tabs for Images, Notes, and Refs include numbers in parentheses, indicating that this record has 5 linked Images, 3 Notes, and 3 literature References.

In the Input screen, any data entry area can be edited. You save any changes by clicking the “Save” button.

Specific Name (Specific Epithet)
xanthochroa

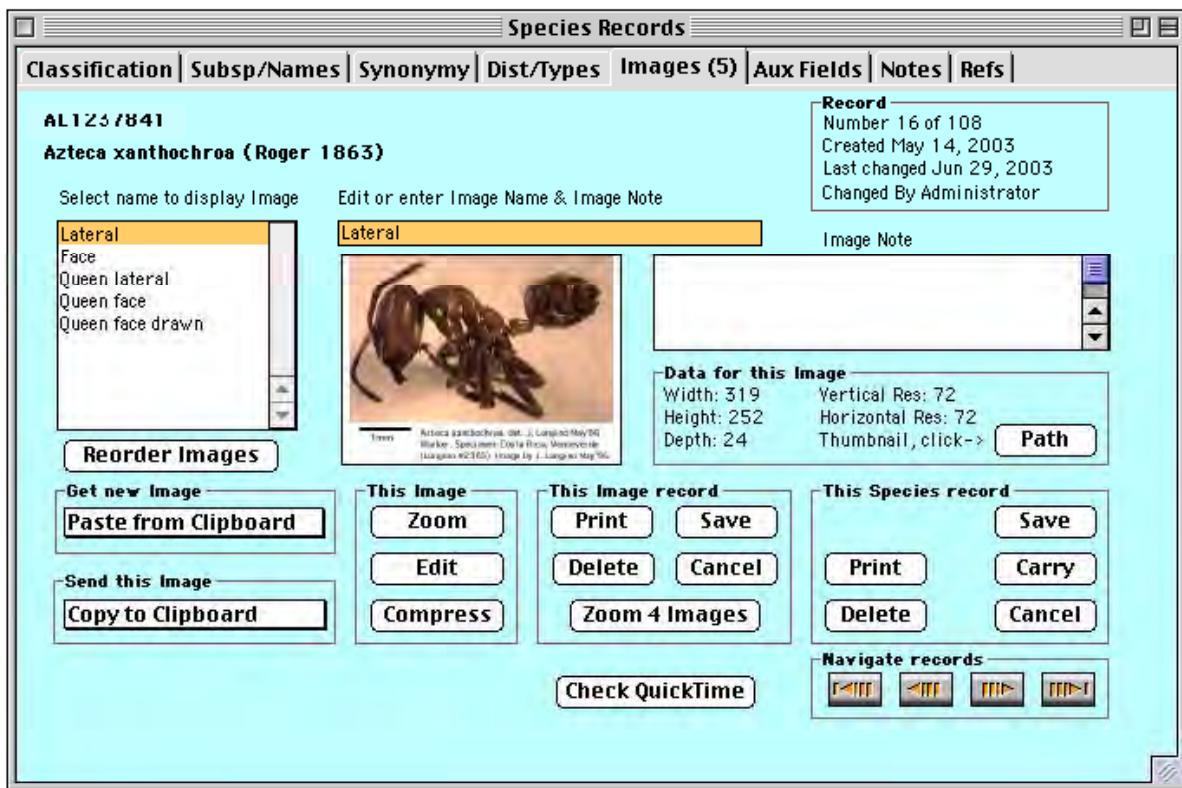
This Species record

(Information in some areas, such as the green “Classification” area on the right of the Species Input screen, showing data from the linked Family and Order records, is for display only, and cannot be edited in this screen.)

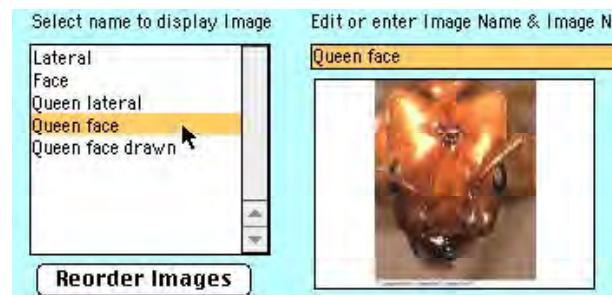
The *Synonymy* panel shows that *Azteca xanthochroa* is a valid name. See Chapter 23, [“Synonymy System.”](#)

Synonymy
Valid Species Code AL1237841
A valid Species name with no synonyms in the database

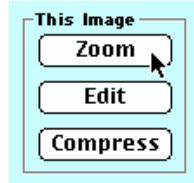
6. To view the Images for this ant Species, click the Image tab (or use the keyboard shortcut; see “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7). The Image tab screen appears, displaying the first Image for this species, with a list of other Images for this Species on the left.



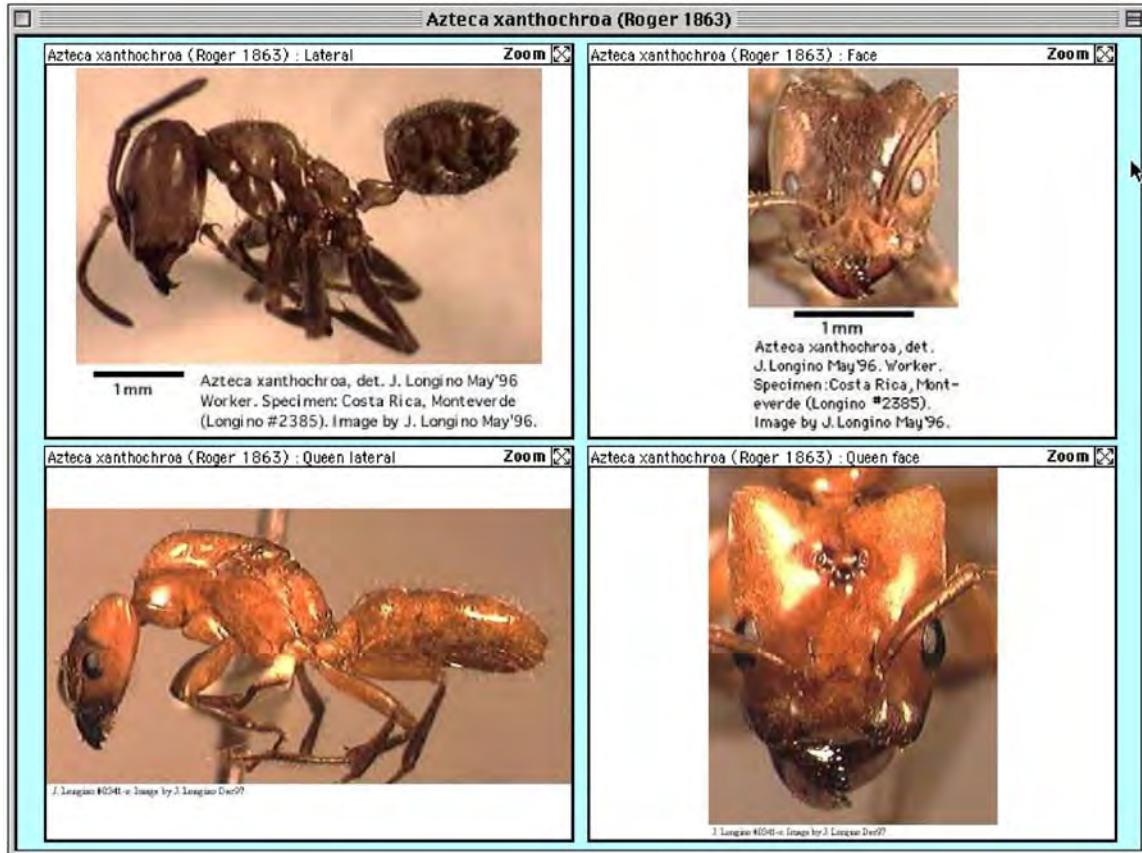
- To display a different Image from the list for this Species, just click the Image name in the list on the left.



- To see the Image at its original resolution, click the “Zoom” button.

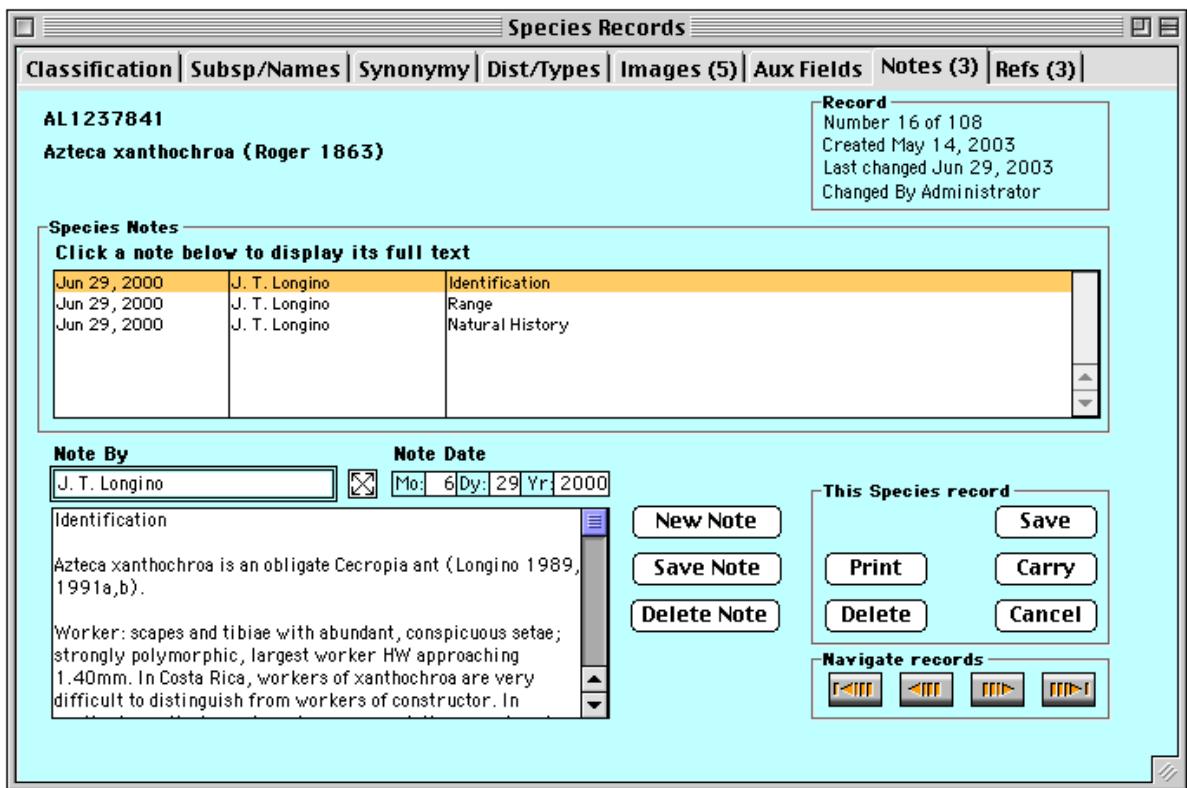


- To see the first 4 Images for this Species at higher resolution, click the “Zoom 4 Images” button.



- The Image tab screen has many other functions: You can Edit, Compress or Delete an existing Image record, create additional thumbnail links with images in external image files, and acquire images from the Clipboard or from imaging devices from within Biota. You can copy images to the Clipboard or export images to disk files in many different formats. For full details, see Chapter 19, [“Images.”](#)
7. To view the Notes for this record, click the “Notes” tab in the Species Input screen.

The Species Notes tab screen appears. Click a Note in the upper panel to display it in full in the lower panel. (See next page.)

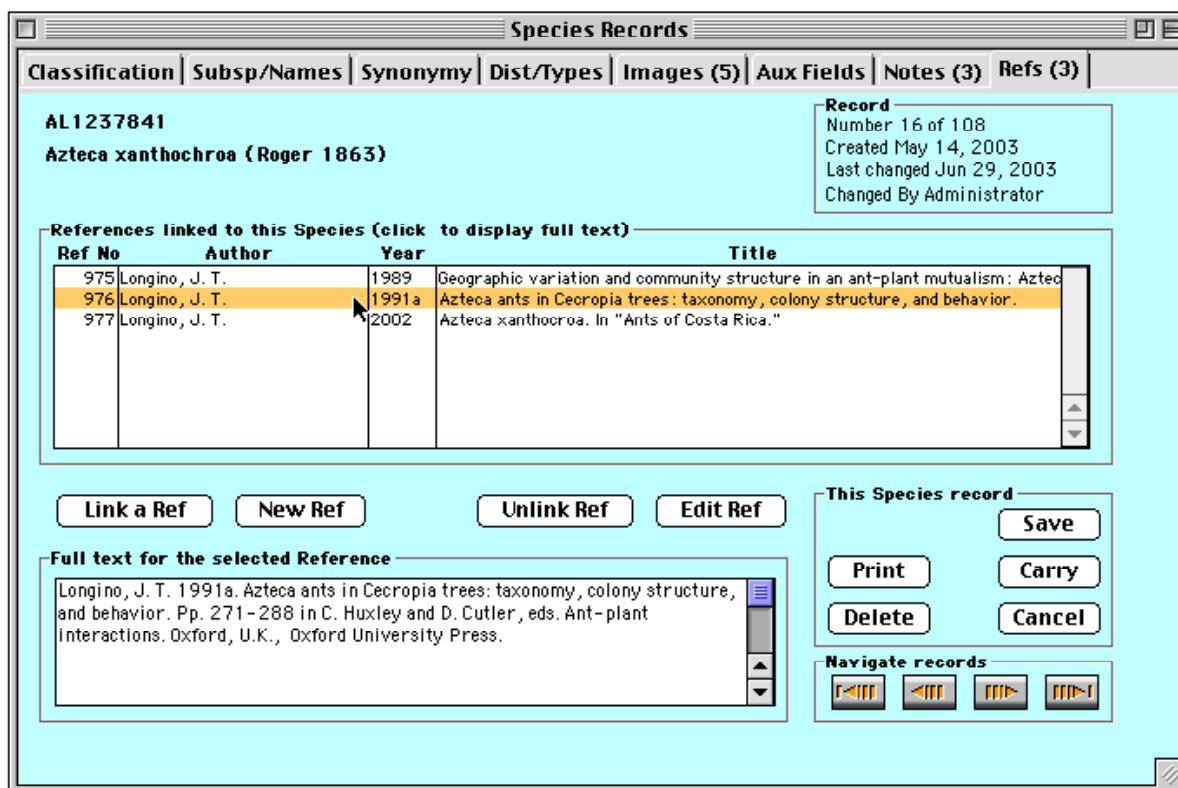


The first of three notes on this ant species has been displayed in the illustration above.

In this same window, you can create new Notes for this Species (using the “New Note” button) or delete the Note displayed (using the “Delete Note” button in the Notes window). See “[Notes Input](#)” in Chapter 11 for details.

8. To view the literature References for this Species record, click the “Refs” tab in the Species Input screen.

The Species References tab screen appears. Click a Reference in the upper panel to display it in full in the lower panel. (See next page.)



The second of three References linked to this Species record has been displayed in the illustration above. (The same Reference record can be linked to any number of other Species, Specimen, Collection or Locality references.)

Using the buttons in the Reference tab screen, you can create new Links to existing Reference records (the “Link a Ref” button); remove existing Links (the “Unlink a Ref” button); create a new, linked record in the References table (the “New Ref” button); or edit the Reference record for any linked Reference (the “Edit Ref” button).

You can also enter new Reference records using the “Reference” command from the Input menu, or import them from reference management software. See Chapter 20, “[References](#).”

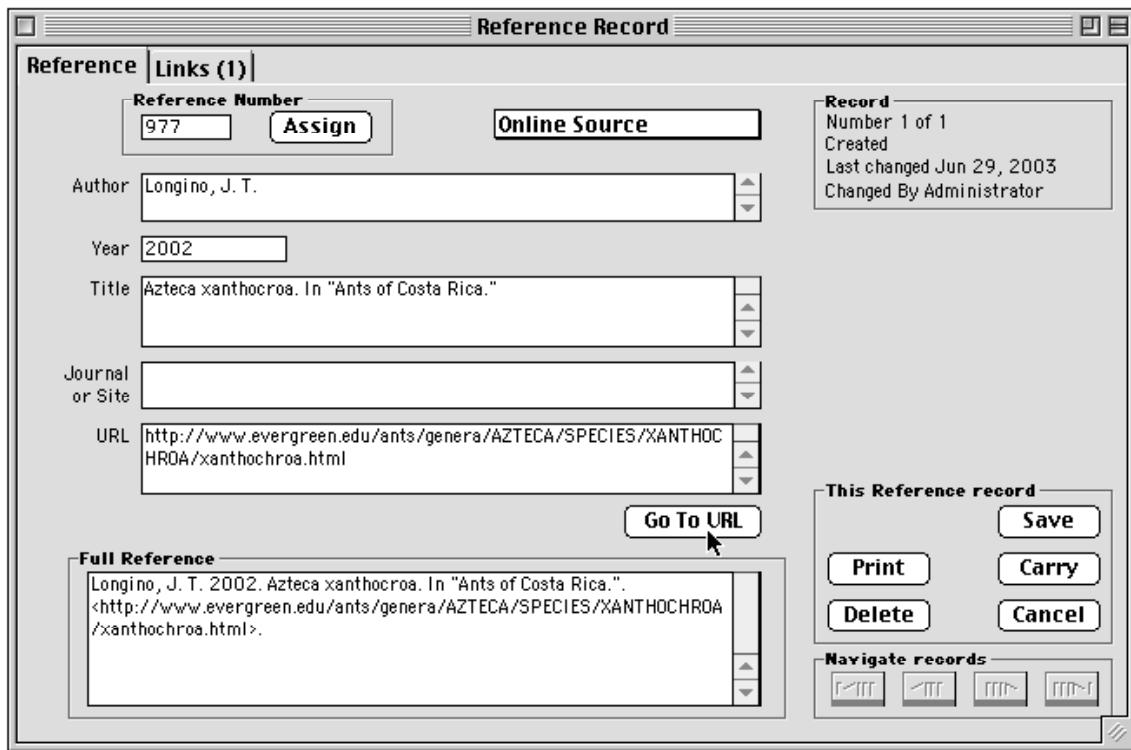
9. For a look at the References table, select the third Reference in the References tab screen:

References linked to this Species (click to display full text)			
Ref No	Author	Year	Title
975	Longino, J. T.	1989	Geographic variation and community structure
976	Longino, J. T.	1991a	Azteca ants in Cecropia trees: taxonomy, colony structure, and behavior.
977	Longino, J. T.	2002	Azteca xanthochroa. In “Ants of Costa Rica.”

Then click the “Edit Ref” button.

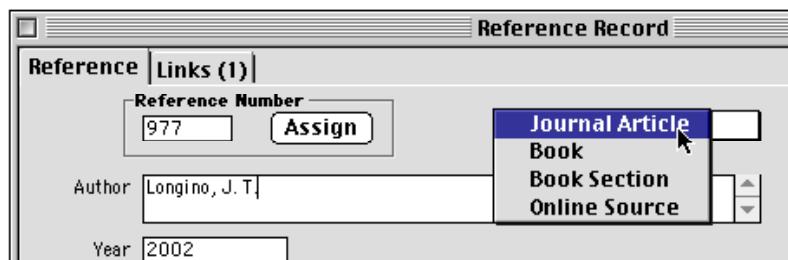


The selected Reference appears, in a new window, in the References Input screen.



Notice that this particular Reference record is of the type “Online Source,” and that the “Go to URL” button is enabled. If you click the “Go to URL” button, your default Web browser application (e.g., Netscape or Internet Explorer) is launched and the referenced Web page for this species, from Longino’s “Ants of Costa Rica,” appears in your browser.

The Reference table also supports three other Reference types: Journal Article, Book, and Book Chapter. Use the Reference Type popup to explore the differences, if you want. (All types include a URL field.)



For full details on Biota’s Reference system, see Chapter 20, “[References](#).”

10. Click the “Cancel” button in the References Input screen (don’t save any changes you made), to return to the Species Input screen.

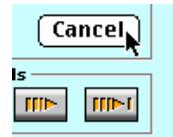
11. To move through the Species records that were listed in the Species Record Listing screen, you can use the record navigation buttons, *from any tab* in the Species input screen. (Left to right, the buttons take you to the First, Previous, Next, and Last record in the current Selection of records.)



Go back to the Images tab and experiment with the navigation buttons. There are keyboard shortcuts for these buttons and for most others. See ["Keyboard Shortcuts for Input Screen Buttons"](#) in Chapter 7.

12. Dismiss the Species Input screen by clicking its “Cancel” button.

The Species Record Listing screen reappears, with the records sorted in the same sorted order they were when you left it.



13. In the Species Record Listing screen, click the “Scroll” button in the “Display Images” panel.

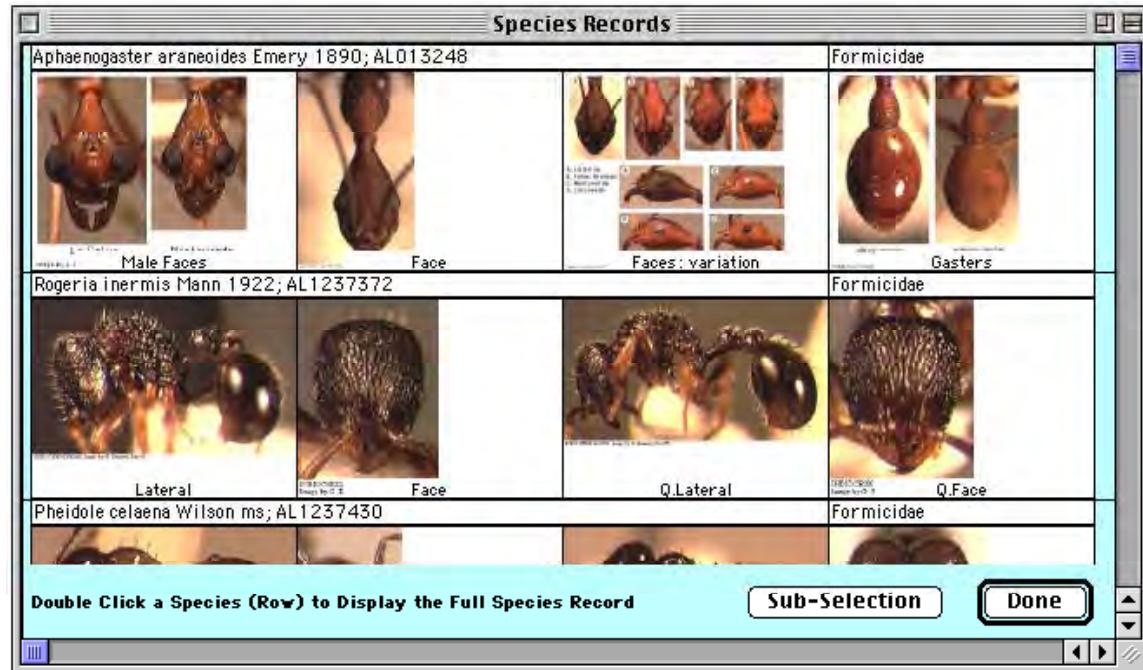
Pheidole	cramptoni	4	0
Prooryctoerous	piotipes	7	0
Pheidole	JTL-048	4	0

Display Images

Change Var Fields **Add Species** **Sort** **Print** **Aux Fields**

Scroll **Page** **Delete Selection** **Sub-Selection** **Done**

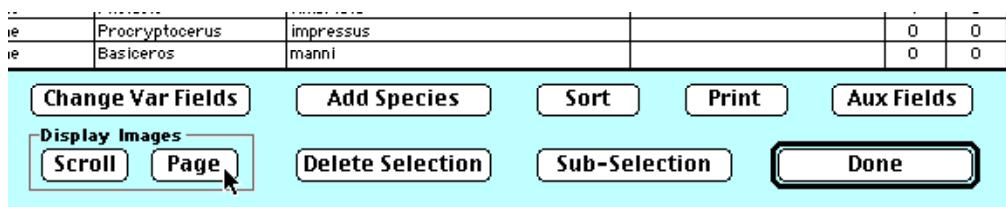
Images for the first few records appear in the Image Record Listing screen.



Each row of Images belongs to one Species record. (The name of the species, its Species Code, and its Family appear above its Image row.) A row of blank frames appears if no Images are linked to a Species record; if fewer than four Images are

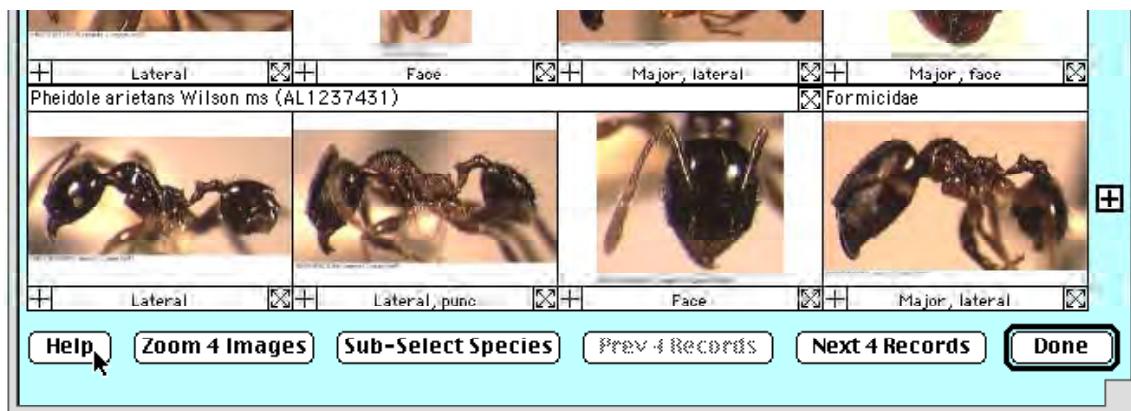
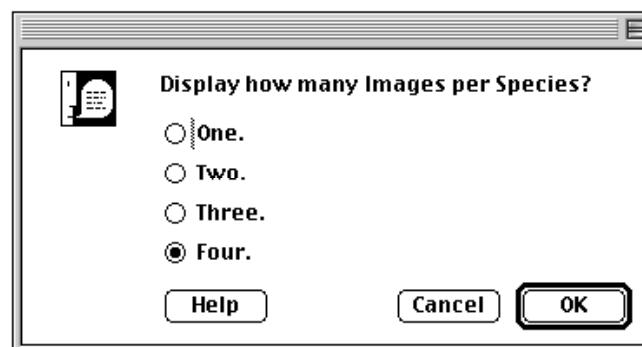
linked, the remaining frames are blank. If the Species records are still sorted by Species Code, the first three records will be ants with Images, of which two are shown above.

14. Click the “Done” button in the Image Record Listing screen to dismiss it. The Species Record Listing screen reappears.
15. In the Species Record Listing screen, click the “Page” button in the “Display Images” panel.



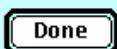
An option screen appears.
Click the “Four” image option,
then the “OK” button.

Images for the first four
Species records appear in the
“Page” Image Record Listing
screen.

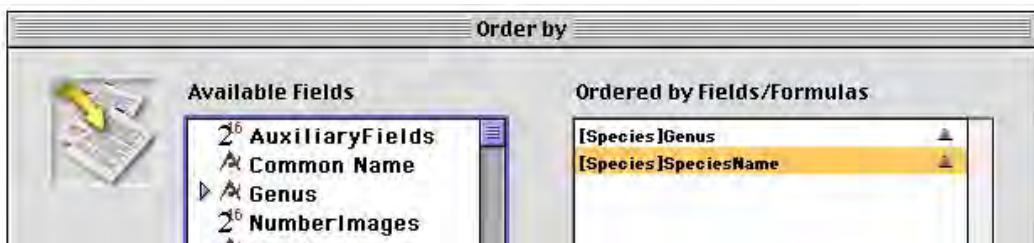


The Page Image display and comparison screen has many special tools. You can get a brief introduction to them, as you explore this screen on your own, by clicking the “Help” button at the bottom left of the Page Image screen, illustrated above.

16. Dismiss the Page Image screen by clicking the “Done” button.
Biota returns you the Species Record Listing screen.



17. Sort the Species records by Genus and Species Name. (See [Steps 2-4](#), earlier in this section, if necessary.)



18. Select a set of records in the Species Record Listing screen. Select any records you wish, but be sure to include the Galápagos finch *Camarhynchus parvulus* (Species Code "camaparv"), which is needed for a later step.
- To select consecutive records, click the first record in the group then hold down the SHIFT key while you click the last record in the group.
 - To select nonconsecutive records, hold down the the CTRL key (Windows) or the COMMAND (⌘) key (Mac OS) or while clicking the individual records.
19. Click the "Sub-Selection" button to dismiss all unselected records.

The Species Record Listing screen is now shows only the Species records you selected.



Note: Dismissing records from a Selection (or including them in one) does not affect the records in the Data File in any way. You can prove it to yourself by choosing All Species from the File menu again, leaving the current window open. The same records can simultaneously be part of any number of different Selections or Record Sets (see Chapter 3, "[Key Concepts](#)").

20. In the Species Record Listing screen, select the record for *Camarhynchus parvulus* (Species Code "camaparv").

Species Records						
Double click a Species to view or modify record					15 Records	
Species Code	Family	Genus	Specific Name, Subsp., Variety	Subgenus	Images	Aux
AL1238658	Formicidae	Basiceros	manni		0	0
bursp	Campanulaceae	Burmeistera	sp.		0	0
cactheli	Fringillidae	Cactospiza	heliotobates		0	0
cactpall	Fringillidae	Cactospiza	pallida		0	0
camaparv	Fringillidae	Camarhynchus	parvulus		0	0
camapaup	Fringillidae	Camarhynchus	pauper		0	0
camapsit	Fringillidae	Camarhynchus	psittacula		0	0
cavcomp	Eriocaceae	Cavendishia	complectens subsp. striata		0	0
cavcuat	Eriocaceae	Cavendishia	cuatrecasasii?		0	0
cavfour	Eriocaceae	Cavendishia	ferrerae		0	0

21. Click the “Delete Selection” button in the Species Record Listing screen (illustrated above). A warning message appears.



22. Click the “OK” button in the warning window shown above. (The deletion will be canceled in the next warning screen).

A second warning screen appears.



If a record you propose to delete has any linked child records in a Core table (see Chapter 3, “[Key Concepts](#)” for definition), a second warning message appears, like the one above.

In this example, there are records for two Specimens of *Camarhynchus parvulus* in the database, which will no longer be linked to any Species record (and thus no longer linked to a Genus record, Family record, or higher ranks) if you confirm the deletion.

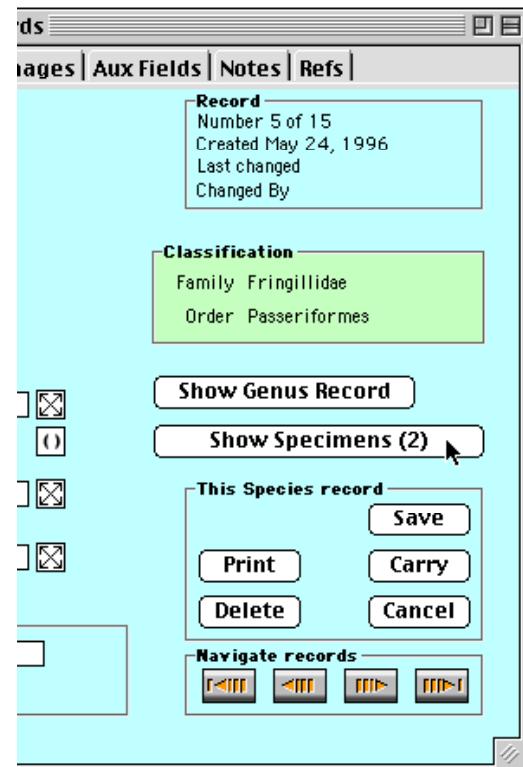
23. Click the Cancel button in the warning screen above to avert the pending deletion. The Species Record Listing screen reappears, with the *Camarhynchus parvulus* record intact. As the warning screen above describes, there is an easy way to take a look at linked Specimen records for *Camarhynchus parvulus*. You will do this next.

Note: If you clicked the “OK to Delete” button in error, the Demo Data File can always be reloaded from the distribution diskette if you later want a full copy—a good example of why you should always make backup copies of your own Data Files.

- 24. Double-click *Camarhynchus parvulus* in the Species Record Listing screen.** The record appears in the Species Input screen. Notice that the “Show Specimens” button indicates that there are 2 linked Specimen records for this Species. (If there are none, the button reads “Show Specimens (None)” and it is disabled—dimmed.)
- 25. Click the “Show Specimens” button in the Species Input screen.**

NOTE: The Input screen for each Core table has an analogous button to display linked child records. The name of the button is always the name of the child table (in plural form); generically, these are called *Child Records* buttons (see “[Linking Fields: Parent and Child Records](#)” in Chapter 3).

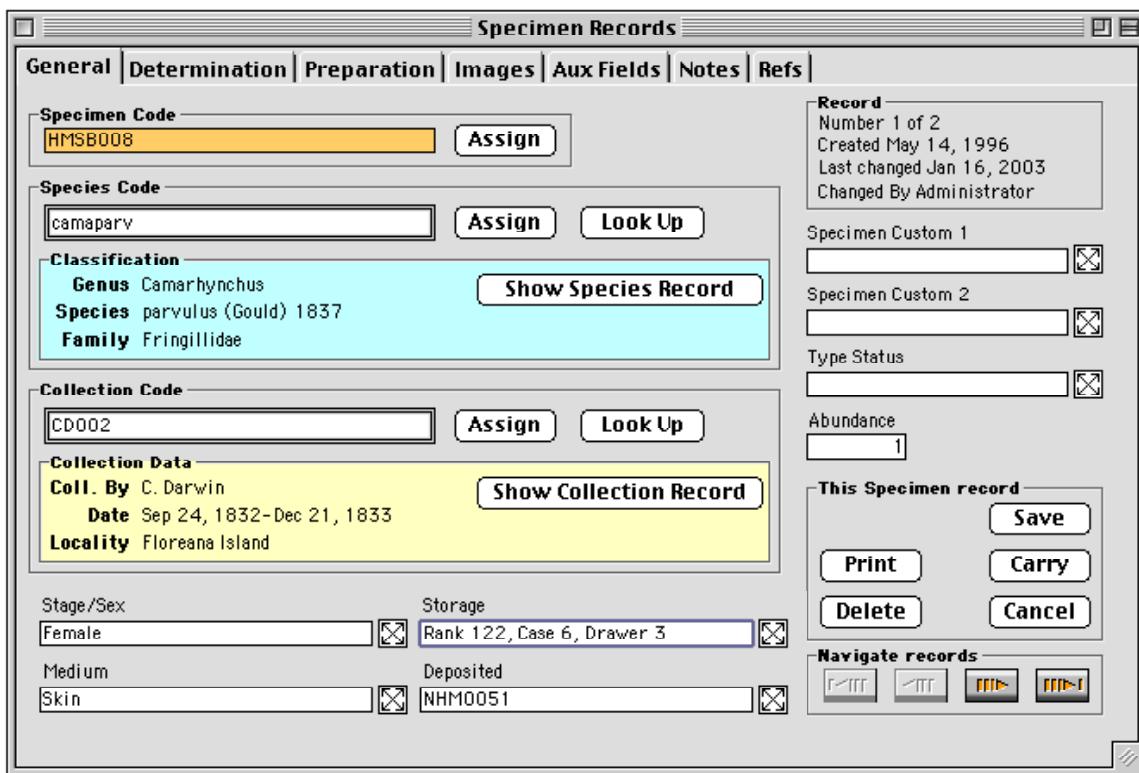
The two Specimen records for *Camarhynchus parvulus* appear in the Specimen Record Listing screen in a new window. The Species Input screen remains open in its own window, although it may be hidden.



Specimen Records										
Double click a Specimen to view or modify record										
Var Field 1 Var Field 2										
Specimen Code	Genus	Species	Collection Code	Collector	Method	Stage/Sex	Host	Storage	Deposite	Img Aux
HMSB008	Camarhynchus	parvulus	CD002	C. Darwin	Shotgun	Female		Rank 12	NHM0051	0 0
HMSB017	Camarhynchus	parvulus	CD004	C. Darwin	Shotgun	Male				0 0

Buttons at the bottom include: 'Change Var Fields', 'Add Specimen', 'Sort', 'Print', 'Aux Fields', 'Display Images', 'Scroll', 'Page', 'Delete Selection', 'Sub-Selection', and 'Done'.

- 26. Double-click one of the records in the Specimen Record Listing screen.** The record appears in the Specimen Input screen. (See next page.)



Like the Species Input screen, the Specimen Input screen is organized by tabs. The tabs for Images, AuxFields (Auxiliary Fields), Notes, and References are identical to those for the Species Input screen—and the same for the Collection and Locality Input screens, as well.

The “General” tab of the Specimen Input screen shows not only fields from the Specimen table, but essential information from the linked Species record (in the blue inset) and the linked Collection record (in the yellow inset). You will see more of this screen later in the tutorial.

(This is the record for a fictitious specimen that exists only in the Demo Data File, although the collector and collection dates are plausible, based on *The Voyage of the Beagle*.)

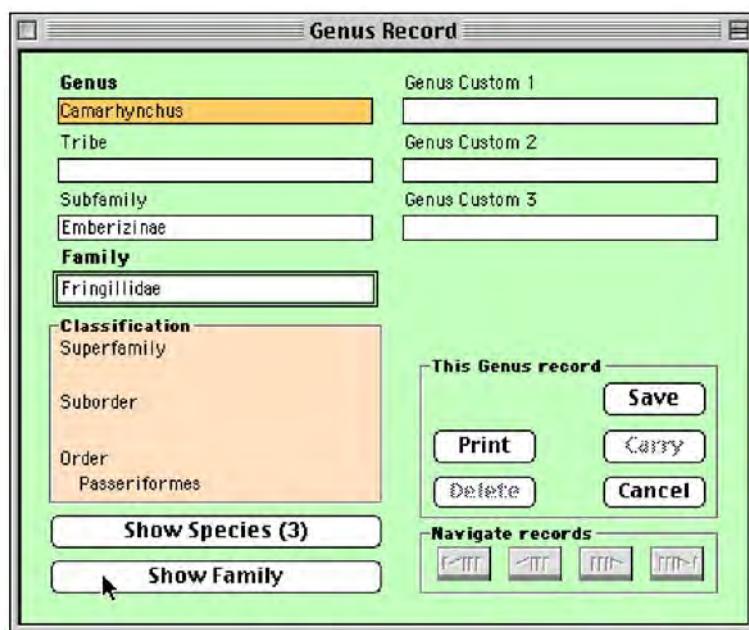
27. Click the “Cancel” button in the Specimen Input screen to dismiss it. The Specimen Record Listing screen reappears.
28. Click the “Done” button in the Specimen Record Listing screen.

The Record Set option screen appears.



29. Click the “Dismiss it” option, then the “OK” button in the Record Set option screen (above). See “[Record Sets](#)” in Chapter 3 for a discussion of the other options offered. You will create a Record Set in the next lesson.
30. Return to the record for *Camarhynchus parvulus* displayed in the Species Input screen.
31. Click the “Show Genus Record” button in the Species Input screen. This is the Parent Record button for the Species Input screen.

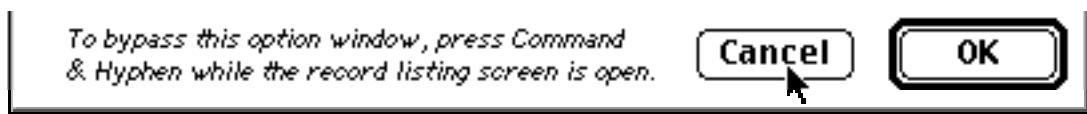
The full Genus record for *Camarhynchus* appears in the Genus Input screen.



If you want to see the full record for Fringillidae, the linked Family record, you can click the “Show Family” (Parent record) button in the Genus Input screen, above, then Cancel the Family Input screen.

The Input screen for each Core table (except for Kingdom and Locality) offers a Parent Record button. These buttons make it easy to display information on parent records—all the way to the top of the taxonomic and place hierarchies (see “[Linking Fields: Parent and Child Records](#)” in Chapter 3).

32. Click the “Cancel” button in the Genus Input screen. The Species Input screen reappears.
33. Click the “Cancel” button in the Species Input screen. The Species Record Listing screen reappears.
34. Click the “Done” button in the Species Input screen. The Record Code option window appears.



Notice the small note in the lower-left corner: “To bypass this option window, press COMMAND and HYPHEN while the Record Listing screen is open.” (This is the Macintosh screen. The Windows version substitutes CONTROL for COMMAND.)

You may not always want to declare the current Selection of records to be a Record Set, add it to the existing Record Set, or save it to disk as a Record Set Pointer File. In the next two steps, you will learn the keyboard bypass explained in the small note, which has the same effect as the “Dismiss it” option in the screen above.

35. Click the “Cancel” button in the Record Set Option window (above). The Species Record Listing screen reappears.
36. This time, dismiss the Species Record Listing screen from the keyboard, bypassing the Record Set option window:
 - **Windows:** Hold down the CTRL key and press the HYPHEN key (above the P key on the keyboard, not the MINUS key in the numeric keypad).
 - **Macintosh:** Hold down the COMMAND key (⌘) and press the HYPHEN key (above the P key on the keyboard, not the MINUS key in the numeric keypad).

NOTE: You can use this keyboard shortcut to dismiss virtually any Record Listing screen, Input screen, or setup screen in Biota. In the case of an Input screen, it is the equivalent of clicking the Cancel button in the screen. There are many useful keyboard equivalents for onscreen buttons and tabs, as well; See [“Keyboard Shortcuts for Input Screen Tabs”](#) and [“Keyboard Shortcuts for Input Screen Buttons”](#) in Chapter 7, and [“Keyboard Shortcuts for Record Listing Screens”](#) in Chapter 10.

Lesson 1 Review

In this lesson, you entered the Biota structure through the Species table by choosing “All Species” from the Find menu. Once “inside,” you learned how to:

- Sort records in the Record Listing screen.
- Delete records from the Record Listing screen.
- Make a Sub-selection of records in the Record Listing screen.
- Display an individual record in the Input screen.
- Move down a hierarchy using Child Records buttons (e.g., the “Show Specimens” button in the Species Input screen).
- Move up a hierarchy using Parent Record buttons in Input screens (e.g., the “Show Genus Record” in the Species Input screen).

Each of the above techniques applies to Record Listing and Input screens throughout Biota’s structure—regardless of how and where you enter the structure (which will depend on the task at hand).

You also learned how to:

- Display Images from Input and Record Listing screens.

- **Display Notes** from Input screens.
- **Display References** from Input screens.

The Images, Notes, and Reference techniques apply identically to the Species, Specimen, Collection, and Locality tables (Loans records also have Notes).

Lesson 2. Creating New Records One Table at a Time

This lesson shows you how to create new records for one table at a time. In Lesson 3, you will learn how to create records in related tables “on the fly,” as they are needed.

The Input screen for each table is the tool you use to create and enter data in new records for that table. As much as possible, all of Biota’s Input screens share the same features. These common elements are discussed in Chapter 7, “[Overview of Record Input Screens](#),” and Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

Step by Step

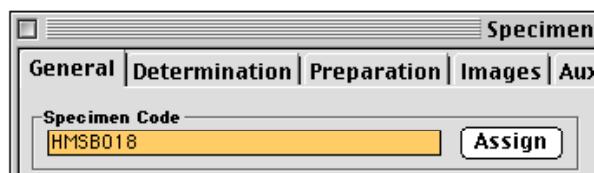
1. **From the Input menu, choose “Specimen.”** The Specimen Input screen appears, with the insertion point (blinking cursor) in the Specimen code entry area. You are going to add new records to the Demo Data File for additional fictitious specimens from Darwin’s visit to the Galápagos Islands.

The screenshot displays the "Specimen Input" window with the following interface elements:

- Top Navigation:** A tab bar with tabs: General, Determination, Preparation, Images, Aux Fields, Notes, and Refs. The General tab is selected.
- Record Information:** A panel on the right labeled "Record" containing fields: Number 0 of 0, Created Jun 29, 2003, Last changed, and Changed By.
- Specimen Code:** A text input field with an "Assign" button.
- Species Code:** A text input field with "Assign" and "Look Up" buttons.
- Classification:** A section with dropdown menus for Genus, Species, and Family, and a "Show Species Record" button.
- Collection Code:** A text input field with "Assign" and "Look Up" buttons.
- Collection Data:** A section with dropdown menus for Coll. By, Date, and Locality, and a "Show Collection Record" button.
- Storage:** A section with dropdown menus for Stage/Sex and Storage.
- Deposited:** A section with dropdown menus for Large and Deposited.
- Buttons:** A panel on the right with buttons: Save, Print, Carry, Delete, Cancel, and a "This Specimen record" group with Save, Print, Carry, Delete, and Cancel buttons.
- Navigation:** A panel at the bottom with buttons for navigating between records.

2. Enter **HMSB018** in the Specimen Code entry area and press the TAB key.

The insertion point moves to the Species Code entry area. Let's say this is a specimen of the Small Tree Finch, *Camarhynchus parvulus*, collected on Santiago Island (James Island, in Darwin's time) on October 9, 1832, when the *Beagle* was anchored there.

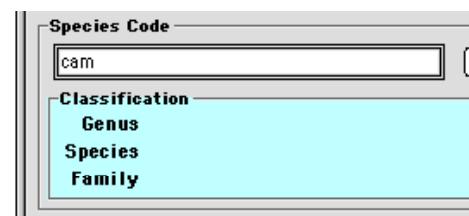


Note: If you get an error message indicating that this record already exists, and you are certain you entered *HMSB018*, it means that someone has already done the tutorial using this copy of the Demo Data File. Either quit Biota and install a fresh copy of the Demo Data File from the distribution CD, or delete the existing *HMSB018* Specimen record. (Select “All Specimens” from the Find menu, find it and delete it).

The next step is to link this Specimen record with the Species record for *Camarhynchus parvulus*, which is done by entering the Species Code for *Camarhynchus parvulus*. Suppose you recall that the Species Code starts with “cam,” but you are not sure of the rest of it.

3. Enter **cam** in the Species Code entry area and press TAB.

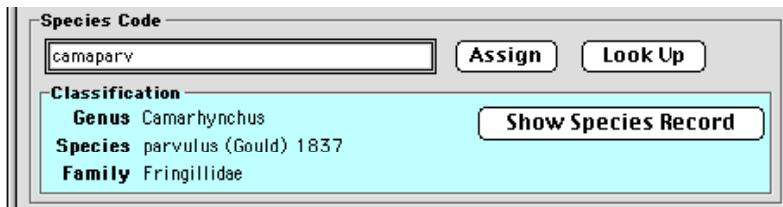
Biota presents a list of all Species records for which the Species Code begins with “cam.” (This way of finding the correct entry for a linking field is called the *wildcard method*.)



Species Records		
Click buttons to sort records		
Species Code	Genus	Species Name
camapary	Camarhynchus	parvulus
camapaup	Camarhynchus	pauper
camapsit	Camarhynchus	psittacula

Cancel Move the green lines to change column width

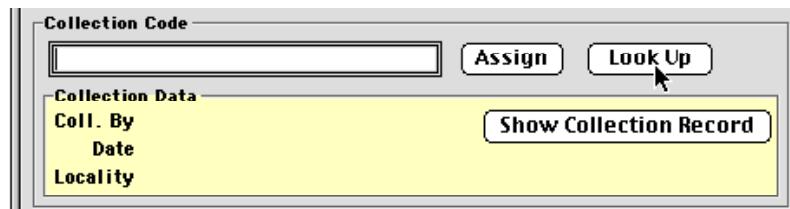
4. Click the line in the Species Records list (above) for *Camarhynchus parvulus*. The Species Code is automatically entered in the Specimen record, with additional information about the Species record you have just linked, displayed in the blue Species information panel.



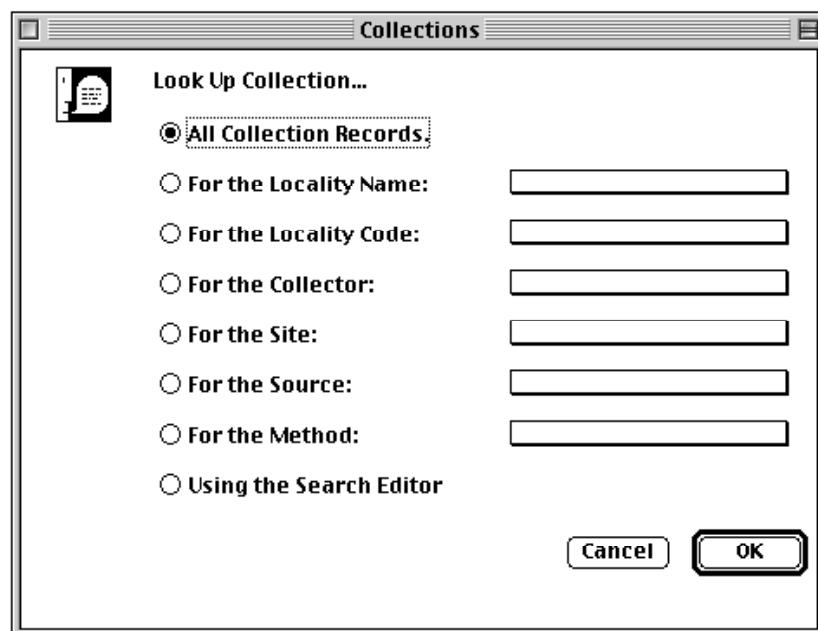
The insertion point moves on to the Collection Code entry area. The next step is to link this Specimen record with the Collection record for Darwin's specimens from Santiago Island on October 9, 1832.

You do not know whether such a Collection record even exists yet, nor its Collection Code if it does. This time, to seek the Collection record, you will use the “Look Up” button instead of the wildcard method you used to find the Species record. (Notice, above, that there is also a “Look Up” button for Species Codes, which you will use later.)

5. Click the “Look Up” button in the Collection Code panel in the Specimen Input screen.



The Look Up Collection option window appears.



This option window helps you narrow the search for existing Collection records—although the first option in the screen (the default) displays them all if you prefer. (If there are hundreds or thousands of Collection records in database, finding a record among those displayed can take a long time.)

Each of the other five option buttons in the Look Up Collection screen limits the search by a different attribute (field) of the Collection records (Locality, Collector, Site, Source, or Method). If you choose the last option in the list, Biota opens the Query Editor (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12) to allow searches not covered by the other options.

6. Click the button labeled “For the Collector” in the Look up Collection window, since you know the record you are looking for will have Darwin listed as Collector.

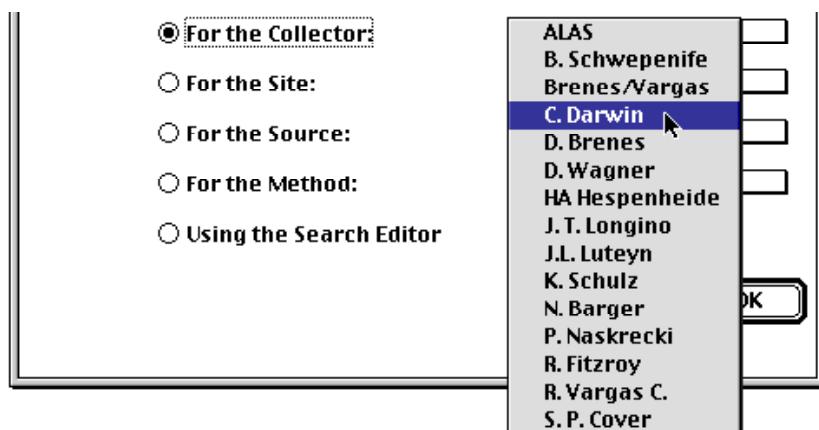
When you click the button, Biota creates a list of all collectors represented in the



database. The first entry from the list (“ALAS” in this case) is displayed in the popup area to the right of the “For the Collector” button to let you know the list has been completed. The rest of the list is hidden in the popup list.

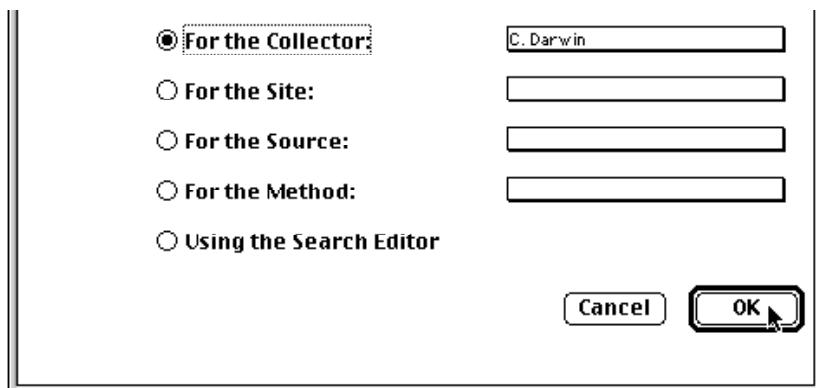
Note: If there are many values, Biota displays the list of values in a scrollable list, instead of a popup menu. See “[Entering Specimen Data: The ‘General’ Tab](#)” in Chapter 11.

7. Click and hold the popup list to the right of the “For the Collector” button to display the list of collectors’ names.



8. Select “C. Darwin” from the popup list (illustrated above).

Biota shows the selected value in the popup area (below).



You can try out the other button and popup lists if you want. No selection is final until you click the “OK” button in the Look Up Collection option window. If you do this, be sure the “For the Collector” button is selected and “C. Darwin” has been selected in the popup before you take the next step.

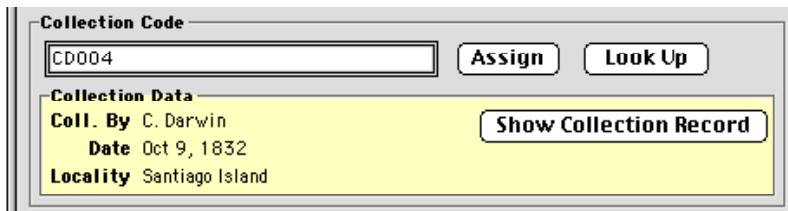
9. Click the “OK” button in the Look Up Collection option window. The Look Up Collection display screen appears, listing all Collection records for “C. Darwin.”

The fourth record is the one you want: Santiago Island on October 9, 1832—but don’t select it just yet.

Look Up Collection						
Sort using the buttons below, then select Collection						4 Records
Locality Code	Collector	Site	Source	Method	Date	Coll. Code
Fernandina	C. Darwin			Shotgun	Sep 30, 1832	CD003
Floreana	C. Darwin			Shotgun	Sep 24, 1832	CD002
SanCristobal	C. Darwin			Shotgun	Sep 19, 1832	CD001
Santiago	C. Darwin			Shotgun	Oct 9, 1832	CD004

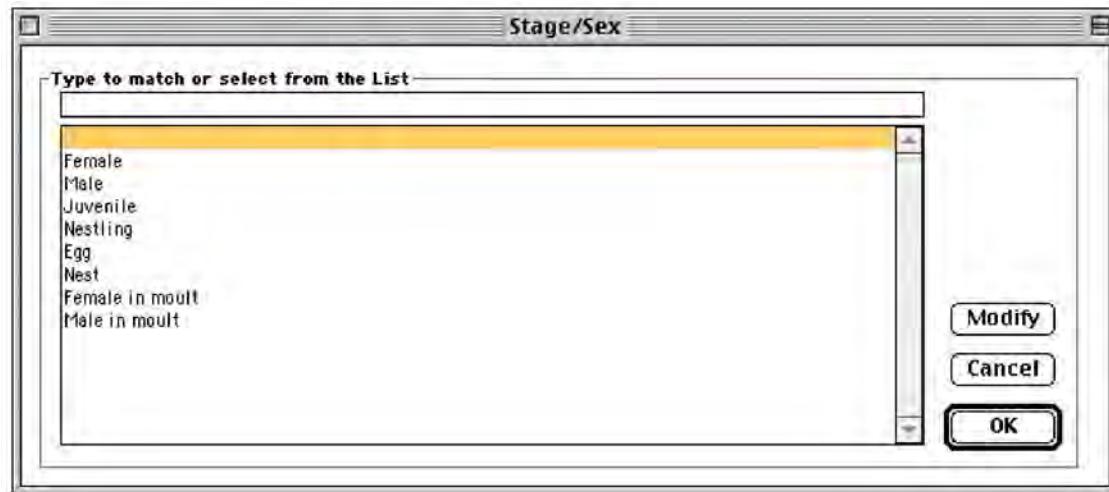
If there were many records in the display screen, you might want to use the Sort buttons at the top of each column to sort the records by the values in that column. Try the “Date” button now.

10. Click the record for Santiago Island, October 9, 1832. The Look Up Collection window is dismissed. The Collection Code for the record you selected is entered in the Specimen record, with additional information about the Collection record you have just linked, displayed in the yellow Collection information panel.



Note: If you want to check the full Collection record, click the “Show Collection Record” button in the Collection Code panel, above, then return to the Specimen Input screen.

The insertion point moves on to the “Stage/Sex” entry area, and an *Entry Choice List* window appears with the title “Stage/Sex.”

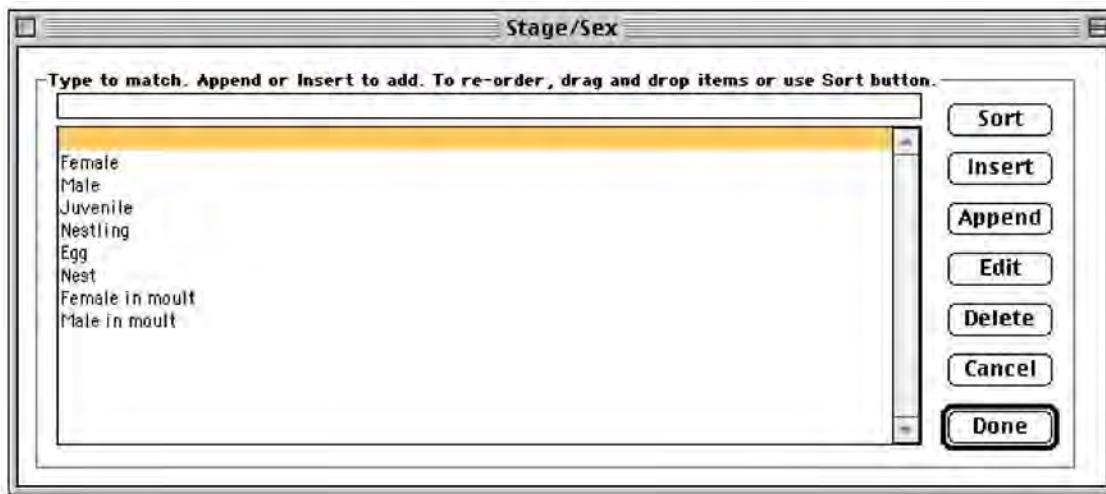


Note: As distributed, the Demo Data File has the List for the [Specimen]StageSex field enabled. If the List does not appear, however, a previous user of the Demo Data File may have disabled it. When you are done with this lesson, choose Entry Choice Lists from the Special menu and enable the List if you like.

Entry Choice Lists are under your control. You can enable or disable a list for most fields (the settings are in “Entry Choice Lists” in the Special menu; see “[Activating or Deactivating Choice Lists](#)” in Chapter 17 for details).

Using the List Editor, you can change the items in the List or the order in which the items displayed.

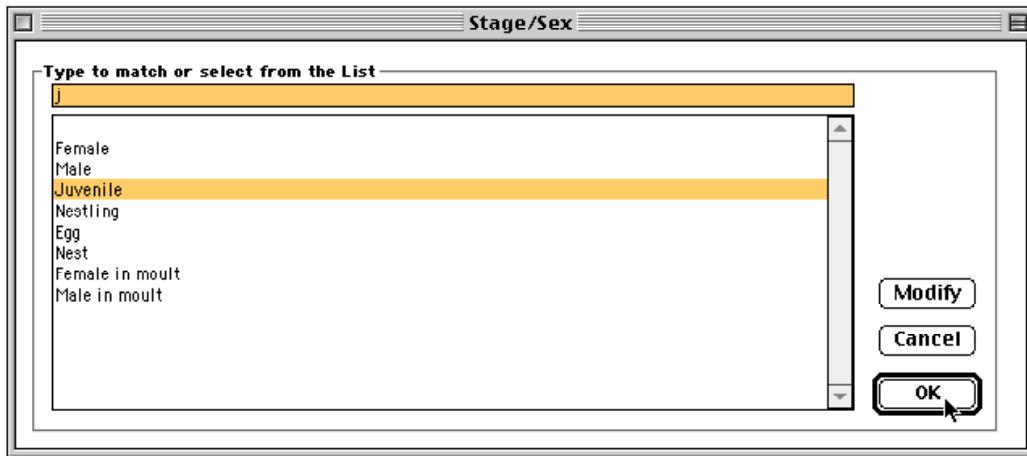
11. To take a look at the List Editor, click the “Modify” button in the Stage/Sex entry choice windows now. A series of editing buttons appears on the right, with brief instructions at the top.



To learn how to use the List Editor, see “[Adding, Deleting, Editing, or Re-ordering Items in a Choice List](#)” in Chapter 17.

Note: You may have noticed that the first item in the Stage/Sex list is blank. Placing a blank item in the first position in the List makes it easy to enter a blank as the default (if that is something you often need to do), or to enter a blank and then change it to an ad hoc entry for which there is no List item. On the other hand, if you don't want blanks or ad hoc entries in your records, don't offer a blank item.

12. Click the “Done” button in the List Editor window. The Editor buttons disappear, but the Stage/Sex Entry Choice List remains. Suppose the Small Tree Finch that Darwin collected was a juvenile of undetermined sex.
13. Type the letter **j** in the “Type to match” entry area at the top of the Stage/Sex Entry Choice List. The entry “Juvenile” is automatically selected in the List, since it is the first (only) entry beginning with the letter **j**.



- 14. Click the “OK” button or press the ENTER key (Windows) or the RETURN key (Mac OS).**

The insertion point moves on to the “Medium” field (intended to record the method of preparation of a physical specimen).



NOTE: To override a Choice List and make a manual entry, click the Cancel button in the Entry Choice List window when it appears, or use the blank entry method outlined in the Note to Step 13.

- 15. Press the TAB key repeatedly, or make any entry followed by TAB if you wish, to move through the fields Storage, Deposited, Specimen Custom 1, Specimen Custom 2, and Type Status.**

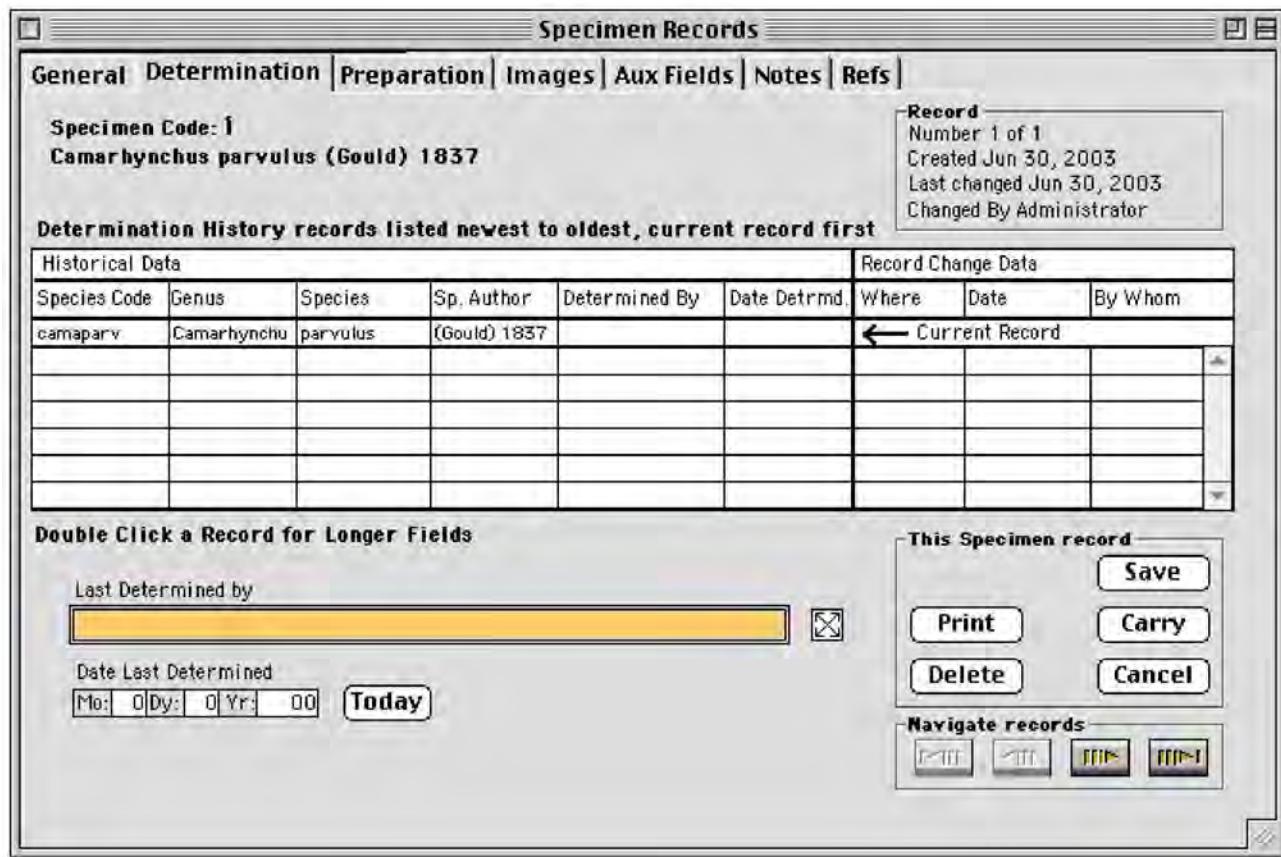
NOTE: Each of the fields you just moved through can be re-named as you require, using the “Core Field Aliases” tool in the Special menu. See Chapter 18, “[Re-Naming Fields](#).” (The “Deposited” field has a special use in the Loans system, however. See “[How Biota Keeps Track of Specimen Loans](#)” in Chapter 21.)

- 16. Press the TAB key again (or make an entry followed by TAB) to move to the “Abundance” field.**

Notice that the Abundance field already has a “1” entered, indicating the default assumption that this record represents a single physical specimen. If, instead, this is a “voucher” record for several specimens (called a “lot” in some disciplines) that share the same Species and Collection data, enter the number of physical specimens that the record represents. If this is a “pseudospecimen” record (see “[Site-Based Species Lists With No Specimens](#)” in Chapter 5), you might want to enter a zero.

17. Press the TAB key again (or make an entry followed by TAB) to leave the “Abundance” field.

The “Determination” tab screen appears, with the insertion point in the “Last Determined By” entry area (highlighted in the illustration below).



(The upper panel in the Determination tab screen will record any future changes in the determinations for this Specimen, if the Determination History system is enabled. See Chapter 22, “[Determination Histories](#).”)

The next step is to record the name of the person who identified this Small Tree Finch specimen. We will pretend that it was last determined by Peter Grant on July 8, 1988.

The “Last Determined By” field of the Specimen table is linked to the Personnel table (notice the double-bordered entry area, which always indicates a link to a parent table).

You could type in the letter *p* to see if “P. R. Grant” appears in pick list, as you did when you entered *cam* in the Species Code entry area to find “camaparv” in Step 3 of this lesson. This time you will use a different method, just to demonstrate it.

18. In the “Last Determined By” entry area, enter @ (the “at” character), then press the TAB key.

All records from the Personnel table are displayed in a choice window. (See next page.)

Last Determined by
@

Personnel Records		
Click buttons to sort records		
Short Name	Last Name	Institution
B. Schwepenife	Schwepenife	CSATS
C. Darwin	Darwin	H. M. S. Beagle
Colwell & Naeem	Colwell & Naeem	UConn & U Minn
D. Lack	Lack	
Darwin & Fitzroy	Darwin & Fitzroy	H. M. S. Beagle
E. Lindquist	Lindquist	Agriculture Canada
HA Hespenheide	Hespenheide	UCLA
INBio	INBio	Instituto Nacional de Biodiversidad
J. T. Longino	Longino	The Evergreen State College
J.L. Luteyn	Luteyn	New York Botanical Garden
Luteyn Mites	Luteyn Mite Collections	University of Connecticut
NYBG	New York Botanical Garden	New York Botanical Garden
P. Naskrecki	Naskrecki	University of Connecticut
P. R. Grant	Grant	Princeton University
R. Colwell	Colwell	University of Connecticut
R. Fitzroy	Fitzroy	H. M. S. Beagle
S. Naeem	Naeem	University of Minnesota
UConn	University of Connecticut	University of Connecticut

This trick works for any linking field (double-bordered entry area). The @ character is Biota's wildcard character.

19. Click the “Last Name” button to sort the list by the “Last Name” (surname) field of the Personnel table.

The list is sorted.



20. Click the entry for “Grant.” The record is entered in the “Last Determined By” entry area of the Specimen record.

The next step is to enter the Date Last Determined.

Last Determined by
P. R. Grant
Date Last Determined
Mo: 7 Dy: 15 Yr: 1988
<input type="button" value="Today"/>

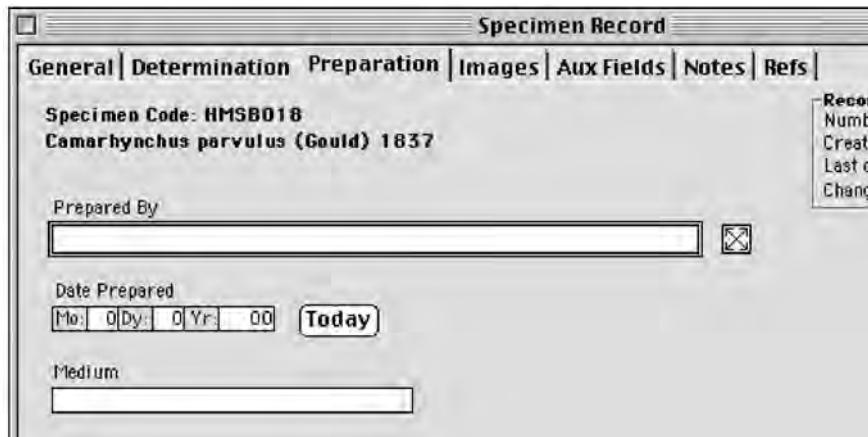
21. Enter 07 in the “Mo” entry area, 15 in the “Dy” area, and 1988 in the “Yr” area.

NOTES:

- a. Do not use the TAB key following each entry. The insertion point moves automatically, as long as you enter 2 digits for month and for day, and 4 for year.
- b. The order of the fields in date entry areas in Biota is determined by the current Control Panel setting in your operating system for Date format. If you have it set to International format, the entry area looks like this instead.
- c. The “Today” button enters the date from your computer’s internal clock.
- d. See “[Dates](#)” in Chapter 9 for complete details on dates in Biota.

Date Last Determined
Mo: 7 Dy: 15 Yr: 1988
<input type="button" value="Today"/>

The “Preparation” tab screen appears, with the insertion point in the “Prepared By” entry area.



(The “Medium” field appears here, as well as on the “General” tab. You can make an entry in either place.)

The next step is to record the name of the person who prepared this Small Tree Finch specimen. We will assume it was done by Darwin himself on some unknown date in 1832.

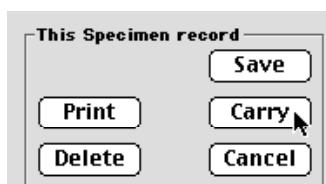
22. Enter “C. Darwin” in the “Prepared By” entry area, and just the year 1832 in the “Yr” entry area. Leave the month and day entry areas blank.

Biota supports *partial dates* (month and year only, or just the year) in the Prepared By or Determined By fields of Specimen records, or in the Collected By field of Collection records.

The record is now complete (for purposes of the Tutorial).

23. Click the “Carry” button in the Specimen Input screen.

Two things happen when you click the “Carry” button. The record you have been working on (HMSB018) is accepted, and Biota displays a new Specimen record with all information except for the Specimen Code “carried over” (copied in) from the record you just completed.



24. Enter **HMSB019** in the Specimen Code entry area of the new record and press the TAB key.

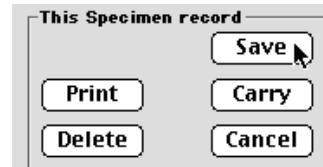
Using the “Carry” button saves time when you are entering a series of records that share information. (You can also click the “Carry” button to use a saved record as a template for a new one; see “[Using an Existing Record as a Template for a New Record](#)” in Chapter 10.)

For the new record HMS019, assume that Darwin also collected a female *Camarhynchus parvulus* on the same day and in the same tree as the juvenile whose record you just completed. Thus only the Stage/Sex field needs to be changed.

25. With the mouse, click in the “Stage/Sex” entry area. The Entry Choice List appears, as in Step 10 above.

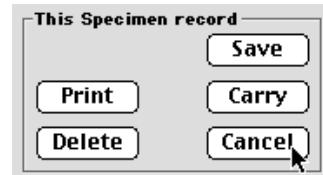
26. Type the letter **f** in the “Type to match” entry area at the top of the Stage/Sex Entry Choice List, then press the ENTER key (Windows) or the RETURN key (Mac OS). “Female” is entered in the record.

27. Click the “Save” button in the Specimen Input screen.
The record is accepted into the Demo Data File and a new, blank Specimen record appears.

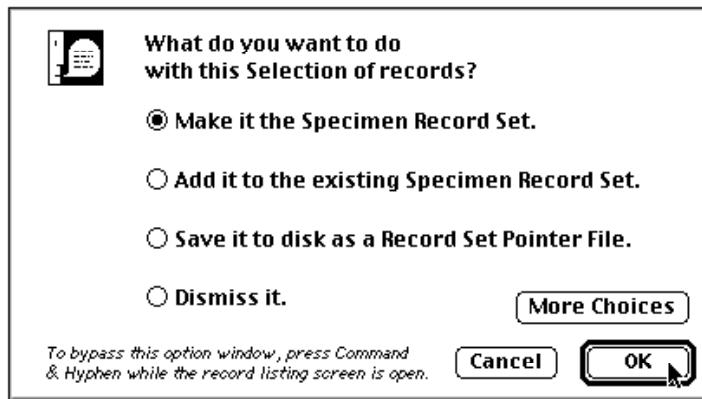


28. Click the “Cancel” button in the Specimen Input screen to dismiss the blank record.

The two records you created appear in the Specimen Record Listing screen.



29. Click the “Done” button in the Specimen Record Listing screen, or press the ENTER key (Windows) or the RETURN key (Mac OS). The Record Code Option window appears.



30. Click the “OK” button in the Record Code Option screen, or press the ENTER key (Windows) or the RETURN key (Mac OS), to accept the default option, “Make it the Specimen Record Set.”

The Specimen Record Listing screen is dismissed and the two records you created are declared the current Specimen Record Set.

NOTE: For all double-bordered (“default”) buttons, like the “Done” button in Record Listing screens and the “OK” button in the Record Set option window, you can always use the ENTER key (Windows) or the RETURN key (Macintosh) to execute the button action, instead of clicking the button with the mouse.

31. From the Display menu, select “Specimen Set.” The Specimen Record Listing screen appears with the two records you created. Once the records are displayed, you can use all the operations for working with records that you have learned.

NOTE: Choosing a command for a Biota table from the Display menu always displays the records in the current Record Set for that table. If the current Record Set is empty, Biota posts a message.

32. **Click the “Done” button in the Specimen Record Listing screen.** The screen is dismissed *without* displaying the Record Set Option window, since these records have already been declared the current Specimen Record Set.

If you had changed the Selection of records after displaying the Record Set (by using the “Sub-Selection” button, the “Add Specimen” button, or by deleting one or more of the displayed records from the database), the Record Set Option window would have appeared.

Lesson 2 Review

In this lesson, you learned how to:

- **Create a Specimen record and link it to a Species Record, to a Collection Record, and to a Personnel record.** The very same techniques apply to creating records for each of Biota’s other tables and to linking them to existing parent records.
- **Use the wildcard entry method** for entering data in linking fields. You used this method to enter the Species Code based on its first few characters, and, later, to display all records from the Personnel table using the @ character.
- **Use a “Look Up” button** to find the right link to a parent table. You used the “Look Up” collection button to find an existing Collection record.

In the Collection Input screen, a “Look Up” Locality button for linking Collection records to Locality records works just like the “Look Up” Collection button you learned about in this lesson.

There is also a “Look Up” Species button in the Specimen Input screen for finding an existing Species record. When you click it, Biota asks for the Genus of the Species you are looking for, then displays all Species records for that Genus in the selection window. You will use this tool in the next lesson.

- **Use an Entry Choice List** to enter data in a field. You can set Entry Choice Lists for many fields in Biota, or have Biota enter a particular value in a field automatically (not demonstrated in the lesson; see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Use the “Carry” button** to accept a record, then use that record as a template for the next new record.
- **Use the “Save” button** to accept a new, single record.
- **Create and display a Record Set.**

For a comprehensive treatment of special features of particular Input screens consult Chapter 8, “[Record Codes](#),” Chapter 9, “[Special Data Types](#),” and Chapter 11, “[Input Table by Table](#).”

Lesson 3. Creating New Records “On the Fly”

In Lesson 2, you learned to link new records to related records in a parent table. The Species, Collection, and Personnel records to which you linked the new Specimen records were, conveniently, already in the Data File. Often, of course, this will not be the case.

When entering a new record or editing an existing one, it is often necessary to create a new record in a parent table. This lesson teaches you how to use Biota’s ability to do this “on the fly” as you create or edit the primary record.

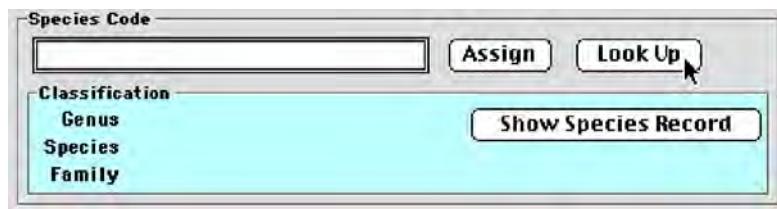
Step by Step

- From the Input menu, choose “Specimen.”** The Specimen Input screen appears. You are going to add a new record to the Demo Data File for yet another fictitious specimen from Darwin’s visit to the Galápagos Islands.
- Enter **HMSB020** in the Specimen Code entry area and press the TAB key.** The insertion point moves to the Species Code entry area.

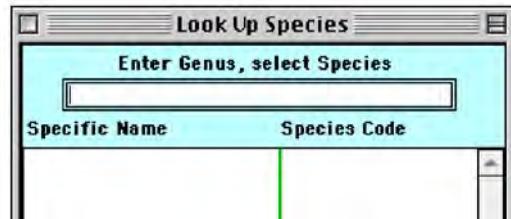
NOTE: If you get an error message indicating that this record already exists, see the Note at [Step 2 in Lesson 1](#).

Let’s say this is a specimen of the Charles Mockingbird, *Nesomimus trifasciatus*, collected by Darwin on Floreana Island (Charles Island, in Darwin’s time) on September 24, 1832.

- To find out if there is already a record for this Species in the database, click the “Look Up” button in the Species Code panel of the Specimen Input screen.**

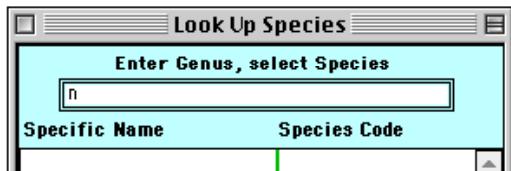


The Look Up Species selection window appears.



You use this tool by entering a Genus name—or the first part of a Genus name using the wildcard method—in the entry area at the top of the window, then press TAB. Biota then looks in the Genus table for matching entries.

- If Biota finds only one match among Genus records, all Species records linked to that Genus record are displayed in the lower panel. You click the one you are looking for to enter it in the Specimen record.
 - If Biota finds more than one match among Genus records, the list of candidates is displayed, as you will see in the next step.
4. Enter the letter “n” in the Genus entry area of the “Look Up Species” window and press TAB.



A list of 5 genera that begin with the letter “n” is displayed, including *Nesomimus*.

Genus Records	
Click buttons to sort records	
Genus	Family
Neoconocephalus	Tettigoniidae
Neocrex	Rallidae
Nesomimus	Mimidae
Notopora	Ericaceae
Nyctanassa	Ardeidae

5. Click the entry for **Nesomimus** in the list of genera (see above). The “Look Up Species” window now shows three Species records for *Nesomimus* species.
If the species you were looking for were here, you would click its name to enter it in

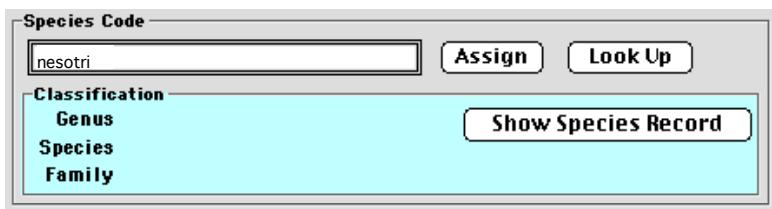
Look Up Species	
Enter Genus, select Species	
Nesomimus	
Specific Name	Species Code
macdonaldi	nesomacd
melanotis	nesomelan
parvulus	nesoparv

the Specimen record. But, clearly, *trifasciatus* is not yet in the database.

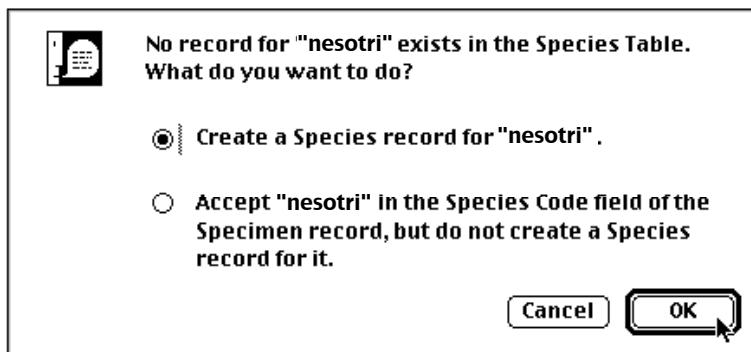
6. Click the “Cancel” button in the Look Up Species window since the record you seek is not listed. You will need to create a new Species record for *N. trifasciatus*.



7. Type “nesotri” in the Species Code entry area of the Specimen Input screen and press TAB.

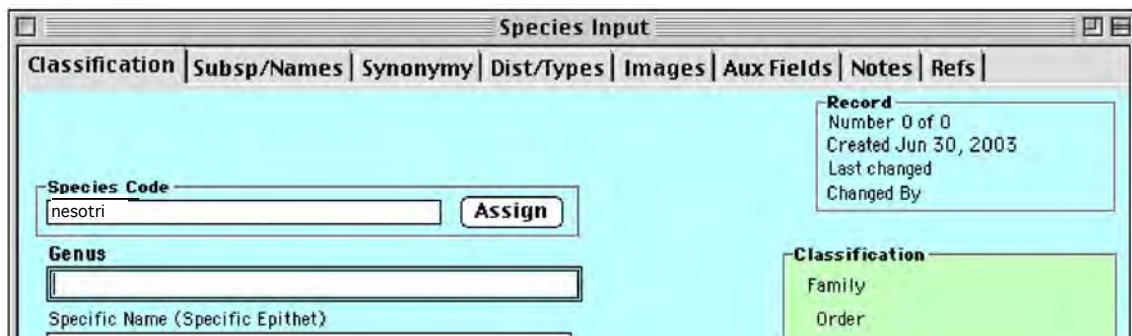


The new record option window appears.

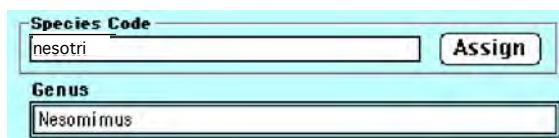


8. With the first (default) option selected, click the “OK” button in the new records option window (illustrated above).

The Species Input screen appears, with the new Species Code already entered, and the insertion point blinking in the Genus entry area.



9. In the Genus entry area, type “nes” and press TAB. The wildcard entry system completes the entry for *Nesomimus*, since no other Genus name in the database starts with *nes*.

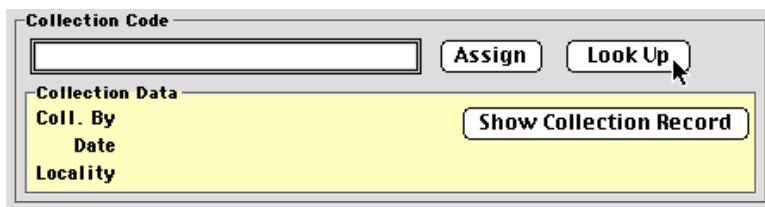


NOTE: If the genus record had not existed, you could create a new one “on the fly,” just as you are in the process of doing for a new Species record. In fact, you could create new records all the way to Kingdom this way, Saving each as you work your way back down.

10. In the Specific Name entry area, type “trifasciatus” and press TAB.
11. Click the “Save” button in the Species Input screen. The Species Input screen is dismissed and you return to the Specimen record in progress.

Genus
Nesomimus
Specific Name (Specific Epithet)
trifasciatus

- NOTE:** If you click the “Cancel” button in the Specimen Input screen now, instead of clicking the “Save” button, the Species record you just created will nonetheless remain in the database.
12. Click the “Look Up” button in the Collection Code panel of the Specimen Input screen to find and enter the Collection Code for the record of Darwin’s collections on Floreana Island for September 24, 1832. If you need help, refer to [Steps 5–10 in Lesson 2](#).



13. In the “Stage/Sex” input area, record the specimen as “Female.”
14. Save the Specimen record.
15. Click the “Done” button in the Specimen Record Listing screen and dismiss the Record Set option screen.

Lesson 3 Review

This lesson covered the creation of new records and how to link them to parent records that you create “on the fly.” In this lesson, you learned how to:

- **Find out if a parent record already exists.** You did this for a Species record from the Specimen Input screen, using the Look Up Species tool.
For higher taxa (e.g., to see whether a Family record exists when you need to link a new Genus record), just enter the first few letters of the name you seek (or @ for all records) and press TAB. Biota will complete the entry if there is just one match, list all candidates if there are several matches, or post a message if nothing matches.
- **Create a new parent record when you need one.** Just enter the new name. Biota gives you the option of displaying the parent record Input screen.

For a comprehensive treatment of special features of particular Input screens consult Chapter 8, “[Record Codes](#),” Chapter 9, “[Special Data Types](#),” and Chapter 11, “[Input Table by Table](#).”

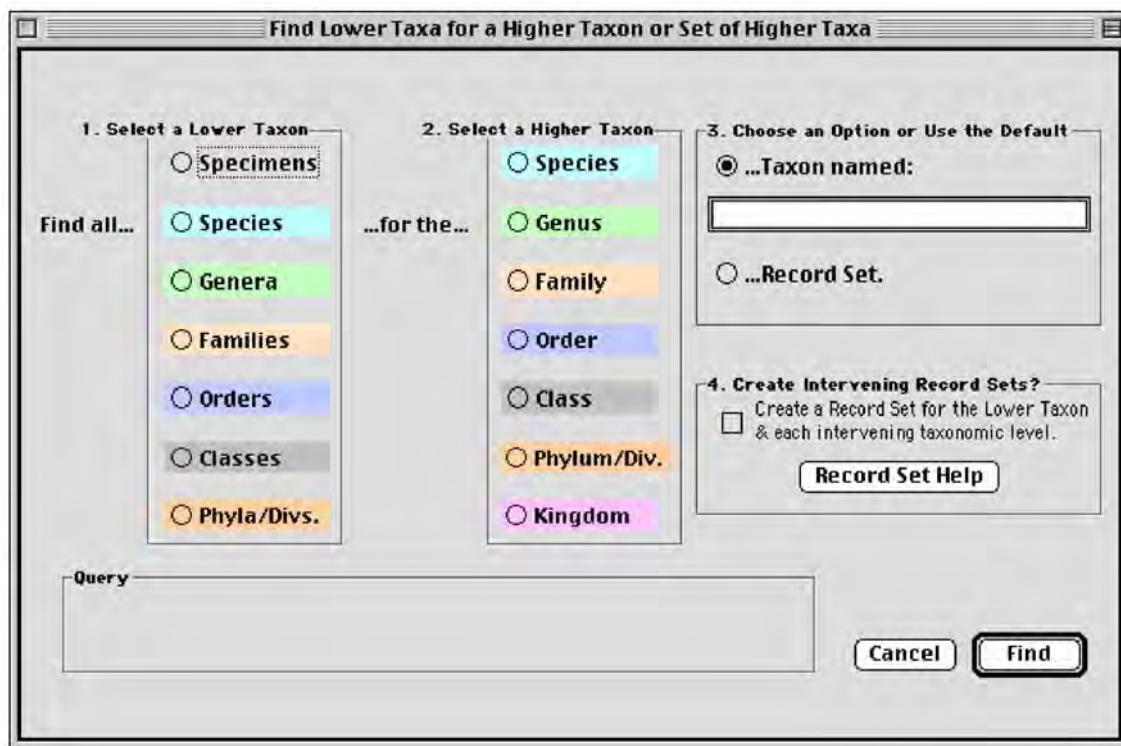
Lesson 4. Finding Records (Queries)

In Lesson 1, you learned how to display all the records for a Biota table by using the “All...” commands from the File menu. In a large database, however, displaying all records is not a very efficient way to find a record.

In this lesson, you will learn two very efficient ways to find records using tools from the Find menu. You will: (1) find records in a table in the taxonomic hierarchy based on a record or records in a higher table, and (2) find records in the place hierarchy (Collection and Locality tables), based on a Species Record Set. Chapter 12, “[Finding and Updating Records](#),” provides a comprehensive reference for Biota’s search and update capabilities, only some of which can be covered in this tutorial.

Step by Step

1. From the Find menu, choose “Lower Taxa for Higher Taxa.” The query setup screen appears.



You will use this tool to find all Species records for the Family Fringillidae (finches) present in the database.

2. In the list of tables in the left panel (the panel labeled “1. Select a Lower Taxon”), click the “Species” button. This is called the *target table*—the table containing the records you seek.

The “Query” panel displays the beginning of the query at the bottom of the screen.

The screenshot shows a window titled 'Query' containing the text 'Find all Species for the ...'. The text is in a black font on a white background, with the first few words of the query underlined in blue.

3. In the list of tables in the right panel (the panel labeled “2. Select a Higher Taxon”), click the “Family” button—the button for the table to be used in the selection criterion (the *criterion table*).

The screenshot shows two panels side-by-side. The left panel, titled '1. Select a Lower Taxon', contains radio buttons for 'Specimens', 'Species' (which is selected), 'Genera', 'Families', 'Orders', 'Classes', and 'Phyla/Divs.'. The right panel, titled '2. Select a Higher Taxon', contains radio buttons for 'Species' (selected), 'Genus', 'Family' (selected), 'Order', 'Class', 'Phylum/Div.', and 'Kingdom'. Below these panels is another 'Query' panel with the text 'Find all Species for the Family'.

The word “Family” is added to the Query.

4. In the entry area beneath the button labeled “...Family named,” type “fri” and press the TAB key. (The entry area is in the upper-right corner of the screen.)

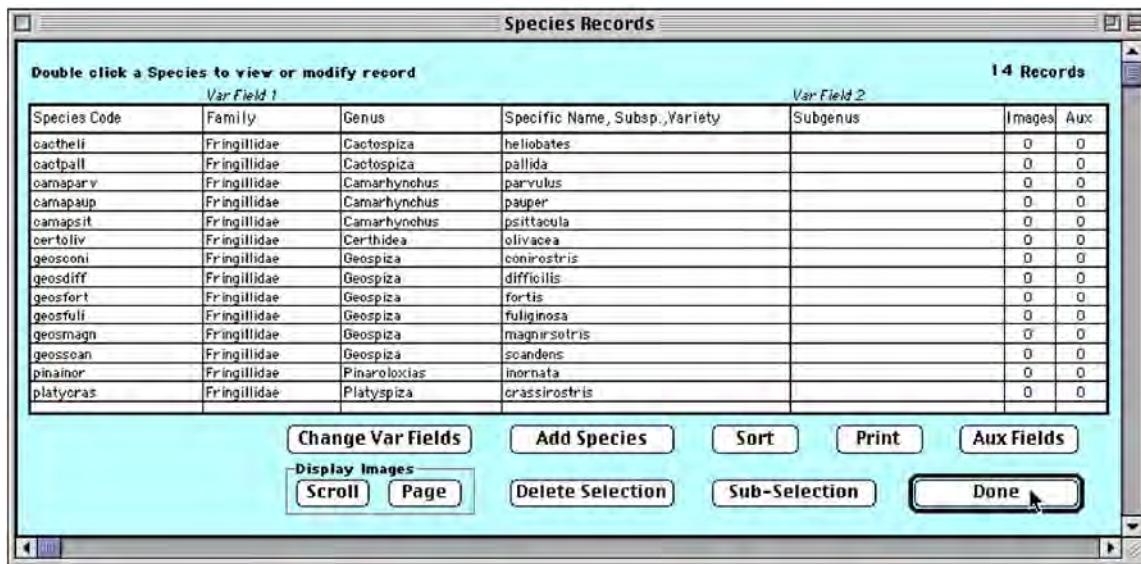
Notice that, instead of entering a Family name, you could have clicked the lower button in the panel to use a Family record set as a search criterion.

Biota completes the entry so that it reads “Fringillidae,” and completes the query to read “Find all Species for the Family Fringillidae.”

The screenshot shows a panel titled '3. Choose an Option or Use the Default'. It contains a radio button labeled '...Family named:' followed by a text input field containing the text 'fri'. Below this is another radio button labeled '...Family Record Set.'

The screenshot shows the 'Query' panel with the text 'Find all Species for the Family Fringillidae.' The 'Find' button is highlighted with a red box and a cursor arrow pointing to it. There are also 'Cancel' and 'Help' buttons.

5. Click the “Find” button to launch the search (above). The 14 Species records for the Family Fringillidae (including species of six different genera) are displayed in the Species Record Listing screen.



The screenshot shows a software window titled "Species Records". At the top, it says "Double click a Species to view or modify record". Below this, there is a table with two columns: "Var Field 1" and "Var Field 2". The "Var Field 1" column contains Species Codes like "caetheli", "caetpall", "camaparv", etc. The "Var Field 2" column contains detailed information such as Family (Fringillidae), Genus (Cactospiza, Cactospiza, Camarhynchus, etc.), Specific Name, Subsp., Variety, Subgenus, Images, and Aux. A total of "14 Records" are listed. At the bottom of the window are several buttons: "Change Var Fields", "Add Species", "Sort", "Print", "Aux Fields", "Display Images", "Scroll", "Page", "Delete Selection", "Sub-Selection", and "Done". The "Done" button is highlighted with a mouse cursor.

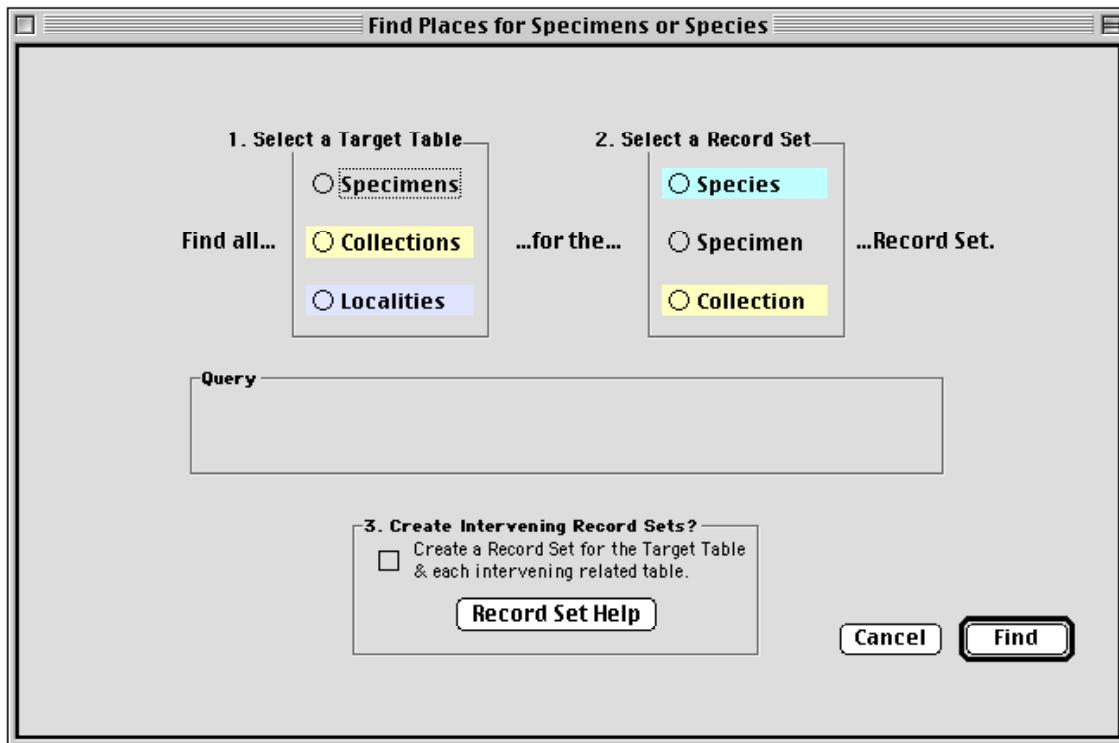
6. Click the “Done” button in the Species Record Listing screen, then click the “OK” button in the Record Set option screen to make these records the current Species Record Set.

In the next group of steps, you will use this Species Record Set to find all Localities linked to these Species records.



Notice that the target and criterion tables in the search just completed are not adjacent in the hierarchy (the Genus table lies between the Species and Family tables). The Record Set you just declared could not be made easily or directly by finding the Family record for Fringillidae, then clicking the “Genera” (Child) record button. Child record buttons are limited to finding groups of records that share a single parent record.

- From the Find menu, choose “Places for Specimens or Species.” The query setup screen appears.

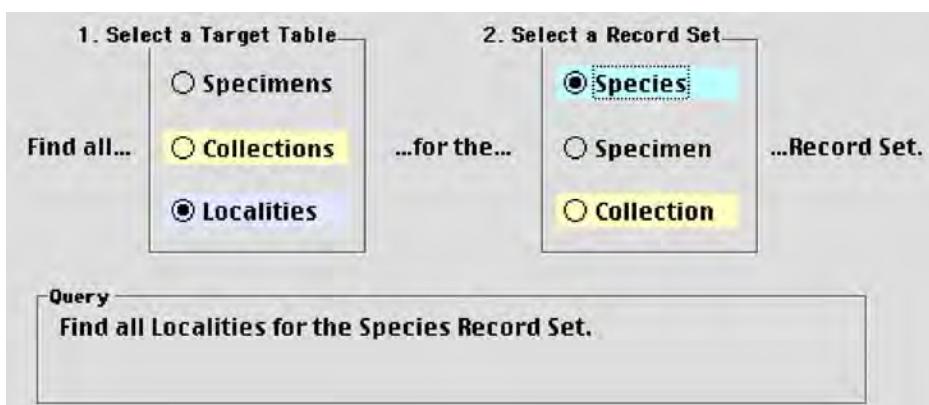
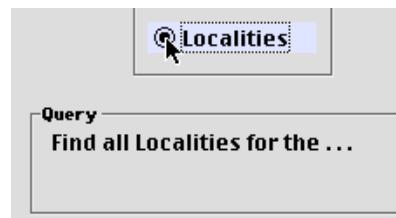


You will use this tool to find all Specimen records linked to the finch Species Record Set, all the Collection records linked to those Specimen records, and all the Locality records linked to those Collection records—all at once.

- In the list of tables in the left panel (the panel labeled “1. Select a Target Table”), click the “Localities” button.

The Query panel displays the beginning of the query.

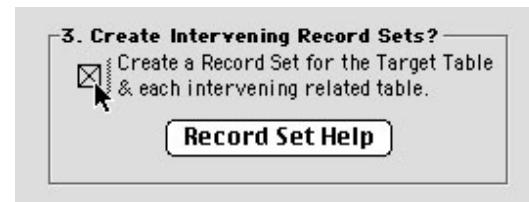
- In the list of tables in the right panel (the panel labeled “2. Select a Record Set”), click the “Species” button.



The Query panel completes the query, “Find all Localities for the Species Record Set.”

- In the panel labeled “Create Intervening Record Sets?” click the checkbox, to set it.

When you set this option, Biota creates Record Sets automatically for the target table records and for the linking records in any intervening tables—in this case, for the Specimen and Collection tables (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).



As you learned earlier in this lesson with the “Lower Taxa for Higher Taxa” tool (which has an identical checkbox), it is not *necessary* to check this option in order to find the target table records you are searching for, nor in order to create a Record Set for them.

- Click the “Find” button to launch the search.

Four Locality records (for four Galápagos Islands) are displayed in the Locality Record Listing screen. Because you checked the checkbox, they have already been declared the Locality Record Set. These are the Localities for Collections of Specimens representing Species in the Species Record set.



Locality Records									
Double click a Locality to view or modify record									
									4 Records
Locality Code	Locality Name	District	Var Field 2	Var Field 3	Var Field 4	Elev	Latitude	Longitude	Img Aux
Fernandina	Fernandina Island		Galápagos Islands	Ecuador			00°26'S	091°30'W	0 0
Floreana	Floreana Island		Galápagos Islands	Ecuador			01°17'S	090°26'W	0 0
SanCristobal	San Cristóbal Island		Galápagos Islands	Ecuador			00°50'S	089°25'W	0 0
Santiago	Santiago Island		Galápagos Islands	Ecuador			00°14'S	090°45'W	0 0

Buttons at the bottom include: Change Var Fields, Add Locality, Sort, Print, Aux Fields, Display Images, Scroll, Page, Delete Selection, Sub-Selection, and Done.

- Without closing the Locality Record Listing screen, select “Specimen Set” from the Display menu. The Specimen Record Listing screen shows the Record Set you just created for all finch Specimen records (including the ones you created in earlier lessons, if you did not delete them).
- Without closing the Locality or Specimen Record Listing screens, select “Collection Set” from the Display menu. The Collection Record Listing screen shows the Record Set you just created for all Collections for the Specimens in the Specimen screen.
(Notice that Biota can open as many simultaneous windows as your computer’s memory can support.)
- Open a few Locality and Collection records to see what the Input screens and their tabs look like, then close them with the “Cancel” button.

15. Click the “Done” buttons in all three Record Listing screens to close them (or use the keyboard shortcut,

Lesson 4 Review

In this lesson, you learned how to:

- **Find records in a table in the taxonomic hierarchy based on a record or records in a higher table.**

You may have noticed in the Find menu that there is an “opposite” tool, “Higher Taxa for Lower Taxa.” It works the same way in reverse (but requires a lower taxon Record Set to be established first). You could use it, for example, to find all Order records that are linked through intermediate tables to a set of Specimen records.

- **Find records in the place hierarchy (Collection and Locality tables), based on a Species Record Set.** You can use the same tool to find records based on other combinations spanning this series of linked tables.

Again, the Find menu offers an “opposite” tool, “Specimens or Species for Places.” It works for the same table combinations, but in reverse order. You could use it, for example, to find all Species records linked through intermediate tables to a set of Locality records.

If you do this based on the Locality set you just created, for example, it will yield not only the finch Species records you started with, but also the Species record for the mockingbird *Nesomimus trifasciatus* that you created in Lesson 3—a nice demonstration of why *both* tools are needed.

- **Create Record Sets automatically for the target table and all intervening tables.** This capability enables you to create linked subsets of your data for several tables at once (for export, for example).

On Your Own—What to Try Next

The lessons in this tutorial have covered many important features of Biota, but there are just as many others you will eventually want to learn about. Here are a few suggestions for next steps on your own.

- **Learn to use the Query Editor.** From the Find menu, choose “Using the Query Editor.” Then see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12, for instructions.
- **Learn to use Record Set Pointer Files.** Read or review “[Record Set Pointer Files](#)” in Chapter 3.
- **Learn how to print or export labels.** Choose a section of Chapter 14, “[Printing Labels](#),” that is relevant to your work.
- **Learn how to create and use Auxiliary Fields and Projects,** in Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).” This feature enables you to create an unlimited number of special fields that you can name as you like, for the Species, Specimen, Collection, or Locality tables.
- **Learn how to customize Biota** by setting preferences, changing the displayed names of fields, adding Choice Lists and default entries, or setting up Record Code Prefixes. See Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#),” Chapter 18, “[Re-naming Fields](#),” and Appendix B, “[Setting Preferences](#).”

- Scan Chapter 4, “[Biota Menus and Menu Items: An Annotated Guide](#)” and/or Chapter 5, “[Overview of Biota’s Tools and Features](#)” for additional items that interest you or solve a problem, and use the links there to find the relevant section of the manual.

PART
2

Entering Data

Chapter 7 Overview of Record Input Screens

Each Core Table (See “[Core Tables](#)” in Chapter 3) in Biota has a screen for listing records (the record Listing screen) and a screen for entering and displaying data for a single record (the record Input screen). This chapter outlines conventions and shortcuts common to Input screens throughout Biota. Details of particular Input screens appear in Chapter 11, “[Input—Table by Table](#).”

Screen Colors

Each of the 14 Core Tables has been assigned its own characteristic screen color, to help you navigate the database. All record Input and Listing screens associated with a particular table share the same background color.

If an Input screen for one table contains information from a linked table, the information from the linked table appears in a panel displaying the table color for the linked table. For example, in the Specimen Input screen below (gray, the default color for the Specimen table), classification information appears in a pale blue panel (the Species table color), whereas collection data are shown in a pale yellow panel (the Collection table color).

The screenshot shows the "Specimen Record" input screen. At the top, there is a navigation bar with tabs: General, Determination, Preparation, Images, Aux Fields, Notes, and Refs. The General tab is selected. Below the tabs are several data entry fields:

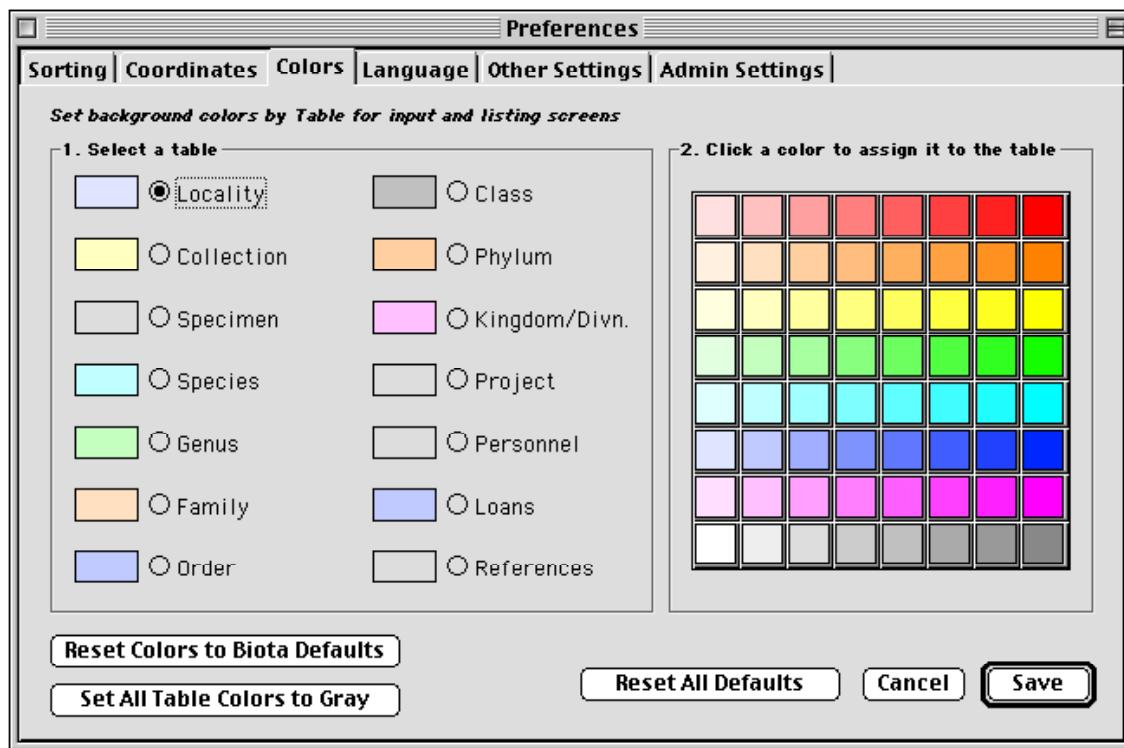
- Specimen Code:** A text field containing "JLL10108" with an "Assign" button to its right.
- Species Code:** A text field containing "plurigi" with "Assign" and "Look Up" buttons to its right.
- Classification:** A panel with a light blue background. It displays:
 - Genus:** Plutarchia
 - Species:** rigida (Benth.) A.C. Smith
 - Family:** EricaceaeA "Show Species Record" button is located at the bottom of this panel.
- Collection Code:** A text field containing "JLL10108" with "Assign" and "Look Up" buttons to its right.
- Collection Data:** A panel with a light yellow background. It displays:
 - Coll. By:** J.L. Lutelyn
 - Date:** May 5, 1984
 - Locality:** Mcpio. SilvaA "Show Collection Record" button is located at the bottom of this panel.
- Stage/Sex:** A text field containing "Fl-Pickled" with a "Storage" section to its right, which includes fields for "JLL Lab" and "NYBG".
- Medium:** A text field containing "FAA" with a "Deposited" section to its right, which includes fields for "NYBG" and "NYBG".

On the right side of the screen, there is a vertical column of buttons and status indicators:

- Record:** Displays "Number 1 of 1", "Created Oct 23, 1992", "Last changed", and "Changed By".
- Specimen Custom 1:** An empty text field with a clear button.
- Specimen Custom 2:** An empty text field with a clear button.
- Type Status:** An empty text field with a clear button.
- Abundance:** A numeric field containing the value "1".
- This Specimen record:** A group of buttons: "Save", "Print", "Carry", "Delete", and "Cancel".
- Navigate records:** A set of five small icons for navigating between records.

To Change the Screen Color Scheme

1. To change the screen color scheme, choose Preferences from the Special menu, then click the Colors tab.

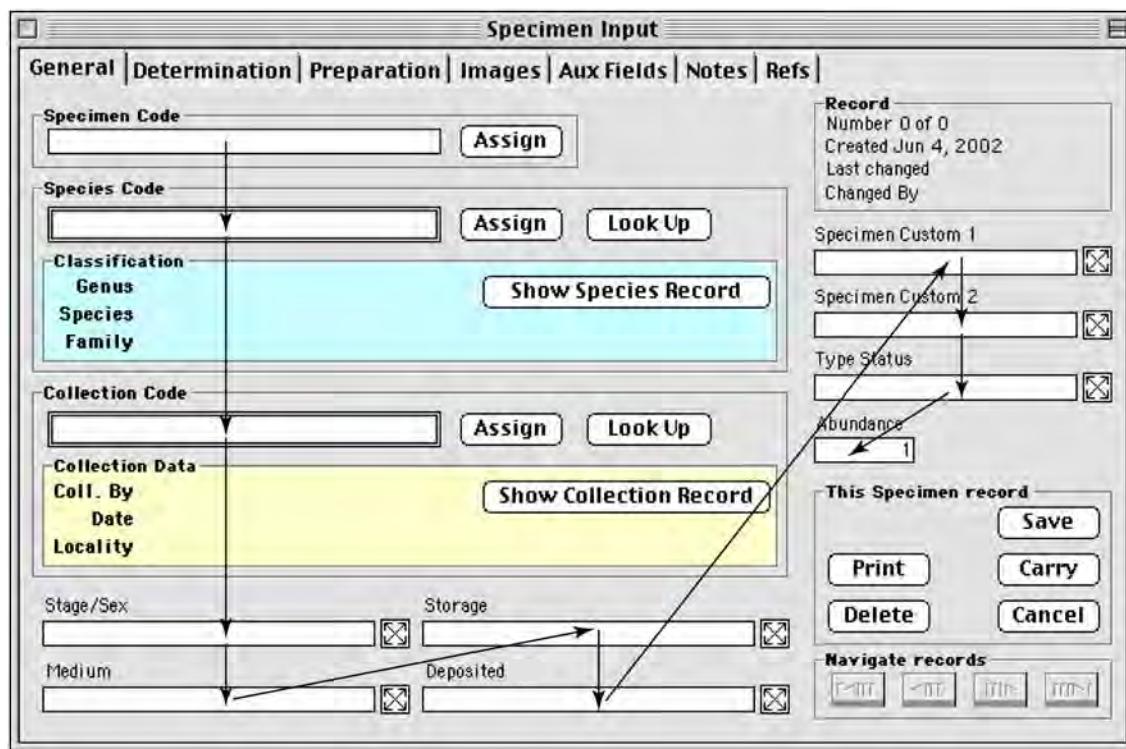


- To set all table colors to Microsoft gray, click the “Set All Table Colors to Gray” button and skip the rest of the steps below.
- To reset all table colors to Biota defaults, click the “Reset Table Colors to Biota Defaults” button and skip the rest of the steps below.
2. Using the radio buttons on the left, select the Core Table color you want to change.
3. In the color palette on the right, click the color you want to assign to the selected table.
4. Repeat Steps 2 and 3 for any other changes you want to make.
5. Click the “Save” button.

NOTE: You can also control the table colors that the onboard Biota Web server uses in Database Client Mode. See “[The Database Client Tab](#)” in Chapter 30.

Entry Areas and Default Entry Order

In all Biota Input screens, you enter data in a series of white, empty boxes (entry areas). For each Input screen, there is a default entry order. Once you have made an entry, you can press the TAB key to move on to the next entry area in the default order. Arrows show the default entry order for the Specimen Input screen, below.



At any time, you can override the default entry order and move directly to any entry area on an Input screen, using the mouse. When you click in another area, the entry in the field you just left is registered, whether or not you first pressed the TAB key.

All entries can be edited using standard screen-editing techniques. For example, an entry can be changed by selecting characters with the mouse and cursor or selecting an entire entry area with a double click, then typing in the new information. If you change an entry, but have not yet pressed the TAB key or clicked in another field, you may select Undo from the Edit menu to restore the previous entry.

Input Screen Tabs and Buttons

Input Screen Tabs

Information on Input screens for many Biota Core Tables are arranged on tabs. From left to right across the top of an Input Screen, tabs particular to that table appear first, with tabs common to several tables following.

In the example below, from the Species Input Screen, the first four tabs (Classification, Subsp/Names, Synonymy, and Dist/Types) appear only for the Species table, whereas the Images, Aux Fields, Notes, and Refs tabs are found in the Input screens for the Specimen, Collection, and Locality tables as well. Notice that, for each of these last four tabs, the number of linked records appear in parentheses after the tab name.



Keyboard Shortcuts for Input Screen Tabs

To avoid using the mouse, you can use keyboard shortcuts to move between tabs in the Input screens for Biota Core tables. The first table below shows the shortcuts that apply to several Core Tables, and the second table below displays shortcuts that apply only to a particular Core Table or Input screen. (See also the next section in this chapter, “[Keyboard Shortcuts for Input Screen Buttons](#),” and “[Keyboard Shortcuts for Record Listing Screens](#)” in Chapter 10, summarized in Appendix C, “[Keyboard Shortcuts](#).”)

FUNCTION	MAC OS	WINDOWS
General tab	COMMAND–G (⌘–G)	CTRL–G
Images tab	COMMAND–I (⌘–I)	CTRL–I
Aux Fields tab	COMMAND–M (⌘–M)	CTRL–M
Notes tab	COMMAND–N (⌘–N)	CTRL–N
Refs tab	COMMAND–R (⌘–R)	CTRL–R

FUNCTION	MAC OS	WINDOWS
<i>Specimen Input screen</i>		
Determination tab	COMMAND–D (⌘–D)	CTRL–D
Preparation tab	COMMAND–B (⌘–B)	CTRL–B
<i>Specimen & Collection (combined) Input screen</i>		
Specimen tab	COMMAND–G (⌘–G)	CTRL–G
Collection tab	COMMAND–H (⌘–H)	CTRL–H
Determination tab	COMMAND–D (⌘–D)	CTRL–D
Preparation tab	COMMAND–B (⌘–B)	CTRL–B
<i>Specimen Series Input screens</i>		
Primary Fields tab	COMMAND–G (⌘–G)	CTRL–G
Other Fields tab	COMMAND–H (⌘–H)	CTRL–H
<i>Species Input screen</i>		
Classification tab	COMMAND–G (⌘–G)	CTRL–G
SubSp/Names tab	COMMAND–H (⌘–H)	CTRL–H

Synonymy tab	COMMAND–B (⌘–B)	CTRL–B
Dist/Types tab	COMMAND–D (⌘–D)	CTRL–D
<i>Collection Input screen</i>		
Host record tab	COMMAND–H (⌘–H)	CTRL–H
Georeference tab	COMMAND–B (⌘–B)	CTRL–B
<i>Locality Input screen</i>		
Georeference tab	COMMAND–B (⌘–B)	CTRL–B
<i>Personnel Input screen</i>		
Create/Edit Group tab	COMMAND–R (⌘–R)	CTRL–R
Create/Edit Note tab	COMMAND–N (⌘–N)	CTRL–N
<i>Project Input screen</i>		
Auxiliary Fields Set tab	COMMAND–M (⌘–R)	CTRL–M
<i>Reference Input screen</i>		
Reference tab	COMMAND–R (⌘–R)	CTRL–R
Links tab	COMMAND–L (⌘–L)	CTRL–L
<i>Loan Input and Loan Return screens</i>		
Loan tab	COMMAND–L (⌘–L)	CTRL–L
Returns tab	COMMAND–R (⌘–R)	CTRL–R

Keyboard Shortcuts for Input Screen Buttons

Keyboard shortcuts are available for most Input screen buttons. (The exceptions are the “Delete” button and a few others that have far-reaching consequences. These require use of the mouse, for safety’s sake.) The table below lists button shortcuts that apply to record Input screens for several tables. (See also the previous section in this chapter, “[Keyboard Shortcuts for Input Screen Tabs](#)”, and “[Keyboard Shortcuts for Record Listing Screens](#)” in Chapter 10, summarized in Appendix C, “[Keyboard Shortcuts](#).”)

FUNCTION	MAC OS	WINDOWS
Any default button (double border), regardless of function	RETURN (⌘–RETURN)	ENTER
“Cancel” button	COMMAND–RETURN (⌘–RETURN)	CTRL–ENTER
“Save” button	COMMAND–S (⌘–S) or COMMAND–J (⌘–J)	CTRL–S or CTRL–J
“Carry” button	COMMAND–K (⌘–K)	CTRL–K
“Print” button	COMMAND–P (⌘–P)	CTRL–P
Next record button 	COMMAND–RIGHT ARROW (⌘–RIGHT ARROW)	CTRL–RIGHT ARROW

Previous record button		COMMAND–RIGHT ARROW (⌘–RIGHT ARROW)	CTRL–RIGHT ARROW
Show parent record button (e.g., “Show Genus” Record on the Species Input screen)		COMMAND–UP ARROW (⌘–UP ARROW)	CTRL–UP ARROW
Show child record(s) button (e.g., “Show Specimens” on the Species Input screen)		COMMAND–DOWN ARROW (⌘–DOWN ARROW)	CTRL–DOWN ARROW
First “Assign” button on a screen		COMMAND–EQUALS (⌘–=)	CTRL–EQUALS (=)
Second “Assign” button on same screen		OPTION–EQUALS (OPTION–=)	ALT–EQUALS (=)
Third “Assign” button on same screen		COMMAND–OPTION–EQUALS (⌘–OPTION–=)	CTRL–ALT–EQUALS (=)
First “Look Up” button on a screen		COMMAND–L (⌘–L)	CTRL–L
Second “Look Up” button on same screen		OPTION–L	ALT–L
First “Today” button on a screen		COMMAND–T (⌘–L)	CTRL–T
Second “Today” button on same screen		OPTION–T	ALT–T
Dismiss screen (without saving; same as “Cancel” button, for Input screens)		COMMAND–HYPHEN (⌘–HYPHEN)	CTRL– HYPHEN

The following table lists shortcuts that apply to only a particular Input screen or tab.

FUNCTION	MAC OS	WINDOWS
<i>Image tab (Specimen, Species, Collection, and Locality Input screens)</i>		
“Zoom” (first image) button	COMMAND–E (⌘–E)	CTRL–E
“Zoom 4” (first 4 images) button	COMMAND–F (⌘–F)	CTRL–F
“Save” image button	COMMAND–Y (⌘–Y)	CTRL–Y
<i>Notes tab (Specimen, Species, Collection, Locality and Loans Input screens)</i>		
“New Note” button	COMMAND–T (⌘–T)	CTRL–T
“Save Note” button	COMMAND–Y (⌘–Y)	CTRL–Y
<i>Reference tab (Specimen, Species, Collection, and Locality Input screens)</i>		
“New Reference” button	COMMAND–T (⌘–T)	CTRL–T
“Link Reference” button	COMMAND–L (⌘–L)	CTRL–L
<i>Specimen Input screen</i>		
“Show Species Record” button (first parent record button)	COMMAND–UP ARROW (⌘–UP ARROW)	CTRL–UP ARROW

“Show Collection Record” button (second parent record button)	OPTION-UP ARROW	ALT-UP ARROW
<i>Input & Identify Specimen Series screen</i>		
“Show Species Record” button (first parent record button)	COMMAND-UP ARROW (⌘-UP ARROW)	CTRL-UP ARROW
“Show Collection Record” button (second parent record button)	OPTION-UP ARROW	ALT-UP ARROW
<i>Loan Input and Loan Return screens</i>		
“Add More Specimens” button	COMMAND-J (⌘-J)	CTRL-J
“Reprint Loan Form” button	COMMAND-P (⌘-P)	CTRL-P
“List Specimens” button	COMMAND-DOWN ARROW (⌘-DOWN ARROW)	CTRL-DOWN ARROW

Entering Data in Linking Fields

For most Biota tables, the record Input screen includes entry areas that link the table with a related table. These special *linking fields* (see “[Linking Fields: Parent and Child Records](#)” in Chapter 3) consistently appear with a double-bordered data entry area in all Biota Input screens (for example, the fields for Species Code and Collection Code in the Specimen Input screen, a portion of which is shown below).

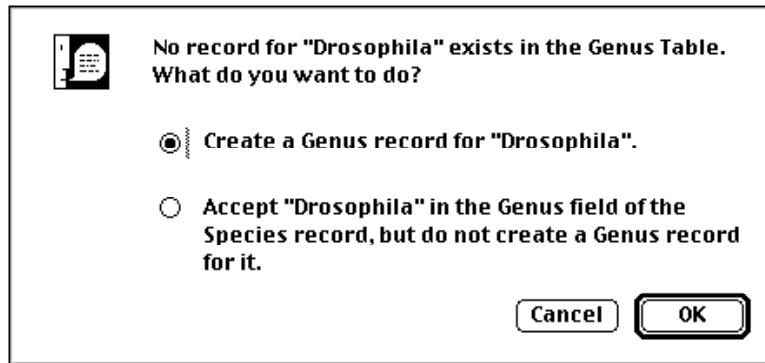
“On-the-Fly” Creation of Linked Records

Double-bordered data entry areas for linking fields work in a special way. Once you enter a value in the field and press TAB, Biota checks to see whether a record already exists for that value in the related (parent) table. If the parent record exists, you can move on to the next field. If it does not exist, Biota offers you the option to create the parent record “on the fly” and then return to the table where you started.

1. **Enter a value for a linking field.** Suppose, for example, you enter the genus *Drosophila* in the Genus entry area of the Species Input screen.

The screenshot shows the "Species Input" window. At the top, there is a navigation bar with tabs: Classification, Subsp/Names, Synonymy, Dist/Types, and Images. The "Classification" tab is currently active. Below the tabs, the species code "012345" is displayed. The main input area contains several fields: "Species Code" (containing "012345") with an "Assign" button, "Genus" (containing "Drosophila"), "Specific Name (Specific Epithet)" (empty), and "Species Author (& Date)" (empty). There are also two small checkboxes at the bottom right of the input area.

2. If your entry already exists in the related table, your entry will be accepted and the cursor will move on to the next field. In the example, if *Drosophila* were already in the Genus table, Biota would accept the entry and you move on to the Specific Name field.
3. If your entry does not match any entry in the related table, Biota presents the screen below. (The screen illustrates the *Drosophila* example.)



- If you choose the first option, “Create a Genus record for Drosophila” (the default), the Input screen for the related table appears (the Genus Input screen, in this example), with the entry you made in the linking field already entered in the correct field of the new Input screen. This method of creating a new parent record “on the fly” is available for all linking fields.

Genus Input

Genus

Drosophila

Tribe

Subfamily

Family

Classification

Superfamily

Suborder

Order

Show Species

Show Family

This Genus record

Save

Print

Delete

Cancel

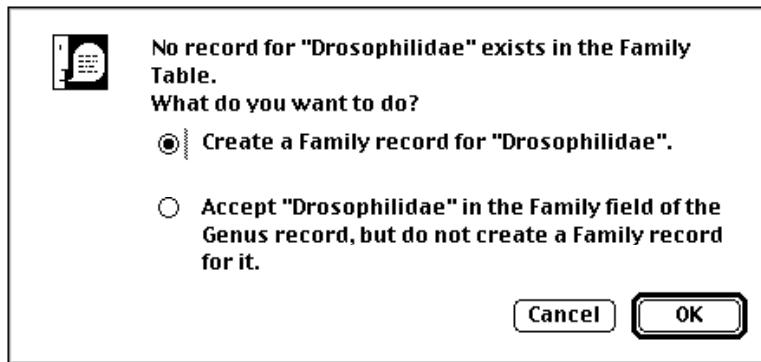
Navigate records

- If you choose the second option, “Accept ‘Drosophila’ in the Genus field of the Species record, but do not create a Genus record for it,” no link to the parent table will exist for this record. In other words, it will be an *orphan record* (see “[Linking Fields—Parent and Child Records](#)” in Chapter 3). You can add a record

in the related table later (a Genus record for *Drosophila*, in this example), but it is generally more efficient to add new, related records when this query appears—or use the table-by-table method outlined in the next section, “[Table-by-Table Creation of Linked Records](#)”.

NOTE: One common exception arises for the “Collected By” field of the Collection table. With historical collections of specimens, you may not want to create a Personnel record for every collector—some of whom may be long deceased and their particulars unknown.

4. **Repeat at additional levels, if necessary.** If you choose the first option (create a new record “on the fly” in the linked table), you may now need to make an entry in a linking (double-bordered) data entry area in the second Input screen. If you do so, the process repeats itself. In the *Drosophila* example, if you make an entry in the Family field on the Genus Input screen that is not in the Family table, Biota will ask if you wish to create a new Family record.



You can continue to create new records in related tables as prompted by Biota. Eventually you will reach a screen for which your entry is already present in the related table, or you will reach a screen that has no linking fields (e.g., the Kingdom Input screen at the top of the taxonomic hierarchy or the Locality Input screen at the top of the place hierarchy).

5. **Accept and return to previous levels.** When you have created the record or records you wish to in related tables, click the “Save” button at the bottom of the current Input screen. The Input screen for the next-lower level will appear.
6. **Enter data in any remaining fields** that you wish to record, then click the “Save” button, at each level.
7. **Continue with this process**, working back down the hierarchy, until you get back to the original screen (the Species Input screen, in the *Drosophila* example).

Table-by-Table Creation of Linked Records

In addition to, or instead of on-the-fly creation of records in related tables, as described in the previous section, new records can simply be entered directly for any table by selecting the corresponding Input command from the Input menu.

For example, you could begin the entry of a hundred specimens by first entering the names of all genera, using the Genus Input screen (choose Input Genus from the Input

menu). Then, when species names are entered, the genera would already be available for wildcard entry (see the next section).

Your choice of approach will depend upon the circumstances. If minimizing the handling of delicate specimens is a consideration, allowing Biota to request new records for linked fields, when needed, permits each specimen to be handled only once when data are entered directly from specimen labels.

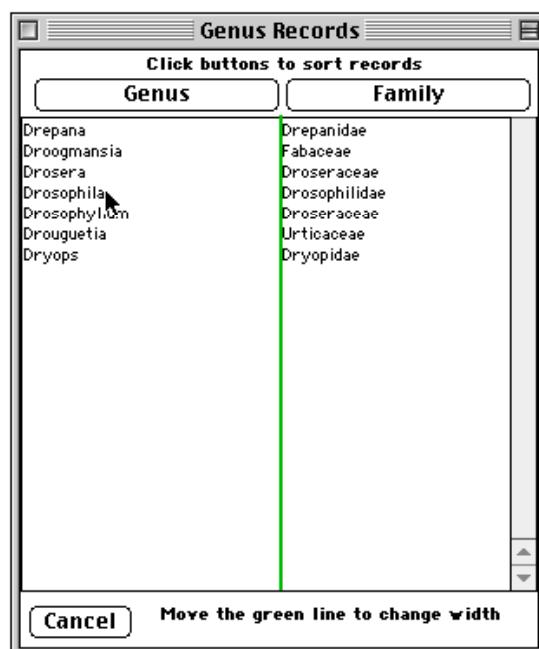
A Powerful Shortcut: Wildcard Data Entry for Linking Fields

For any double-bordered linking field (but not for any other fields), you can save much time and effort by using the *wildcard entry* option.

- 1. Enter the first letter, or the first few letters** of a linking-field value (taxonomic name, Personnel Short Name, or Record Code (Specimen Code, Species Code, Collection Code, or Locality Code) that you know or suspect is already recorded in the related table.

NOTE: To get a full list of *all* records in the related table, enter @ (the wildcard character in Biota), in place of any letters in the linking field entry area.

- 2. Press the TAB key.**
- 3. If only one record in the related table matches your entry,** the match will be entered in the linking field automatically.
- 4. If more than one entry in the related table begins with the sequence of characters you entered,** all matching values will appear in an alphabetized, scrolling list. For example, if you entered the two letters *dr* in the entry area for Genus in the Species input screen and there were existing records for several genera beginning with *Dr* in your Data File, Biota would present a pick list of the options, as shown below.



5. **If you see the entry you want**, just click it in the list and it will be entered in the linking field. (*Drosophila* is being clicked in the illustration.)
6. **A second (or second and third), "helper" field is also listed.** In the example above, Family is listed for each Genus.
7. **The values in the list can be sorted** by either column by clicking once on the column header button. (For example, to sort the Genera in the window above by Family, you would click the “Family” button in the window.)
8. **If Biota enters a value automatically that you did not intend**, it means your intended value is not present in the related table. Select the incorrect entry with the mouse and enter the correct value manually. For example, suppose you wanted *Drosophila*, so you entered “Dr” in the Genus entry area. If *Drymlys* were in fact the *only* genus in the Genus table starting with *Dr*, Biota would complete your entry as *Drymlys*. You would then have to change the entry manually to *Drosophila* (spelled out fully), then proceed as in Step 3, above.

Overriding Wildcard Input for Linking Fields

In one rather uncommon circumstance, you may need to override Biota's wildcard entry for linking fields. This circumstance is best explained with an example.

Suppose you are entering a new Species record for the species *Musanga recta*, and you have an existing record in the Genus table for the genus *Musanga*. As explained in the previous section, you can type “musa” in the Genus field of the Species input screen and Biota will automatically fill in *Musanga* (or display it in a choice window along with any other existing Genus names that begin with the letters “musa”).

Instead, however, suppose you need to create a Species record for *Musa nana*. If you enter “musa” in the Genus field of the Species input screen, Biota will incorrectly complete the entry as *Musanga*. In this case, you need to force Biota to allow creation of a new Genus record for *Musa*.

In general terms, when you need to create a parent record on the fly for a Linking field value that precisely matches the initial letters of a longer value in the Key field of the parent table, you need to override the wildcard lookup. (See why the example was better?)

You can override the wildcard lookup of parent records in any double-bordered linking field very simply.

1. **Type in the value** for which you want to create a new parent record (*Musa* in the example).
2. **Depress the OPTION key (Macintosh) or the ALT key (Windows) while pressing the TAB key** to enter the new value. Biota will offer to create the new parent record.
3. **Create the new parent record** in the normal way (see “[“On-the-Fly’ Creation of Linked Records](#)” earlier in this chapter).

Chapter 8

Record Codes

Record Code Concepts

As introduced in Chapter 3 (“[Key Concepts](#)”), the Key fields for the Specimen, Species, Collection, and Locality tables rely on *Record Codes*, rather than actual names of taxa or places, although Record Codes can be names if you wish. In Biota, *Record Code* is a general term for Specimen Codes, Species Codes, Collection Codes, and Locality Codes.

For any Record Code, you may use any combination of up to 30 ASCII characters that you wish. The only restrictions on Record Codes are that each record *within a table* must have a unique Record Code, and a Record Code may not start or end with a space character (Biota enforces both restrictions, in case you forget). On the other hand, careful planning of a Record Code system for your particular database can enhance the usefulness of the database you create. Some examples appear later in this chapter.

If you want, you can use the same code for records in *different* tables. Although this might seem a useful approach for related records, it makes little sense when many records in one table (e.g., many Specimen records) are linked to a single record in a related table (e.g., a Species record), since each of the “many” records will require a different Record Code. In general, it is likely to be less confusing to use Record Codes that are globally unique throughout a Data File.

An exception to this rule of thumb concerns the Input Specimen and Collection tool (Input menu), which is used primarily to enter data for historical specimens that have a one-to-one relationship between Specimen and Collection records (see “[Specimen and Collection Combined Input](#)” in Chapter 11). This tool automatically creates a Collection record linked to each Specimen record you enter, with identical Specimen and Collection Record Codes. (If you prefer, you can use the Record Code Settings tool to automatically assign a sequential Collection Record Code. (See “[Assigning New Record Codes Automatically During Data Entry](#)” later in this chapter.)

Why Does Biota Require and Display Record Codes?

In database applications designed for business (such as airline reservation systems) or for scholarly applications (such as literature reference management programs)—unique identifiers for records are normally created automatically and are often never seen by the user. Each record can be found by other criteria, though often less efficiently. When the airline reservation agent gives you a “record locator” (the automatically generated unique Record Code for your reservation) the airline hopes you will use it when you call to reconfirm or change your plans, because it saves the company time and money over having the agent find your record by date, flight, and name. Likewise, in Biota, the Record Code is the fast lane to the record.

User control over Record Codes has a number of advantages:

- **You can design a system of codes** that is meaningful in your research or institution.

- You can avoid conflicts (identical codes) when combining data from two or more Biota Data Files.
- Museums and herbaria can use an established system of accession numbers or collection codes.
- You can use unique records codes you have already created for data imported from existing flatfiles or field notebooks. This advantage is especially applicable to Collection Codes and Specimen Codes, for which a collector's own scheme of unique codes may be appropriate.
- Accessible Record Codes permit you to use machine-readable barcodes or image codes to identify records uniquely (see Appendix K, “[Barcodes](#)”). Biota offers special support for Specimen and Species Record Code recognition, especially for barcodes (see “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” later in this chapter), although barcodes may be used for Collection and Locality Codes, as well.

Why Does Biota Require Species Codes?

You may wonder why Biota uses Record Codes for the Species table, while relying on scientific names in the Key Fields for higher taxon tables (Genus, Family, Order, etc.). Species Codes are necessary for several reasons.

- Specific epithets are not unique. Specific epithets (specific names) are obviously unsuitable as unique identifiers of Species records because of the redundancy of published specific epithets among genera.
- Temporary groupings of specimens are often needed. In revisionary systematics and especially in biotic inventory projects, Species records are often needed to unite groups of Specimen records, long before a specific epithet can be applied to those specimens.
- Unidentified or undescribed species. In a relational database, a Species record is required to connect Specimen records to a Genus record, when the genus is known but the species is uncertain or undescribed.

Guidelines and Suggestions for Designing Record Code Systems

Although you may use any system you wish, this section provides some suggestions for designing Record Code systems, based on the experience of Biota users. The four tables that require you to create Record Codes for new records differ in how Biota users generally assign Record Codes.

Specimen Codes

For some groups of organisms (vertebrates, for example), traditions of unique specimen codes or accession numbers for individual specimens have long existed, in museums and herbaria. Whenever possible, it makes sense to use such an existing system for assigning Specimen Codes to records in a Biota Data File.

The use of barcodes for individual specimens or specimen lots (see “[Setting Up for Automatic Record Code Prefix Recognition](#)” later in this chapter) suggests another obvious recommendation: simply use the specimen barcode (or possibly an abbreviated version of it; see “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” later in this chapter).

[Record Codes](#)” later in this chapter) as the Specimen Code for Biota records (see Appendix K, “[Barcodes](#)”).

Sequential Specimen Codes

A special consideration in designing a code system applies to Specimen Codes. The Series menu (Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”) provides a set of powerful input, search, and specimen-identification utilities. These utilities can be used to their greatest advantage only if Specimen Codes for related groups of Specimen records can be assigned Specimens Codes that end with a consecutive *integer counter* (including leading zeros as necessary; see the Warning below), with or without an *alphanumeric prefix*.

WARNING: Because Record Code fields are alphanumeric, sorts on record fields treat numerals “alphabetically.” Thus, Record Codes A1, A20, and A100 will sort in the order: A1, A100, A20. Likewise, codes 3, 5, 31, and 40 will sort in the order: 3, 31, 40, 5. To avoid this problem, use imbedded or leading zeroes: A001, A020, A100; 03, 05, 31, 40. These series will sort in the order listed.

A “group” of specimens, in this sense, may share any characteristic that you consider important or convenient, such as being from the same mass collection or lot, from the same locality, from the same collector, or from the same species.

For detailed instructions on how to set Biota up to use commercial barcodes as sequential counters with the Series tools, see “[Setting Up for Automatic Record Code Prefix Recognition](#)” later in this chapter.

Unified Record Code Systems: Specimen, Collection, and Locality Codes

In some cases, it may make sense to create a joint system of Collection Codes and Specimen Codes. A group of specimens from the same collecting event share the same Collection Code, which may form a prefix for their Specimen Codes. For example, if the Collection Code is Peru89-01234, the Specimen Codes for three specimens from that collection might be Peru89-01234:001, Peru89-01234:002, and Peru89-01234:003.

A vegetation study that used Biota to keep track of trees, shrubs, and seedlings in a complex layout of sites, transects, and quadrats designed a three-level nested system of Record Codes for the Locality, Collection, and Specimen tables. Each site/transect combination had a Locality record, with the Locality Code made up of a site abbreviation and transect number, for example, LOC2. The quadrats within the LOC2 transect each had a Collection record, with Collection Codes of the form LOC2-T034, LOC2-T035, etc. for the tree (T) quadrats of the transect. Smaller quadrats on the same transect used for shrubs (S) had Collection Codes such as LOC2-S011, LOC2-S012, and so on, with a third series for the even-smaller seedling quadrats. Finally, each plant species that occurred within each quadrat was recorded in a separate Specimen record, with the Abundance field registering the number of individuals of that species in that quadrat. The Specimen Codes for trees were of the form LOC2-T034-003, LOC2-T034-004, or, for shrubs, LOC2-S012-026, LOC2-S012-027, and so on.

Biota could easily find all the Specimen records for a particular locality, transect, or quadrat in this study, using fields and relations, regardless of what values had been assigned for Record Codes. In practice, however, the use of meaningful Record Codes helped the researchers and data input personnel keep track of progress and make

sense out of patterns more easily—especially once records were exported to text files for statistical or spatial analysis.

NOTE: You can ask Biota to enter alphanumeric Record Code prefixes automatically. For manual input of the rest of the code (integer or alphanumeric), after the prefix, you can use Entry Choice Lists to enter the prefix (see “[Using Entry Choice Lists to Enter Record Code Prefixes](#)” later in this chapter). For automatic generation of unique integer counters appended to a prefix you specify (but with the integers not under your control), see “[Assigning New Record Codes Automatically During Data Entry](#)” later in this chapter.

WARNING: If you use a hierarchical system for Locality, Collection, and Specimen Codes, be sure to avoid ending up with Collection or Specimen Codes too long for the Record Code field (30 characters maximum), as records accumulate.

Locality Codes

For biogeographical databases of all kinds, Locality Codes present special problems. First of all, of course, one must decide at what level in the hierarchy of places a “locality” will be defined, but this is an issue that will depend on the nature of your data.

There exist place-name authority lists (gazetteers), complete with established locality codes, for some place names within countries and smaller political entities. Obviously, if these are appropriate and available, one would do well to use the established codes as Biota Locality Codes. If you wish, you can import place name lists for use in Biota’s Entry Choice List system (see Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#)”).

Otherwise, if you are on your own to invent Locality Codes, the most meaningful approach is probably to base the Locality Code closely on whatever you enter for the Locality Name field of the Locality record. The Locality Name field is a text field, and may thus contain up to 32,000 characters (not that you would normally use that many). With this approach, if the Locality Name entry is longer than 30 characters, you will have to abbreviate it to a unique but recognizable form, 30 characters or fewer, to create a Locality Code. When you need to find an existing Locality record to link a Collection record, you can, of course, use the Lookup Locality tool (see “[Entering Collection Data: The 'General' Tab](#)” in Chapter 11). However, for Locality Codes that abbreviate Locality Names, it is faster to use the wildcard data entry system (see “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7).

Species Codes

One obvious way to create Species Codes is to concatenate the generic name (or its initial characters) with the specific epithet (or its initial characters), e.g., *glycinemax* for *Glycine max*, or *drosophmelano* for *Drosophila melanogaster*. For combinations longer than 30 characters (a rather common circumstance), you will need to abbreviate either the genus or the epithet or both. Some Biota users settle on a standard system, such as the first *N* characters of the genus (if there are that many) followed by the first *M* characters of the specific name (if there are that many), with a numerical suffix in case of ambiguity. *N* plus *M* should not exceed 29, to allow for a numerical suffix if necessary.

You can leave a space or use a separator character between the genus and species names or abbreviations if you like (e.g., *glycine max* or *drosoph_melano*). For some taxa or institutions, there may be established codes for species that should be used instead.

Especially for systematics databases, this approach has the slight disadvantage that a species may subsequently be reassigned to a different genus, or its epithet changed for various reasons. If this happens, and you wish to use Species Codes based on species names, you can always change the Species Code when you change other parts of the Species record. Biota will automatically offer to change the Species Code in linked Specimen records (see “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12).

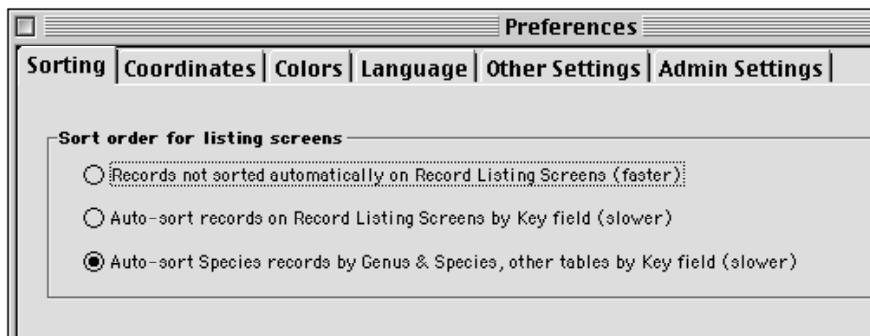
In survey work and systematic revisions, Species Codes are usually needed long before there are secure names to apply to the corresponding Species records. Fortunately, temporary Species Codes are easily accommodated by Biota—there is a special utility to create them automatically, if you wish (see Chapter 25, “[Temporary Taxa for Approximate Determinations](#)”).

Or, you can create your own temporary Species Codes, which you need to link Specimen records (and thus Collection and Locality data as well) to known affinities at higher taxonomic ranks. A “species” that starts out with the Species Code *hystrix_hairy#1* can later be changed to *Hystrix_hirsuta* when it has been described or determined authoritatively, by making a single change in the Species record (see “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12).

Sorting Records by Record Codes

As the default, Biota displays records for all tables except Species sorted by the Key field for each table in Record Listing screens. This means that Specimen, Collection, and Locality records will be sorted by Record Code, and taxon tables—Genus and above—by taxon name. As the default, however, Species records are sorted by Genus, then by Species Name (specific epithet), rather than by Species Code.

In the Sorting tab of the Preferences screen (Special menu), you can switch to either of two other options, or return to the default.



- **Records not sorted automatically on Record Listing screens (faster).** Records will appear in the order they were created. This option produces faster displays and is therefore useful for large data files when you intend to sort records on some other criterion anyway, once they are displayed.
- **Auto-sort records on Record Listing screens by Key field (slower).** With this option selected, records for *all* tables are sorted by Key field, *including* Species records (which are sorted by Species Code).
- **Auto-sort Species records by Genus and Species, other tables by Key field (slower).** This is the default setting when you create a new Data File or click the “Reset All Defaults” button on the Preferences screen.

NOTE: You can sort records any way you wish by using the “Sort” button on each Record Listing screen, once they are displayed (see “[Sorting Records in Record Listing Screens](#)” in Chapter 10).

WARNING: Because Record Code fields are alphanumeric, sorts on record fields treat numerals “alphabetically.” Thus, Record Codes A1, A20, and A100 will sort in the order: A1, A100, A20. Likewise, codes 3, 5, 31, and 40 will sort in the order: 3, 31, 40, 5. To avoid this problem, use imbedded or leading zeroes: A001, A020, A100; 03, 05, 31, 40. With their leading or embedded zeros, these series will sort in the order listed.

Using Entry Choice Lists to Enter Record Code Prefixes

Once you decide on a system of Record Codes for your database, Biota offers some help with the input process. If you plan to enter the same prefix for the Record Codes in a series of records, but you need to control the remainder of each Record Code yourself, using an Entry Choice List can save you time and mistakes. (If you want to set the prefix, but let Biota create a unique integer counter to complete each Record Code, see the next section, “[Assigning New Record Codes Automatically During Data Entry](#).”)

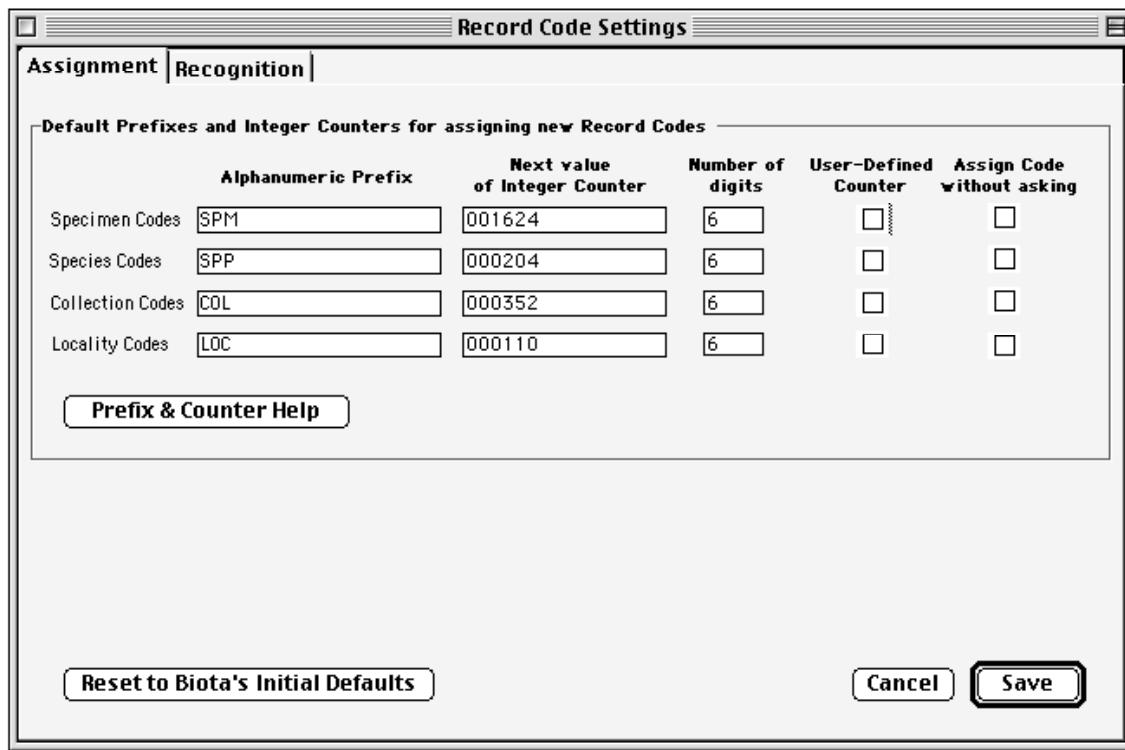
You can activate and set up an Entry Choice List for any Record Code field ([Species] Species Code, [Specimen] Specimen Code, [Collection] Collection Code, or [Locality] Locality Code), using the procedures described in detail in Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#).” If you prepare the list of entry options with the Record Code prefix you are currently using as the first (or only) option, you can enter it simply by pressing the RETURN or ENTER key.

NOTE: An alternative way to enter a Record Code prefix automatically, with no integer counter, is to set it up for automatic entry using the Assignment tab of the Record Code Settings screen (Special menu), with the “Number of Digits” setting at zero. See “[Assigning New Record Codes Automatically During Data Entry](#)” later in this chapter.

Assigning New Record Codes Automatically During Data Entry

You can create and apply your own complete system of Record Codes (a general term for Specimen Codes, Species Codes, Collection Codes, and Locality Codes), one at a time, or you can rely on Biota to generate Record Codes automatically, based on settings you specify in the Prefix settings screen.

All settings for automatically generated Record Codes are found in the Assignment tab of the Record Code Settings screen (Special menu).



In this screen, you can control the following settings, independently for Specimen Codes, Species Codes, Collection Codes, and Locality Codes:

- Set the alphanumeric prefix (any alphanumeric string up to 26 characters in length) for Records Codes.
- Set a starting value for the sequential integer counter part of the Record Code.
- Set the number of digits in the integer counter (up to 9 digits), to control formatting.
- Specify whether Biota should use the user-defined integer sequence or the internal record sequence number as the integer counter part of automatically generated Record Codes.
- Specify whether automatically generated Record Codes are also to be entered automatically by Biota, without your confirmation, or, instead, through use of the “Assign” buttons on input screens.

The Format of Automatically Generated Record Codes

A Record Code of the form *A1B2CD01234* is said to be made up of the *alphanumeric prefix A1B2CD* and *the integer counter 01234*. In other words, a Record Code prefix generally ends with the *rightmost nonnumeric character* in the Record Code (although you can end a prefix with a numeral if you wish), and the integer counter comprises any remaining characters (which must all be digits).

When Biota generates Record Codes automatically, you can tell Biota to base the integer counter either on a starting integer you specify in the Record Code Settings screen, or on the *sequence number* for the corresponding table—the number of records entered in the table since the Data File was created. The sequence number increases by one every time a record is created, no matter how many records are later deleted.

In either case, leading zeros are automatically added to the integer counter, if necessary, to make all instances of the counter carry the number of digits you specify in the Record Code Settings screen, so that alphabetic sorting will work correctly (see the Warning at the end of the section “[Sorting Records by Record Codes](#)” earlier in this chapter).

The length of a Record Code (a Specimen Code, Species Code, Collection Code, or Locality Code) may not exceed 30 characters, whether created manually or automatically. For automatically created Record Codes specified in the Record Code Settings screen, the maximum length of an alphanumeric prefix is 26 characters and the maximum length of the integer counter is 9 characters—potentially totaling 35 characters—but Biota enforces a total of no more than 30 characters when you set the specifications. For example, if you enter a 22-character prefix in the Record Code Settings screen, the integer counter may not be set any longer than 8 characters. Dialog screens guide you through the process, as illustrated in the next section.

Setting Record Code Prefixes and Lengths

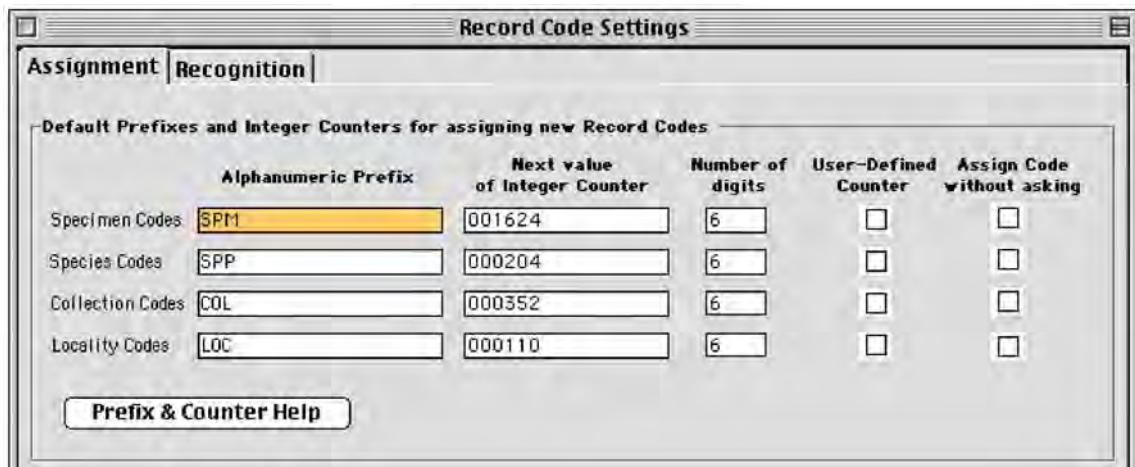
When you first create a new Biota Data File (an “empty” database; see “[Creating an Empty Biota Data File While Launching Biota](#)” in Chapter 3), Biota assigns the following default Record Code settings:

- **LOC** for the Locality Code alphanumeric prefix.
- **COL** for the Collection Code alphanumeric prefix.
- **SPM** for the Specimen Code alphanumeric prefix.
- **SPP** for the Species Code alphanumeric prefix.
- **Six digits for the integer counter** for each table (Locality, Collection, Specimen, and Species)
- **The User Defined Counter option off** (unchecked), for each table. (Sequence numbers will be used to create the counters, with this setting.)
- **The Assign Without Asking option off** (unchecked), for each table. (The “Assign” buttons on input screens must be used to generate the automatic Record Codes, with this setting.)

With these default settings 999,999 unique Record Codes can be generated for each of the four tables. If you need more than that, you must modify the prefix or the number of digits in the integer counter.

To change the default prefix, to adjust the number of digits in the integer counter, or to change the settings for automatic generation of integer counters and Record Codes, take the following steps:

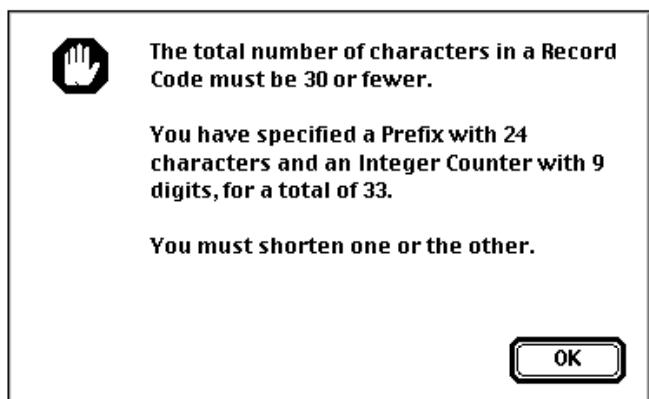
1. Select Record Code Settings from the Special menu. The Record Code Settings screen appears.



2. Enter or edit the Record Code prefix settings in the Assignment tab of the screen. You can enter any prefix you want for each of the four Record Codes (Locality Code, Collection Code, Specimen Code, and Species Code), up to 26 characters for each prefix.

NOTES:

- a. **Leading space characters** are not permitted in a Record Code prefix, but you may include internal space characters if you wish.
- b. **If you want to use the integer counter alone to generate Record Codes,** leave (or make) the alphanumeric prefix setting blank.
- c. **If the number of characters you specify** as a prefix plus the number of digits set for the integer counter exceeds 30, Biota posts a message such as the one shown here.



3. Set the “User-Defined Counter” checkbox option.
 - To use your own integer counter sequence, as specified in the next step of these instructions, the checkbox for the appropriate table must be checked.
 - To use the sequence number (the number of records entered in the table since the Data File was created) as the integer counter for a table, the checkbox must be unchecked.
4. If the “User-Defined Counter” checkbox is checked, you may edit the user-defined counters shown in the entry areas labeled “Next Value of Integer Counter.”

NOTE: If the “User-Defined Counter” checkbox is *unchecked*, the value shown in the “Next Value of Integer Counter” entry area is the sequence number for the table, which cannot be edited or deleted.

5. Specify the number of digits for the integer counter in “Number of Digits” entry areas. You may enter any value between 3 and 9. Thus, the maximum number of unique records with a particular prefix can vary from 999 (for 3 digits) to 999,999,999 (for 9 digits). If the number you specify plus the number of characters in the alphanumeric prefix exceeds 30, Biota posts a message such as the one shown in [Step 2](#), above.

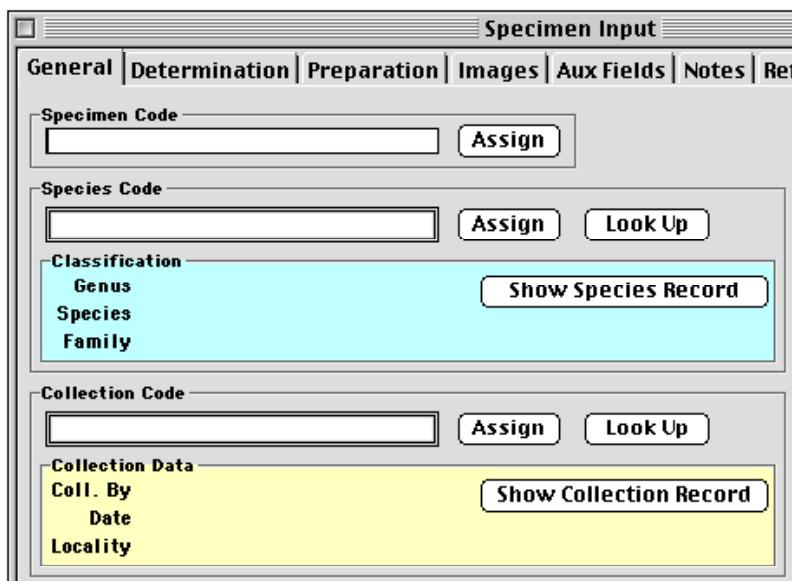
WARNING: If you set the number of digits for the counters too low and you reach the limit, Record Codes will begin to repeat, and Biota will post a Duplicate Key Error message (see “[Duplicate Key Errors](#)” in Chapter 3). At that point, you must change to a different prefix.

6. Set the “Assign Code Without Asking” checkbox option.
 - If the checkbox for a table is checked, Biota will automatically create and enter a Record Code, according to your specifications in Steps 2-5, above, for the table indicated.
 - If the checkbox for a table is unchecked, you must use the appropriate “Assign” button in input screens to enter a Record Code created according to your specifications in steps 2-5 above, for the table indicated. (Using “Assign” buttons to enter automatically generated Record Codes is discussed in the next section, “[Assigning New Record Codes Using an ‘Assign’ Button: Step by Step](#)”.)
7. Click the “Save” button. Until you change them again, the settings you have established will be used for all subsequent new Record Codes automatically created by Biota.

NOTE: The settings you establish using the Record Code Settings screen are recorded in your Biota Data File. They remain just as you set them until you change them, regardless of how many times you start up or shut down Biota. If you start a new Data File, you will have to set them again.

Assigning New Record Codes Using an “Assign” Button: Step by Step

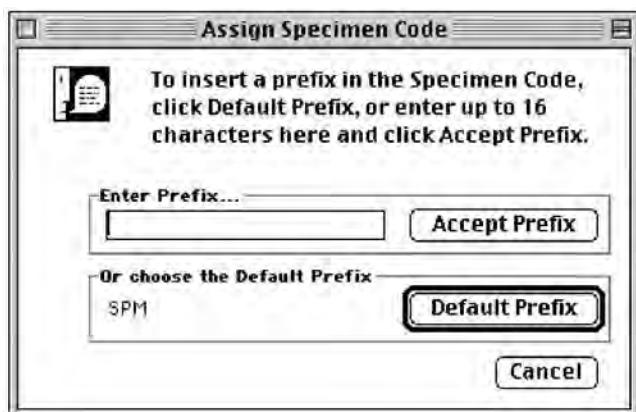
“Assign” buttons are used to enter automatically-generated Record Codes while creating or modifying records. These buttons appear in the Input screens for the Specimen, Species, Collection, and Locality tables. Each of these Input screens has an “Assign” button for its own Record Code, plus an “Assign” button for “on-the-fly” creation of new



Record Codes for parent tables (Species and Collection tables for Specimen records and the Locality table for Collection records). The Specimen Input screen appears below as an example, with its three “Assign” buttons.

Here are the steps you follow to assign automatically generated Record Codes using an “Assign” button, while creating or modifying records.

1. **Click the “Assign” button.** During data entry, you may elect to click the “Assign” button next to a Record Code entry area, instead of typing in a Record Code or having Biota enter an automatically generated Record Code without asking (see the previous section, “[Setting Record Code Prefixes and Lengths](#)”). A dialog window appears, offering two options.



2. Choose an option for assigning the Record Code.

- **Default Prefix.** If you click the “Default Prefix” button (or press the RETURN or ENTER key), Biota creates and assigns a Record Code that begins with the Default Prefix shown in the window, followed by an integer counter.
- **Enter Prefix, Accept Prefix.** Alternatively, you may type up to 26 characters in the “Enter Prefix” entry area as an *ad hoc* prefix for the record you are currently creating or editing. Then click the “Accept Prefix” button in the dialog window. Biota creates and assigns a Record Code that begins with the *ad hoc* prefix you entered, followed by an integer counter.

NOTE: For either option, the integer counter is created according to specifications set in the Record Code Settings screen (see the previous section, “[Setting Record Code Prefixes and Lengths](#)”).

Setting Default Prefixes for Recognizing Specimen and Species Record Codes

Biota has the capacity to recognize, automatically, particular Specimen Code and Species Code prefixes that you specify, whether the codes were created by you, generated by a commercial producer of barcodes, or assigned automatically by Biota. The codes you specify are recognized automatically wherever these Record Codes are required in the Biota interface—including Input screens, search query screens, and Loans screens.

Here's how it works. When you enter any value in a Specimen Code or Species Code entry area, either manually or using a barcode reader, Biota checks to see if the value you entered begins with an alphanumeric prefix you specified in the Recognition tab of the Record Code Settings screen (Special menu). If the entry does not start with a specified alphanumeric prefix you have specified, it is treated as an ordinary entry.

Thus, Specimen Codes and Species Codes whose attributes you have specified in the Recognition tab of the Record Code Settings screen can be freely mixed with Record Codes with other prefixes, barcodes of any origin, Biota-generated codes, *ad hoc* codes you make up for each specimen, and any existing Specimen codes (e.g., museum or herbarium accession numbers) or Species codes (from authority files), all in the same database.

There are two reasons you might want to exploit Biota's ability to recognize particular prefixes.

- **To use the Specimen Series tools.** To use the tools of the Series menu (Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”) efficiently, either from the keyboard or using barcodes and a barcode reader, you need to use automatic Specimen Code recognition. (See the next section of this chapter, “[Using Alphanumeric Specimen Codes with the Series Tools](#).“)
- **To abbreviate or change Specimen Code or Species Code prefixes entered as barcodes.** To substitute an abbreviated barcode prefix for a long barcode prefix or to replace a barcode prefix with a different prefix in Specimen Codes or Species Code, you can instruct Biota to recognize specified barcode prefixes and make the substitutions automatically in records. (See “[Substituting Different Prefixes for Barcode Prefixes in the Data File](#)” later in this chapter.)

Using Alphanumeric Specimen Codes with the Series Tools

Much time and effort can often be saved by using commands from the Series menu to enter, update, or find consecutive series of Specimen Codes—although the Series tools can also be used for nonconsecutive Specimen Codes (Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”).

If you are using Specimen Codes that have an alphanumeric prefix followed by an integer counter (see “[The Format of Automatically Generated Record Codes](#)” earlier in this chapter), you can tell Biota to look for that particular prefix, and when it finds it, to use the integer part of the Specimen Code as a starting or stopping point to create a series of new Specimen records, to find an existing series, or to find and update an existing series.

There are two ways to tell Biota to look for a particular Specimen Code prefix.

- **Manual input of the prefix.** You can enter the alphanumeric prefix manually. Click the “Prefix” button in any Series screen, then use the Enter Prefix/Accept Prefix option (see “[Assigning New Record Codes Using an “Assign” button: Step by Step](#)” earlier in this chapter). Unless you need to do this for only one or two series of Specimen Codes, this method is likely to be far less efficient than the automatic Specimen Code prefix recognition (below).
- **Automatic Specimen Code prefix recognition.** With this approach, you use the settings of the Recognition tab of the Record Code Settings screen to inform Biota about the alphanumeric prefix for the Specimen Codes you are using. (See the next section of this chapter.)

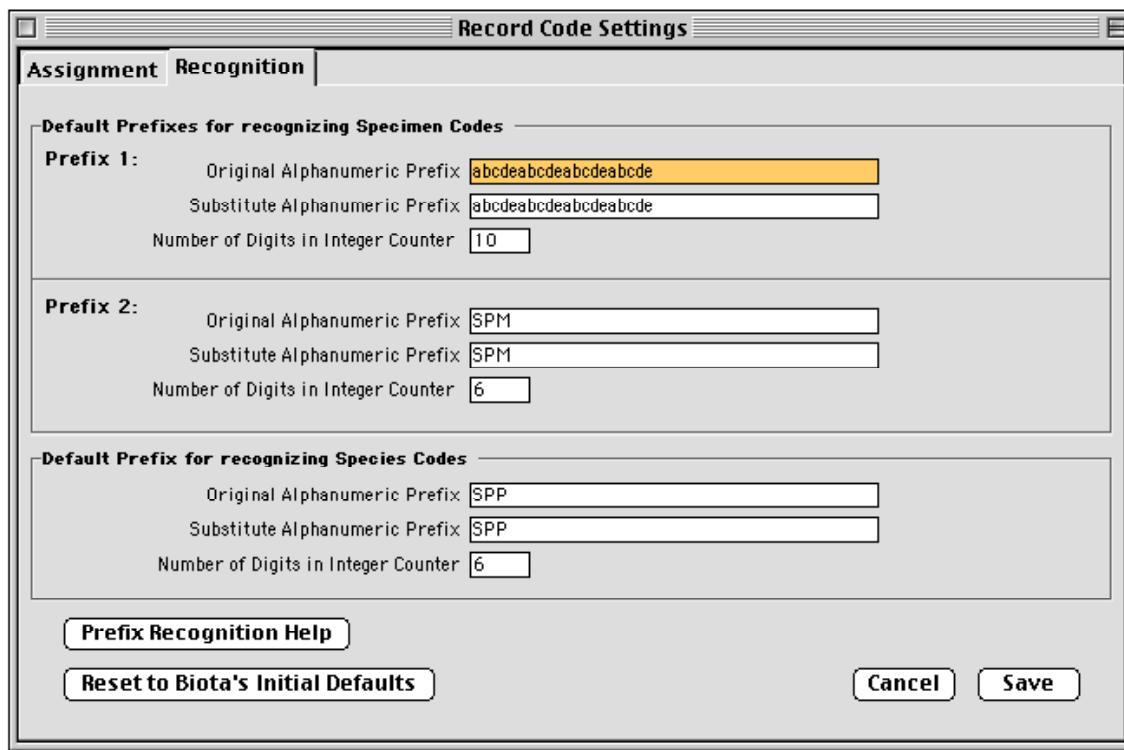
Setting Up for Automatic Record Code Prefix Recognition

Follow these steps to set Biota up to recognize Specimen Code prefixes and/or Species Code prefixes automatically.

1. **Select Record Code Prefixes from the Special menu.** The Prefix setting screen appears.
2. **Click the Recognition tab.**



Notice that you may specify two *different* Specimen Code recognition profiles and one Species Code recognition profile. The primary reason for offering two different Specimen Code recognition systems is to permit a mixture of two different systems



of Specimen barcodes to be used simultaneously (for example, Specimen barcodes for your own institution's collection and barcodes for specimens on loan from another institution, bearing a different prefix).

3. **Enter the Original Record Code prefixes.** In the entry areas labeled “Original Alphanumeric Prefix,” enter the alphanumeric prefix that appears in the full Specimen Codes and/or Species Codes you will use. *These prefixes may be up to 20 characters in length.*
4. **Enter the Substitute (or repeat the Original) Record Code prefixes.**
 - **If you want to use Original Specimen Code prefixes with the Series tools:** In the entry areas labeled “Substitute Alphanumeric Prefix,” *repeat precisely the same alphanumeric prefix* that you entered in the corresponding entry area labeled “Original Alphanumeric Prefix.” *Prefixes may be up to 20 characters in length.*
 - **If you want to substitute different prefixes for barcode prefixes:** In the entry areas labeled “Substitute Alphanumeric Prefix,” enter the alphanumeric prefix that you want Biota to substitute for the full Specimen Codes and/or Species Codes on barcode labels you will use. *Prefixes may be up to 20 characters in length.* (See the next section of this chapter, “[Substituting Different Prefixes for Barcode Prefixes in the Data File](#),” for details and warnings about substituting prefixes for barcode prefixes.)
5. **Enter the number of digits for the integer counter.** Finally, in the fields labeled “Number of Digits in Integer Counter,” enter the number of digits that follow the

alphanumeric prefix in your Specimen Codes or Species Codes, so Biota can correctly format the regenerated Record Codes. *Integer counters may be up to 10 digits in lengths.*

Substituting Different Prefixes for Barcode Prefixes in the Data File

A barcode reader is simply an alternative to the keyboard for entering data. If you read a barcode into a text document or a Biota field, you will simply see whatever is coded on the barcode label. (See Appendix K, “[Barcodes](#),” for general information on barcode readers and barcodes.)

Specimen barcodes usually have a long alphanumeric prefix, identifying country, institution, and series, followed by a long, unique integer counter. (For example, barcodes for specimens collected by or for the Instituto Nacional de Biodiversidad in Costa Rica—INBio—all start with INBIOCRI00, followed by a unique, seven-digit integer.) Some projects also use barcode labels for Species Codes, in which case the barcode for a species can be attached to the species label in specimen storage units.

Although the complete barcode is essential on the specimen itself, it may not be necessary in your database—but see the warning at the end of this section. Biota allows you to use either the original barcode (with any mixture of barcode prefixes from different institutions or collections), or to strip off all or whatever part of the prefix you specify and replace it with a substitute (perhaps abbreviated) prefix, or with none.

If you want, you can specify a substitute for a particular alphanumeric barcode prefix using the Recognition tab of the Prefix Setting screen (see the previous section, “[Setting Up for Automatic Record Code Prefix Recognition](#)”). You can do this separately and independently for Specimen Codes (two different prefixes can be recognized and two different prefixes substituted) and Species Codes. Each time a Specimen Code or Species Code is entered, Biota checks to see if it begins with the specified prefix. If so, the prefix is replaced by the substitute prefix you have specified, followed by the *original* value of the integer counter.

- **For example**, if the original barcode reads *IntlMusNatHist001234*, and you have specified that *IntlMusNatHist* is to be replaced by *IMNH*, Biota will assign the Specimen Code *IMNH001234* to a new Specimen record when you scan in the barcode in the Specimen input screen.
- **Later, suppose you search for the record** using the “By Specimen Code” tool from the Find menu, or the “Find Specimen Series” tool from the Series menu. You can find the record by entering either the shortened code, which is actually on the record in the Data File, or the full, original barcode (*IntlMusNatHist001234*), which Biota will recognize and translate to the abbreviated equivalent to make the search.

If you want to use barcodes for Species Codes, you can shorten or replace Species barcode prefixes in the same way.

WARNING: Abbreviating or substituting prefixes in institutional specimen barcodes is generally not advisable. Prefixes that have been designed to be universally unique are best recorded in full, to avoid ambiguity when data are pooled in aggregated databases. *Even if you do not substitute, however, you need to register the Original Prefix, with an identical “Substitute Prefix,” in the Prefix setting screen to be able to use the Series commands. See “[Setting Up for Automatic Record Code Prefix Recognition](#)” earlier in this chapter.*

NOTE: Long barcodes, and long Record Codes in general, will not be visible in full in some Biota Record Listing screens. To view the complete Record Code, you may have to open the record in the Input screen by double-clicking it in the Record Listing screen.

Chapter 9

Special Data Types

Certain special data types are notoriously troublesome in biodiversity databases. This chapter describes how Biota handles intermediate taxonomic levels (ranks), dates, and geographical coordinates (latitude and longitude).

Intermediate Taxonomic Levels (Subtaxa and Supertaxa)

Biota's taxonomic tables (Species, Genus, Family, Order, Class, Phylum, and Kingdom) represent only the obligatory levels (ranks) of the Linnean hierarchy, in the sense that every organism must be assigned to a taxon at each of the seven levels. In fact, of course, systematists use many intermediate levels in classifying organisms: Subclasses, Suborders, Superfamilies, Cohorts, Tribes, and so on.

The Dilemma of Intermediate Levels

The problem is that each group of organisms (or each group of taxonomists) uses different intermediate levels, so that even sister taxa are frequently classified to different numbers of levels. For this reason, it is not feasible to create a separate table for each possible intermediate level (e.g., a Subfamily table), since some child records (e.g., Genus records) would have a Subfamily parent but others only a Family parent.

The ideal (and cladistically correct) solution is to implement a recursive taxonomic design. A recursive taxonomic rank system allows an indefinite and potentially unlimited number of taxonomic levels within any clade.

There are some practical drawbacks to the recursive design, however. In addition to providing the programmer with a permanent source of migraines, recursive relations can produce a significant computational overhead, slowing operation of many features of a database. For example, in a recursive design, finding all Specimens for an Order requires following each branch and subbranch of a clade from its ordinal root to each specific or subspecific tip, then finding all specimens for each tip, tip by tip. In contrast, a strictly hierarchical model requires a single command (a single line of program code) to do the same search.

The key consideration in electing to use a traditional design for Biota, however, was to simplify for the user, both in concept and in fact, the processes of importing and exporting text files. It is much easier to conceptualize these processes when the table and field structure of the database is only one step away from the form in which most biologists are used to listing taxa on paper or the computer screen.

How Biota Handles Intermediate Taxonomic Levels

Biota uses fields within the obligatory taxon tables (Species, Genus, Family, Order, etc.) for intermediate taxonomic levels (see Appendix A, "[Biota Tables, Fields, and Relational Links](#)"). For example, the Family Formicidae (the ants) is divided into several subfamilies (Myrmicinae, Formicinae, etc.), and each subfamily is further classified into tribes (e.g., within the Subfamily Myrmicinae: Tribes Cephalotini, Attini, Dacetini, etc.).

Biota treats membership in a particular Tribe and subfamily as attributes of each Genus record. Thus, the Genus table in Biota contains two fields for taxonomic levels between the generic and the familial level: [Genus] Tribe and [Genus] Subfamily (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). Each ant genus gets its own Genus record, with the appropriate values in the [Genus] Tribe and [Genus] Subfamily fields. In other words, there is no single record for a Tribe or Subfamily, as there must be for each taxon in the database at the obligatory levels. Nonetheless, you can search, sort, select, and display, and therefore print or export records based on intermediate taxonomic levels.

For groups not requiring certain intermediate taxonomic levels (or if you choose to ignore them), simply leave the fields for intermediate levels blank.

Default Names for Intermediate Taxon Fields

Biota provides predefined fields for the following intermediate taxonomic ranks (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

[Species]	Subgenus
[Species]	Section
[Genus]	Tribe
[Genus]	Subfamily
[Family]	Superfamily
[Family]	Suborder
[Order]	Superorder
[Order]	Subclass
[Class]	Subphylum
[Phylum]	Subkingdom
[Kingdom]	Superkingdom

Renaming an Intermediate Taxon Field

If the organisms you work with require a name for an intermediate taxonomic level that does not correspond to the default names listed above, you can rename any of these fields to suit your needs (see Chapter 18, “[Renaming fields](#)”).

Defining Additional Intermediate Levels

If you need more intermediate levels than Biota has provided with default names (see “[Default Names for Intermediate Taxon Fields](#)” earlier in this chapter), use one of the many Custom fields (e.g., [Genus] Genus Custom1, see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) and rename it appropriately (see Chapter 18, “[Renaming fields](#)”).

Remember, an intermediate level is always an attribute (field) of the next *lower* obligatory level.

Updating Intermediate Taxa

To add intermediate taxonomic names to existing records, rename an existing intermediate taxon, or specify certain records to be recorded as a new intermediate taxon, take these steps.

1. **Define a Record Set** (see “[Record Sets](#)” in Chapter 3) for the records you want update.
2. **Use the Find and Replace tool** (see “[Updating Records Using the Find and Replace Tool](#)” in Chapter 12) from the Special menu to add or change the intermediate taxon name for all records in the Record Set.

Dates

Date information appears in many places in Biota tables and records. You can record the date of a collecting event (or the beginning and ending dates for a collecting period), the date each specimen was prepared, the date each was last determined, the date a Note record was added to a parent record, and the date a Specimen Loan was made or returned.

Automatically Recorded Dates

For Specimen, Species, Collection, Locality, Personnel, Loans, References, and Project records, Biota automatically registers the date each record was created and the most recent date it was changed. (The identity of the user making the most recent change is also recorded, if this option is enabled in the “Admin Settings” tab of the Preferences screen. See Appendix B, “[Setting Preferences](#)”).

If the Determination History option has been activated, the current date is recorded any time the determination of a specimen is updated, directly or indirectly (see Chapter 22, “[Determination Histories](#)”).

Date Formats in Biota: U.S. and International Formats

Along with preserving other endangered historical curiosities such as inches and acres, the USA stands alone in placing the day of the month first, followed by month and year, while the rest of the world does it the sensible way, day-month-year, from smallest to largest unit of time.

Fortunately for the user, Biota does not care which way you set the date format (International vs. US) in your computer’s operating system (Windows or MacOS). Biota figures out which OS date setting is in use and observes the following conventions:

- **On Input screens, Record Listing screens,** and in printed reports, dates always match the system setting.
- **In the Sort and Query Editors,** all dates match the system setting. When using the Search Editor for a date field, be sure to enter the date using the same format as the system setting.
- **On labels,** all dates are in International format, regardless of the system setting. On labels, you can choose to express the month as either the English three-letter abbreviation (12 Apr 1994) or with Roman numerals (12 IV 1994).
- **In the Import and Export Editors,** if you select a date field to import or export, Biota offers a choice of International, US, or ANSI (YYYYMMDD) date format, regardless of the system setting.
- **In all other Export tools,** dates match the system setting.
- **All Biota Data Files are completely date-cross-compatible,** regardless of the current system setting, the system setting under which they were created, the Biota

version under which they were created (all the way back to Version 1 in 1995), or the platform (Windows or Mac OS) on which they were created.

- **If you change the Date Format setting in your operating system** after launching Biota, you will be reminded by an appropriate message.



Entering Dates

To enter a date in a record, you enter numerals in three separate, labeled fields, as shown here. (The entries *Dy:*, *Mo:*, and *Yr:* are simply guides to the fields, which are always present. You enter only the numbers.)

- **If your computer operating system is set to International date format:**

Collected By	<input type="text" value="C. Darwin"/>		
Date Collected (or Date Started)	Date Collection Completed (Optional)		
<input type="text" value="Dy: 30"/> <input type="text" value="Mo: 9"/> <input type="text" value="Yr: 1832"/> <input type="button" value="Today"/>	<input type="text" value="Dy: 3"/> <input type="text" value="Mo: 10"/> <input type="text" value="Yr: 1832"/> <input type="button" value="Today"/>		

- **If your computer operating system is set to US date format:**

Collected By	<input type="text" value="C. Darwin"/>		
Date Collected (or Date Started)	Date Collection Completed (Optional)		
<input type="text" value="Mo: 9"/> <input type="text" value="Dy: 30"/> <input type="text" value="Yr: 1832"/> <input type="button" value="Today"/>	<input type="text" value="Mo: 10"/> <input type="text" value="Dy: 3"/> <input type="text" value="Yr: 1832"/> <input type="button" value="Today"/>		

Entering Today's Date

To enter today's date (more precisely, the date set in your computer's operating system), click the "Today" button next to a date entry area or use the keyboard equivalent.

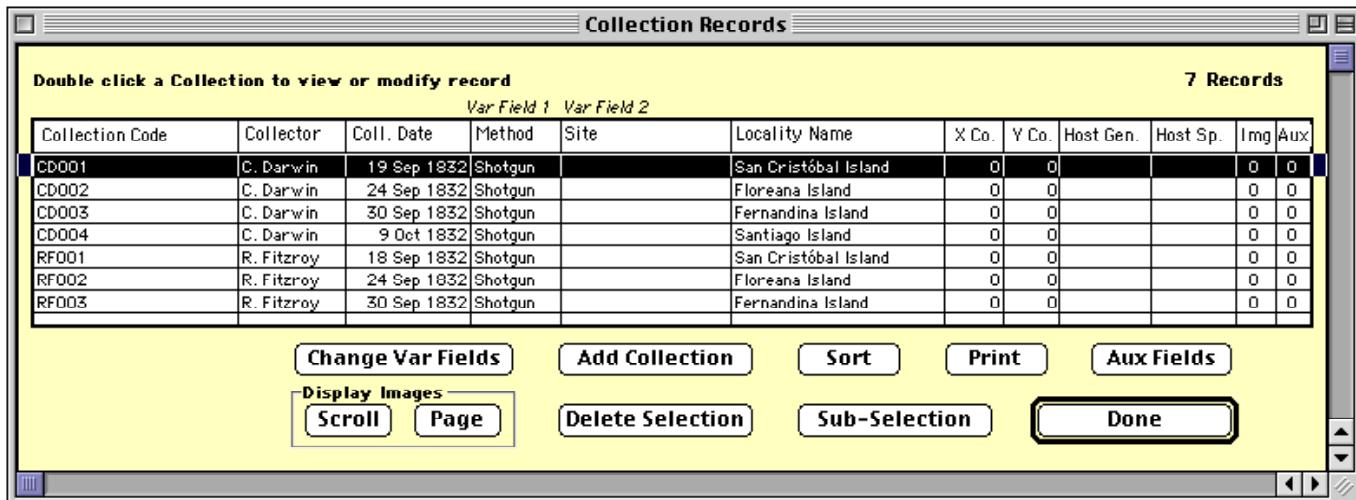
FUNCTION	MAC OS	WINDOWS
First "Today" button on a screen	COMMAND-T (⌘-L)	CTRL-T
Second "Today" button on same screen	OPTION-T	ALT-T

Entering a Default Date

You can use the Field Value Defaults tool (Special menu) to enter any date automatically as the default, for any user-enterable date field. See Chapter 17, "[Default Entries and Entry Choice Lists \(Pick Lists\)](#)."

Date Displays on Record Listing Screens

In Record Listing screens, Biota displays dates in International or US date format, according to your operating system setting. The three-letter English abbreviation is used for the month, to avoid any ambiguity in work settings that use both systems.



Partial dates (see the next section in this chapter, "[Partial Dates](#)") are displayed as Month (abbreviated) Year, or Year.

Collection Date ranges (see "[Collection Date Ranges](#)" later in this chapter) are displayed in condensed format, but may nonetheless be too long to be seen in full in a Record Listing screen. To view a Collection Date range in full, you may need to open the record in the Input screen by double-clicking it in the Record Listing screen.

Partial Dates

Partial dates are allowed in several of Biota's date fields. Especially for historic specimens, the exact dates of collection, preparation, and determination are often not

known. Instead, collection dates on specimen labels often show only month and year, or just the year. *For collection, preparation, and determination dates*, Biota allows you to enter dates in any of three formats:

- **International date format:**
 - ◊ **Complete date:** DD/MM/YYYY (e.g., enter 17/05/1975 for 17 May 1975)
 - ◊ **Month-year date:** MM/YYYY (e.g., enter 00/05/1975 for May 1975)
 - ◊ **Year-only date:** YYYY (e.g., enter 00/00/1975 for 1975)
- **US date format:**
 - ◊ **Complete date:** MM/DD/YYYY (e.g., enter 05/17/1975 for May 17, 1975)
 - ◊ **Month-year date:** MM/YYYY (e.g., enter 05/00/1975 for May, 1975)
 - ◊ **Year-only date:** YYYY (e.g., enter 00/00/1975 for 1975)

How Biota Handles Partial Dates

For most purposes, there is no reason to pay any attention to how Biota handles partial dates internally. *But if you need to import or export partial dates, you will need to read this section and the next one.* In addition, you may want to read this section to understand how records are sorted when some records have complete dates and some have partial dates.

Biota keeps track of complete and partial dates by means of a second, internal Date Flag field paired with each of the date fields that allow partial dates (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). Thus, Date Determined is paired with a field called Date Det Flag, an integer field of length 1 that has the value 0 if you enter a complete date for Date Determined, the value 1 if you enter a month-year date, and the value 2 if you enter a year-only date.

Partial dates are actually recorded as complete dates (4th Dimension accepts only complete dates in a date field). For screen display, labels, or printed reports, however, Biota displays or prints only month and year from records with month-year dates and only the year for year-only dates (as flagged by the corresponding Date Flag field).

Specifically, Biota uses the following internal conventions to record complete and partial dates:

- **Complete date** (e.g., 17 May 1975): Biota records the complete date plus a 0 in the corresponding Date Flag field.
- **Month-year date** (e.g., May 1975): Biota records the *first* day of the month (1 May 1975), plus a 1 in the corresponding Date Flag field.
- **Year-only date** (e.g., 1975): Biota records the *last* day of the year (31 December 1975), plus a 2 in the corresponding Date Flag field.

Importing and Exporting Partial Dates

The only time you will ever see or need to be concerned with Date Flag fields is if you need to export partial dates using the “Export by Tables and Fields” tool (see Chapter 27, “[Exporting Data](#)”) or import partial dates using the “Import by Table and Fields” tool (see Chapter 28, “[Importing Data](#)”).

For importing partial dates, you can use any convention you wish (e.g., middle day of the month for month-year dates, middle day of the year for year-only dates), as long as you import the correct Date Flags.

Collection Date Ranges

Sometimes specimens are collected automatically in traps or nets over a period of time (even seeds in seed traps), so that the exact date of capture for a specimen is not known. Or, specimens are known to have been collected on a certain expedition or cruise for which the start date and end date are known, even though no specific collection date was recorded for individual specimens.

In such cases, you may enter the first date for the collection period in the “Date Collected” field and the last date for the collection period in the “Date Collection Completed” field (internally called “DateCollEnd”), both in the Collection table. Both fields allow any mixture of complete and partial dates.

Collected By			
C. Darwin			
Date Collected (or Date Started)	Date Collection Completed (Optional)		
Mo: 9 Dy: 30 Yr: 1832	Today	Mo: 10 Dy: 3 Yr: 1832	Today

Collection Date Ranges on Labels and in Exported Text Files

Collection Dates and Collection Date ranges are always printed or exported in International format for labels, condensed “intelligently” (see “[Collection Labels](#)” in Chapter 15) and in some kinds of exported text files (see Chapter 27, “[Exporting Data](#)”).

If both the Date Collected field and the Date Collection Completed (internally, “Date Coll End”) fields have been entered in a Collection record, a Collection or Locality label made using that record will include the date range, condensed if possible. Here are the rules with examples:

COSTA RICA: Cartago Cerro de la Muerte, La Georgina Cordillera de Talamanca Elev 3100m, 9°41'0"N83°52'0"W coll. R. Colwell, 9-12 Jan 1976	COSTA RICA: Cartago Cerro de la Muerte, La Georgina Cordillera de Talamanca Elev 3100m, 9°41'0"N83°52'0"W coll. R. Colwell, Jan-Mar 1976
COSTA RICA: Cartago Cerro de la Muerte, La Georgina Cordillera de Talamanca Elev 3100m, 9°41'0"N83°52'0"W coll. R. Colwell, 29 Jan-2 Feb 1976	COSTA RICA: Cartago Cerro de la Muerte, La Georgina Cordillera de Talamanca Elev 3100m, 9°41'0"N83°52'0"W coll. R. Colwell, Jan 1975-Mar 1976

- Complete dates in the same month:** The label for a collection made between 9 January 1976 and 12 January 1976 would read 9-12 Jan 1976.
- Complete dates in the same year, but not the same month:** The label for a collection made between 29 January 1976 and 2 February 1976 would read 29 Jan-2 Feb 1976.
- Month-Year dates in the same year:** A collection made during the period January through March in 1976 would be labeled Jan-Mar 1976.
- Month-Year dates in the different years:** A collection made during the period December 1975 through March 1976 would be labeled Jan 1975-Mar 1976.
- One date complete, one partial:** You can even use a complete date for Date Collected and a partial date for Date Collection Completed, or vice versa, but no

attempt is made to condense the label format. A collection made between an unknown day in December 1975 and 20 January 1976 would be written Dec 1975–20 Jan 1976 on a label, to avoid ambiguity.

Spatial Coordinates

Information on collection of specimens has always included geographical data, with steadily increasing precision as the centuries have passed. At present, two trends in georeferencing are evident.

First, museums and herbaria are struggling to add geographical coordinates to historical specimen data based on place names. This is a difficult and tedious task that can be automated to only a certain degree by using geographical place name databases and Geographic Information Systems (GIS). How to interpret a collector's notation "25 km NW Guadalajara, Jalisco, Mexico" requires human judgment: Did the collector mean 25 km along a road or in a direct line? Was the distance measured from the center of the city or from the edge (and if the edge, where was the edge at the time of collection)? How precisely was the distance measured? And, of course, many older collections use political units as their only locality data: "Bolivia," or "Park County, Colorado" or historical political units like "Veragua." What do you enter in a database for the latitude and longitude of Bolivia?

Second, more recent collections usually carry specific latitude and longitude information (or the equivalent in UTM, Lambert, or other coordinate systems). Collectors now use Geographic Positioning System (GPS) devices that provide latitude and longitude information accurate to within a few meters, and GPS units of even greater accuracy will soon be in the backpack, or pocket, or on the wrist of every collector of new specimens. Again, however, the problem of precision arises for coordinate data. If a collector used a large-scale map to guess at the coordinates of a collecting site, the precision will be less than if a high-resolution topographic map was used, and far less than if a GPS device was used. For these reasons, specimen databases need to provide a way to record not only geographical coordinates, but also a way to record and display their estimated level of accuracy.

Meanwhile, ecological studies often require a way to record the spatial coordinates of quadrats or sampling sites within a grid or geographical locality.

Options for Recording Spatial Coordinates in Biota

Biota's data structure (see Appendix A, "[Biota Tables, Fields, and Relational Links](#)") provides three ways to record geographical coordinate data and to indicate its accuracy.

- **The X Coordinate, Y Coordinate, and XY Accuracy fields** of the Collection table. (See the next section in this chapter, "[Spatial coordinate fields in the Collection table](#).")
- **The Latitude, Longitude, and Lat-Long Accuracy fields** of the Locality table. (See "[Latitude and Longitude \(Locality Table\)](#)," later in this chapter.)
- **The three Alternate Coordinates fields** of the Locality table. (See "[Alternate Coordinates \(Locality Table\)](#)," later in this chapter.)

Spatial Coordinate Fields in the Collection Table

The Collection table offers three fields for recording spatial coordinates: X Coordinate, Y Coordinate, and XY Accuracy. These fields have several possible uses.

Because Collection records have a many-to-one relation with Locality records (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”), you might use a single Locality record to register approximate or historical coordinates for a named place (for example, a watershed, region, or county) as the parent record for many Collection records. The linked Collection records might be a mixture of modern and historical records for latitude and longitude. The modern records might include GPS readings (in decimal degrees), while the historical records leave these fields blank.

Alternatively, for a quadrat-based sampling study, you could use the X Coordinate and Y Coordinate fields of the Collection table for quadrat coordinates and a parent Locality record to identify and record Latitude and Longitude for the plot grid.

Input for these fields is located on the Georeference tab of the Collection Input screen.

NOTE: The X Coordinate and Y Coordinate fields of the Collection table are real number fields, whereas the XY Accuracy field is alphanumeric. Values for the X Coordinate may take any numeric value, negative or positive.

Latitude and Longitude (Locality Table)

Biota stores Latitude and Longitude data in units of decimal degrees—the standard system used in Geographic Information Systems (GIS) work. Nonetheless, Biota offers three unit systems for the entry and display of latitude and longitude values in the Locality table. You can enter data using any of the three systems and freely use different systems for different records in the same data file. As you make an entry in any of the systems, Biota instantly translates the value into the other two and displays all three versions in the Coordinates panel of the Locality input screen. See “[Entering Locality Data: The 'General' Tab](#)” in Chapter 11 for details and instructions.

- **System 1: Degrees/Minutes/Seconds (DMS).** This is the traditional system found in most gazetteers and atlases—but see the important warning, below.
- **System 2: Integer Degrees, Decimal Minutes.** This is the system used by most Geographical Positioning System (GPS) instruments.
- **System 3: Decimal Degrees.** This is the system used in Geographical Information Systems (GIS).

WARNING: Some gazetteers list Latitude and Longitude values in DMS, but use a *format* that looks like Integer Degrees with Decimal Minutes. For example, $24^{\circ} 48.39$ actually means $24^{\circ} 48' 39''$ in these gazetteers. The easiest way to detect this deceptive format is to see if you can find any values in the gazetteer to the right of the “decimal point” that exceed 59. If not, those values are Seconds, not the decimal part of true Decimal Minutes.

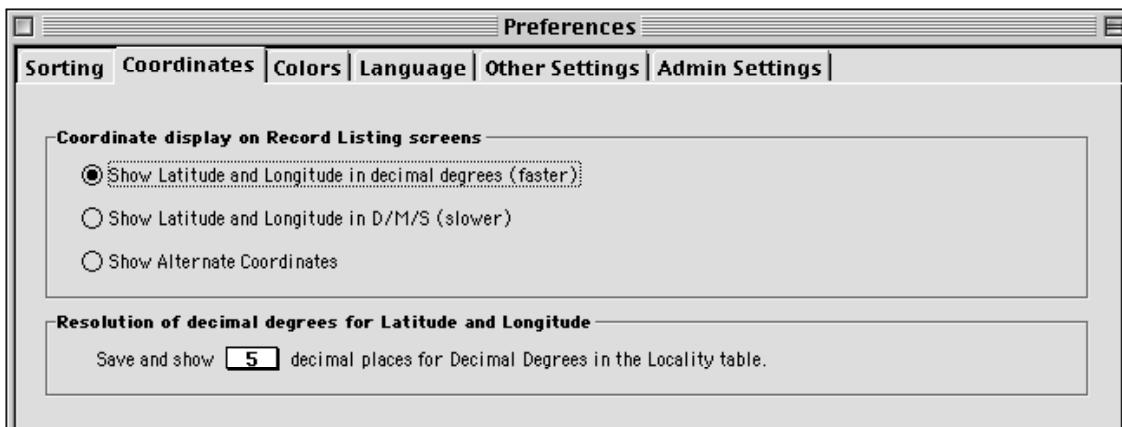
Conversion Formulas for Latitude and Longitude Unit Systems

Here are the formulas Biota uses to convert to and from Decimal Degrees (the internal storage format in Biota), where *Int* means the integer part of a real number, *Abs* means absolute value, and *Round* means round to the nearest integer:

- **Degrees** = *Int [Abs (Decimal Degrees)]*
- **Decimal Minutes** = *[Abs (Decimal Degrees) — Degrees] * 60*
- **Minutes** = *Int (Decimal Minutes)*
- **Decimal Seconds** = *(Decimal Minutes — Minutes) * 60*
- **Seconds** = *Round (Decimal Seconds)*
- **Decimal Degrees** = *Degrees + (Minutes/60) + (Seconds/3600)*

Setting the Display Format and Internal Resolution for Latitude and Longitude

Using settings in the Coordinates tab of the Preferences screen (Special menu), you can control the onscreen display for the geographical reference fields of the Locality table and the resolution for decimal degrees of latitude and longitude.



- In the upper panel of the Coordinates tab, “Coordinate display on listing screens,” you can select one of three options for coordinates in Record Listing screens.
 - ◊ **Show Latitude and Longitude in decimal degrees.** Because Latitude and Longitude are stored internally by Biota in decimal degrees, display in this format is faster than for the second option.
 - ◊ **Show Latitude and Longitude in D/M/S** (Degrees/Minutes/Seconds). This option is slower than the preceding option, because Biota must compute the degree/minute/seconds (DMS) equivalents for each record as it is displayed.
 - ◊ **Show Alternate Coordinates.** This option is explained in the section “[Alternate Coordinates](#)” later in this chapter.
- In the lower panel of the Coordinates tab, “Resolution of decimal degrees for Latitude and Longitude,” use the popup list to set the number of decimal places that Biota records internally for decimal degrees of Latitude and Longitude. You can select any setting from zero through 6 decimal places. The default value is 5 decimal places. (Spatial resolution at 6 decimal places is about 1 cm.)
This setting also controls the number of decimal places shown for decimal degrees in the Georeference tab of Locality Input screen, as well as the display in Record

Listing screens when the “Coordinate display on listing screens” option is set to “Show Latitude and Longitude in decimal degrees.”

Setting Latitude and Longitude Display Resolution for Individual Locality Records

In individual Locality records, you can use special key words in the “Lat-Long Accuracy” field (the “Accuracy” input area in the Georeference tab of the Locality Input screen) to control the display, printing, and export of Latitude and Longitude data.

- **Degrees and Minutes only option.** In particular Locality records, Latitude and Longitude data may be accurate to Degrees and Minutes, but not to Seconds, especially for most historic data and for coordinates taken from maps. You can tell Biota to display, print, and export only Degrees, Minutes, and Hemisphere by entering the value “Minutes” (or “Minutos,” for the Spanish interface) in the Lat Long Accuracy field. (Do not enter the quotation marks.)
- **Degrees only option.** Likewise, if the Latitude and Longitude values in a Locality record are accurate only to Degrees, you can enter “Degrees” (or “Grados”) in the Lat Long Accuracy field to instruct Biota to display, print, and export only Degrees and Hemisphere.

If you enter any other value besides “Minutes,” “Minutos,” “Degrees,” or “Grados” (in either lowercase, uppercase, or mixed case) in the “Lat Long Accuracy” field or if you leave the field blank, Biota displays, prints, and exports full data for Degrees, Minutes, and Seconds for each record in which either Latitude or Longitude or both are not blank (zero).

This format option affects the Locality Input and Record Listing screens and the Collection Input screen (if the DMS display option is set); exported or printed locality labels of all kinds (see Chapter 15, “[Printing Labels](#)”); exported Specimen Flatfiles and Specimens Examined Lists (see Chapter 27, “[Exporting Data](#)”); and exported Web pages (see Chapter 33, “[Exporting Static Web Pages](#)”).

Alternate Coordinates (Locality Table)

In cartography and in Geographic Information System (GIS) software, the spherical coordinate system used for latitude and longitude (also called GRS for Geographic Reference System or Global Reference System) forms the underlying basis for all map projections, for transformations among map projections and map coordinate systems (latitude/longitude is not considered a map projection), and for adjustment of coordinates for different models of the Earth’s shape (“datums”). Biota offers full support for latitude/longitude entry and display (see “[Latitude and Longitude \(Locality Table\)](#),” earlier in this chapter).

Other coordinate systems, however, are used for geographical reference data in many parts of the world and are often found in label or catalog data for historic specimens. Biota accommodates alternate (non-latitude/longitude) geographical coordinate systems, such as UTM or Lambert coordinates, or the Township-Range-Section system of U.S. Public Land Surveys, by means of three “Alternate Coordinate” Core fields in the Locality table.

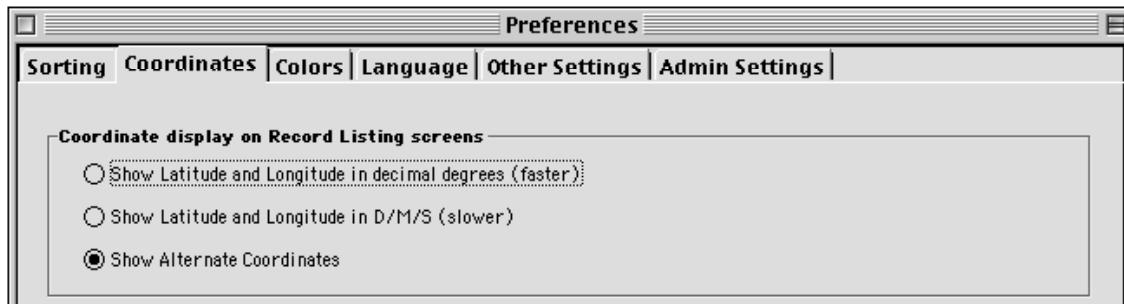
- **The default names** of the Alternate Coordinate fields are “Alternate Coordinate 1,” “Alternate Coordinate 2,” and “Alternate Coordinate 3.” (The internal names are “Alt Coordinate 1,” “Alt Coordinate 2,” and “Alt Coordinate 3.”) Each is an 80-character alphanumeric field.

- **The fields may be renamed** (see Chapter 18, “[Renaming Fields](#)”). Some examples are presented in the section “[Suggestions for Use of the Alt Coordinate Fields](#),” later in this chapter.
- **The fields support Entry Choice Lists (Pick Lists)**, if you wish to activate and create them (see Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#)”).

NOTE: Although intended primarily for coordinate data, the Alternate Coordinate fields can be used for any alphanumeric locality data you wish. (If you use the fields for non-coordinate data, be sure to uncheck the “Show Alternate Coordinates” display option in the Coordinates tab of the Preferences screen; see “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#),” earlier in this chapter.)

Setting the Display Format for Alternate Coordinates in the Locality Record Listing Screen

In the Coordinates tab of the Preferences screen (Special menu), you can set Biota to display data from the Alternate Coordinates fields instead of Latitude and Longitude in Record Listing screens.



In the upper panel of the Coordinates tab, “Coordinate display on listing screens,” select “Show Alternate Coordinates.” (The other options on the Coordinates tab are explained in the section “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#),” earlier in this chapter.)

Suggestions for Use of the Alt Coordinate Fields

Dozens of map projections and map coordinate systems are used in cartography (for example, ARC/INFO GIS software supports 38 map projections¹). Here are suggestions for using Biota's Alternate Coordinate fields for three systems commonly used by biologists for recording collection or observation sites for specimens. (Other coordinate systems can be similarly accommodated, as necessary.)

- **UTM (Universal Transverse Mercator) Rectangular Coordinates.** In the UTM system, Earth is divided into 60 zones, each spanning six degrees of longitude between 84°N and 80°S latitude. UTM coordinates are always positive, seven-digit integers that represent the number of meters east (the *easting* or “X” coordinate on

¹ Snyder, J. P. 1992. *Map Projections and Coordinate Management: Concepts and Procedures (ARC/INFO User's Guide)*. Redland, CA: Environmental Systems Research Institute, Inc.

a map) and north (the *northing* or “Y” coordinate on a map) of the southwest corner of the UTM zone. (There are actually two sets of coordinates for each zone, one for the Southern and one for the Northern Hemisphere.) Thus, coordinate values alone are not sufficient to identify a point on Earth; the UTM Zone and hemisphere must also be specified. (In addition, the *datum*—the ellipsoid used to model Earth—affects UTM coordinates and all other map coordinate values.)

In the United States, USGS (U.S. Geological Service) and BLM (Bureau of Land Management) topographic maps (except for older ones) have a UTM grid, or at least UTM tick marks in the margins, with the UTM coordinate value for each grid line in the map margins. (UTM grids on many U.S. topographic maps are actually “alien grids,” since many of the maps themselves are not Universal Transverse Mercator projections but Lambert or Polyconic projections. UTM coordinates can nonetheless be read accurately off such maps.²) The UTM Zone for any map that includes UTM coordinates can usually be found in the map legend (on U.S. topographic maps, in lower-left corner).

For UTM coordinates, if all three Alternate Coordinate fields are available, it would be logical to use the Alternate Coordinate 1 field for the easting value (which, by convention, is the first of the pair), Alternate Coordinate 2 for the northing value, and Alternate Coordinate 3 to record the UTM Zone (including the hemisphere, if you are likely to have data from both the Northern and Southern hemispheres in your Data File). You can rename the fields appropriately (see Chapter 18, “[Renaming Fields](#)”). You might consider preceding the easting value by “UTM” so that labels (see below) clearly indicate what the coordinates are. The Alternate Coordinates panel of the Coordinates tab of the Locality Input screen would then appear as below (for San Vito de Java, Costa Rica).

Alternate Coordinates	
UTM Easting	UTM 0283220
UTM Northing	0975500
UTM Zone	Zone 17

NOTE: Be sure to include leading zeroes for coordinate values so that all have exactly seven digits—otherwise, alphanumeric sorts will not make sense.

- **Lambert Rectangular Coordinates.** In some countries (Costa Rica, for example), Lambert rectangular coordinates appear on high resolution maps prepared in the Lambert Conformal Conic projection (with no UTM grid or tick marks superimposed). As with UTM (see above), the Lambert coordinates are northings and eastings from the southwest corner of a particular, named Lambert zone, defined by a standard point of origin. The recommendations for UTM, above, are easily applied to Lambert coordinates.

² Thompson, M. M. 1987. *Maps for America: Cartographic Products of the U.S. Geological Survey and Others*, Third Edition. Washington, D. C.: U.S. Department of the Interior, Geological Survey, U.S. Government Printing Office.

- **Township, Range, and Section (TRS).** The TRS system has been used in the United States since 1785 for Public Lands Surveys. TRS is neither a map projection nor a unified coordinate system, but rather, a series of more than 30 independent, historically fixed land surveys, each ranging in the four cardinal directions from a different, largely arbitrary point of origin, covering twenty-nine States³. In effect, TRS data combine large scale coordinates (*Township* for the north-south coordinate, *Range* for the east-west coordinate) with *Section* data, which identify land areas within Townships.

Despite the idiosyncratic nature of TRS data, museums and herbaria in Public Lands States sometimes need to database specimens that are referenced to TRS data. To avoid ambiguity, the named *principal meridian* that uniquely identifies each Public Lands Survey should be specified for the TRS data for each locality record in a database—although the combination of State plus County or Parish can also suffice (e.g., Biota's State/Province and District fields).

If all three Alt Coordinate fields are available, one option for recording TRS data (which follows legal land title usage), is to use Alternate Coordinate 1 for Township (north-south), Alternate Coordinate 2 for Range (east-west) and principal meridian, and Alternate Coordinate 3 for Section (and subsection) data (e.g., with semicolons separating fields, “T18S; R1E of 6th Principal Meridian; NW1/4 of NW1/4 of Sec. 29”). Alternatively, with three fields, Alternate Coordinate 1 could be Township, Alternate Coordinate 2 could be Range and Section, and Alternate Coordinate 3 the principal meridian name, as shown in this example, with data for a site in Colorado.

Alternate Coordinates	
Township	T8S
Range & Section	R72W, Sect 12
Principal Meridian	6th PM

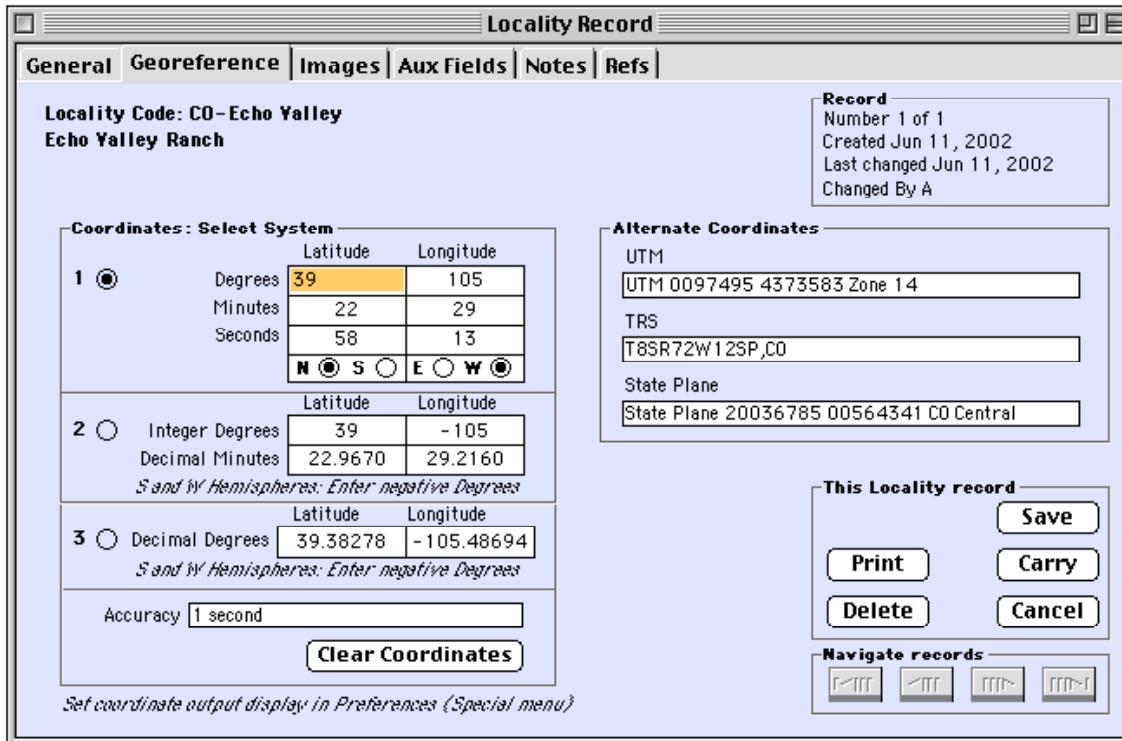
If two of the Alternate Coordinate fields are used for TRS data, one field could accommodate Township, Range, and Section data (e.g., “T18SR1E, NW1/4 NW1/4 of Sec. 29”) and the other the principal meridian (“6th Principle Meridian”).

If only one field is to be used for TRS data, the principal meridian could be omitted, or incorporated as a code, as in the example on the next page for “More than one non-latitude/longitude system.”

NOTE: If you intend to use the utility program TRS2LL (see the Note in the section “[Converting Non-Latitude/Longitude Coordinates to Latitude and Longitude](#),” later in this chapter) to convert TRS data to latitude and longitude, or the reverse, be sure to study the TRS format required for TRS2LL input and follow it in your Biota Data File, either in a single Alt Coordinate field or split among Alt Coordinate fields in a format easily combined in a text editor.

³ Thompson, M. M. 1987. *Maps for America: Cartographic Products of the U.S. Geological Survey and Others*, Third Edition. Washington, D. C.: U.S. Department of the Interior, Geological Survey, U.S. Government Printing Office. Pp. 80-87.

- **More than one non-latitude/longitude system.** If you need to record coordinates for records using more than one non-latitude/longitude coordinate system, you should consider using a single field for each system. (The 80 characters allowed for each field should be sufficient.) Here is an example for Latitude and Longitude, UTM, TRS, and the State Plane System (a third system used for US States), with data for a site in Colorado. (The TRS data are in the format required for the transformation program TRS2LL; see the Note in the section “[Converting Non-Latitude/Longitude Coordinates to Latitude and Longitude](#),” later in this chapter)).



Alternatively, you could use Locality Auxiliary Fields (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”), defined as you wish, but they will not appear on standard Biota labels and reports (see “[Latitude/Longitude and Alternate Coordinates on Labels or Reports and in Exported Text Files](#)” later in this chapter).

Converting Non-Latitude/Longitude Coordinates to Latitude and Longitude

Biota itself does not convert non-latitude/longitude coordinates (or TRS data) to latitude and longitude, or the reverse. Utility programs exist to do so, however, and Biota’s data import-export tools make it painless to get data in and out of your Biota Data File for such conversions.

Take the following steps to convert non-latitude/longitude coordinates to latitude and longitude. (The reverse process is analogous.)

1. Enter the non-latitude/longitude coordinates in the Alternate Coordinate fields.
2. Use the Export Editor to export the coordinate data to a text file (see Chapter 27, “[Exporting Data](#)”). Export only Locality Code and the appropriate Alternate

Coordinate fields for each Locality record affected—plus Country, State/Province, and or District (County) if needed by the conversion utility.

NOTE: If the non-latitude/longitude coordinate data are in Locality Auxiliary Fields, use the Export Auxiliary Fields tool instead of the Export Editor (see “[Exporting Auxiliary Field Values](#)” in Chapter 16.)

3. **Using a utility program with the text file as input, transform the map coordinates to Latitude and Longitude.** The Latitude and Longitude values must be in decimal degrees. If they are not, you will need to transform them to decimal degrees using the formulas in the section “[Conversion formulas for latitude and longitude unit systems](#)” earlier in this chapter.
4. **Use the “Import Update” capability of Biota’s Import Editor** (see Chapter 28, “[Importing Data](#)”) to add the Latitude and Longitude data to the existing Locality records, leaving the Alternate Coordinate data intact.

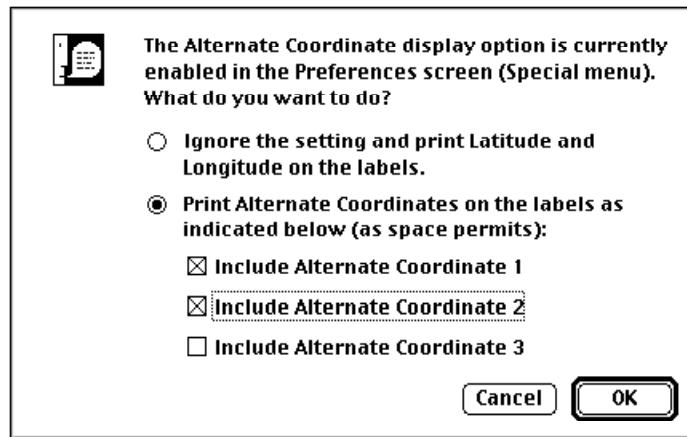
NOTES:

- a. **To transform UTM to Latitude and Longitude or the reverse** (as well as to and from State Plane coordinates, for specific ellipsoids), an easy-to-use, interactive shareware program by John Banta, called “Coordinate Transform,” is available from SeisSoft Co. at www.connect.net/jbanta/Welcome.html. A commercial, file-based version is also available. The U.S. Geological Survey also offers a variety of software for cartographic transformations (available through www.usgs.gov).
 - b. **To translate TRS data into latitude and longitude or the reverse**, for most U.S. Public Lands states, a freeware program called TRS2LL is available from Martin Wefald (<http://www.geocities.com/jeremiahobrien/trs2ll.html>). The Latitude/Longitude output (for estimated Section centers) is already in decimal degrees, but you *must add the minus sign to all longitude values* to indicate location in the Western Hemisphere (TRS is endemic to the U.S.), before importing into Biota.
-

Latitude/Longitude and Alternate Coordinates on Labels or Reports and in Exported Text Files

For geographic reference data on Locality labels that Biota prints or exports, and in the standard printed report for the Locality table, you can choose between either Latitude and Longitude (expressed in the Degrees/Minutes/Seconds system, see “[Latitude and Longitude \(Locality Table\)](#)” earlier in this chapter) or Alternate Coordinate field values.

- **To print or export label data that includes Alternate Coordinates** on pin, slide, or vial Locality labels or herbarium labels (see Chapter 15, “[Printing Labels](#)”) take the following steps:
1. **Set the display format** in the Coordinates tab of the Preferences screen (Special menu) to the Alternate Coordinates option, as shown in the section “[Setting the Display Format for Alternate Coordinates in the Locality Record Listing Screen](#)” earlier in this chapter.
 2. **Create a Specimen Record Set** that includes the Specimen records for which you want to print or export data for Locality labels.
 3. **Choose a Locality label style for Specimens from the Labels menu.** (The Specimen Locality label tools are “Pin Labels: Locality,” “Slide Labels: Locality,” “Vial Labels: Locality,” and “Herbarium Labels.”) An option screen appears.
 4. **Click the Alternate Coordinates option** to enable the Alt Coordinate field checkboxes.



If you have defined Aliases for the Alternate Coordinate fields, the Aliases appear in the option screen by the checkboxes, instead of the default Alternate Coordinate field names. (See Chapter 18, “[Renaming Fields](#).”)

5. **Check the checkbox for each of the three fields you want to include** on the labels or report, as shown above.

WARNING: It is up to you to ensure that the data you intend to show on labels or a Locality report can be accommodated in the space available.

- **To print or export label data that includes Latitude and Longitude** for pin, slide, or vial locality labels or on herbarium labels (see Chapter 15, “[Printing Labels](#)”), you can use either of two methods:

Either: Set the display format in the Coordinates tab of the Preferences screen (Special menu) to either of the Latitude/Longitude options, as shown in the section “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#)” earlier in this chapter.

Or: Follow the steps, above, for printing Alternate Coordinates but choose the Latitude/Longitude (default) option in [Step 4](#), above.

- **To include Alternate Coordinate data in exported Collection label data**, see the instructions in Chapter 15, “[Printing Labels](#).”
- **To include Alternate Coordinate data in exported Specimen flatfiles or Loan records**, check the appropriate boxes in the “Export Specimen Flatfile” setup screen (see “[Exporting Specimen Flatfiles](#)” in Chapter 27).
- **To include Alternate Coordinate data in exported Specimen Web pages**, check the appropriate boxes in the “Specimen Fields” options screen (see Chapter 33, “[Exporting Static Web Pages](#)”).
- **To display Alt Coordinate fields in the Locality Record Listing screen, in addition to Latitude and Longitude**, see the section “[Changing the Fields Displayed in a Record Listing Screen](#)” in Chapter 10.
- **To include Alternate Coordinates on the standard printed Locality Report**, set the display format in the Coordinates tab of the Preferences screen (Special menu) to the Alternate Coordinates option, as shown in the section “[Setting the Display Format for Alternate Coordinates in the Locality Record Listing Screen](#)” earlier in this chapter.

Chapter 10

Working With Records

In Record Listing and Input Screens

Every Core table in Biota (see “[Core Tables](#)” in Chapter 3) uses the same standard format for listing records. These *Record Listing screens* all share many functions that are explained in detail in this chapter. Once you know how to use the standard Record Listing screen for one Biota Core table, you know how to use them all.

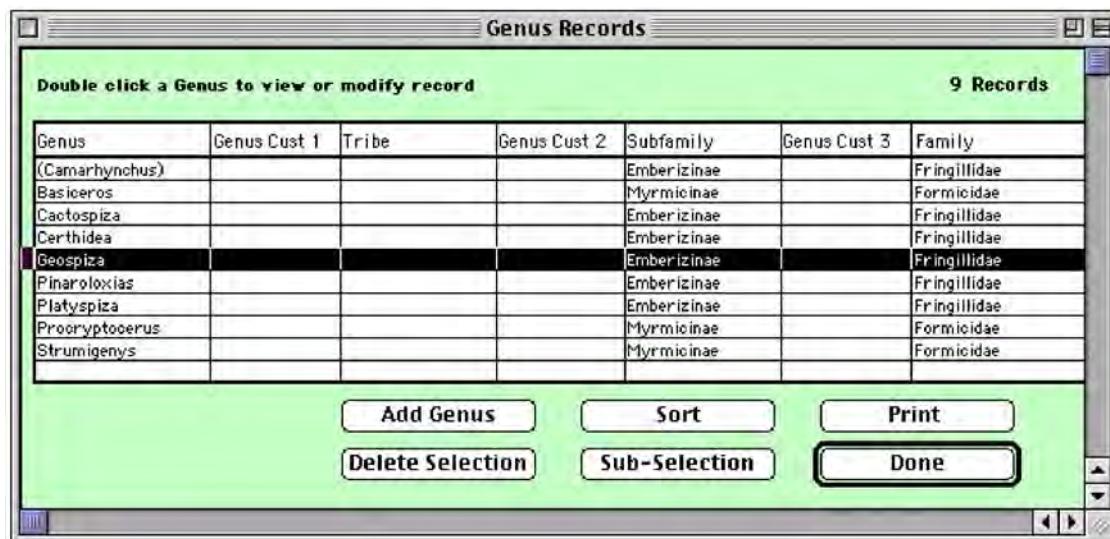
Biota also uses two other kinds of screens to list records, which differ in some important ways from the standard Record Listing screens for Core tables. These are explained in other chapters.

- **Record Listing screens for Auxiliary Fields.** See Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#),” if you need help with viewing or manipulating information in Auxiliary Fields.
- **Record Listing screens for Images.** See Chapter 19, “[Images](#),” if you need help working with Image Listing screens.

In the rest of this chapter, the term *Record Listing screen* refers the standard Record Listing screen.

Displaying Records in a Standard Record Listing Screen

Biota offers many tools for finding records (see Chapter 12, “[Finding and Updating Records](#)” and Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”). For every tool in the Find menu (and the record-finding tools in the Series menu), records are displayed in the standard Record Listing screen for the appropriate table.



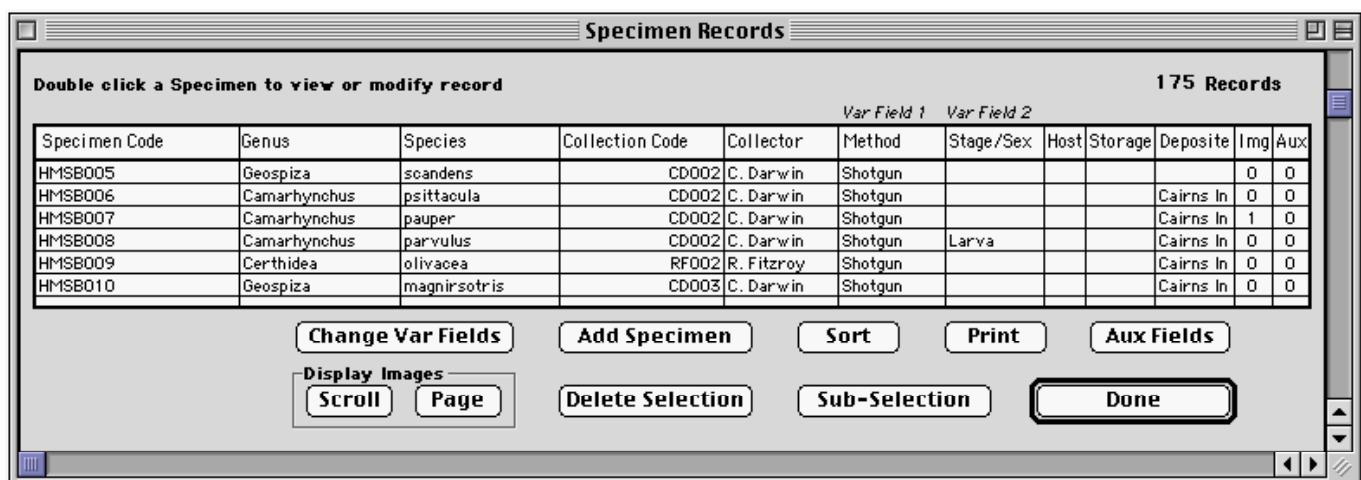
Here are the Genus records for a group of records for Galápagos Finches, shown in the Genus Record Listing screen.

Changing the Fields Displayed in a Record Listing Screen

You can change the fields displayed in certain columns of the Specimen, Species, Collection, and Locality Record Listing screens. The columns are labeled Variable Field 1 and Variable Field 2 (as well as 3 and 4, in the Locality Record Listing screen). You control the display using the button labeled “Change Var Fields” found at the base of the Record Listing screen.

For example, to change the fields displayed in the Specimen Record Listing screen, follow these steps. (The procedure is identical for the Species, Collection, and Locality Record Listing screens.)

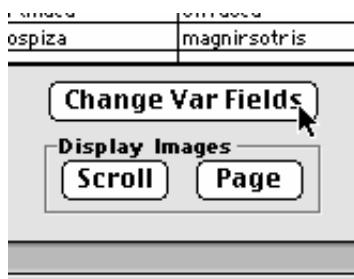
1. **Display any selection of records** in the Specimen Record Listing screen, using tools from the Input, Series, Find, or Display menus.



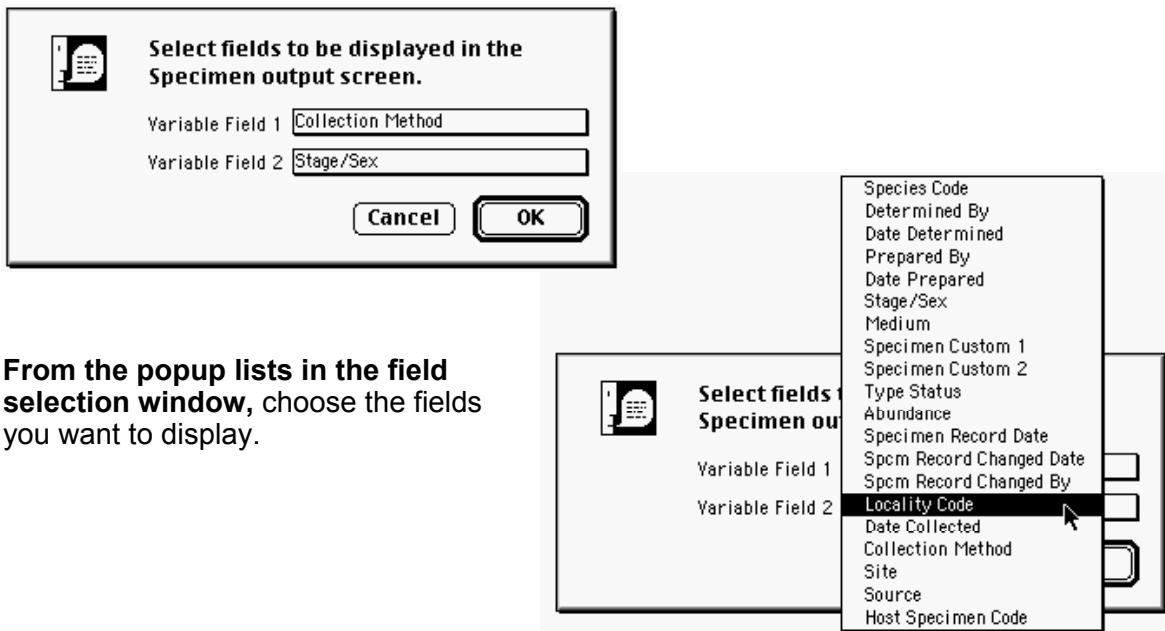
Notice the labels Var Field 1 and Var Field 2 above the columns that currently display the [Specimen] Method and [Specimen] Stage/Sex fields (the default fields displayed in these columns).

Var Field 1	Var Field 2
Method	Stage/Sex
Shotgun	

2. **To change the fields displayed, click the “Change Var Fields” button, found on the lower left of the Record Listing screen.**



The Variable Fields selection window appears, showing the current field for each of the two Var Field columns in the Record Listing screen.



- From the popup lists in the field selection window, choose the fields you want to display.

The selection of records is re-displayed, showing the fields you selected for display ([Collection] Date Collected and [Collection] Locality Code, in the example below).

Var Field 1		Var Field 2	
Collector	Date Coll.	Loc. Code	Host
C. Darwin	Sep 24, 183	Floreana	
C. Darwin	Sep 24, 183	Floreana	
C. Darwin	Sep 24, 183	Floreana	
C. Darwin	Sep 24, 183	Floreana	
R. Fitzroy	Sep 24, 183	Floreana	
C. Darwin	Sep 30, 183	Fernandina	

n Sort Print /

NOTE: Each time you launch Biota, all Variable Fields in Record Listing screens are set to the default fields (see the next section, "[Fields Available for Display in Record Listing Screens](#)"). If you change the fields displayed using the method above, the changes remain in effect for the duration of the current Biota session unless you change them again. (With Biota4D running under 4D Server, each Client has independent control over Variable Fields.)

Fields Available for Display in Record Listing Screens

The previous section, "[Changing the Fields Displayed in a Record Listing Screen](#)," explains how to use the Variable Fields feature of the Specimen, Collection, Locality,

and Species Record Listing screens. Here are the fields you can display for each of these screens.

NOTE: In the lists that follow:

- (a) **An asterisk indicates a field that can be re-named** using the Core Field Alias (see Chapter 18, “[Renaming Fields](#)”). If you have defined an Alias for such a field, the Alias, not the Internal Field Name listed below, appears in the popup lists for field selection as well as in the Record Listing screen header.

- (b) **A number symbol (#) indicates a “Record Changed By” field.** These fields are available only if the checkbox “Show Record Changed By field in Input screens” is checked in the “Admin Settings” tab of the Preferences screen (Special menu).



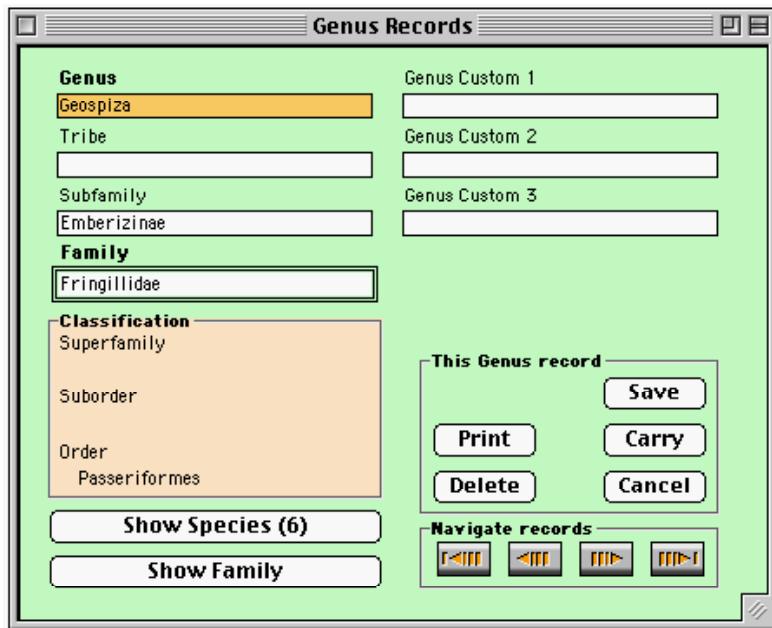
- **In the Specimen Record Listing screen**, you can display any of the following 20 fields in either of two Variable Field columns:
 - ◊ **Fields of the Specimen table:** Species Code, Determined By, Date Determined, Prepared By, Date Prepared, Stage/Sex*, Medium*, Specimen Custom 1*, Specimen Custom 2*, Type Status*, Abundance, Specimen Record Date, Specimen Record Changed Date, and Specimen Record Changed By#.
 - ◊ **Fields of the Collection table:** Locality Code, Date Collected, Collection Method*, Site*, Source*, and Host Specimen Code.
 - ◊ **Default fields:** [Collection] Method* and [Specimen] Stage/Sex*.
- **In the Collection Record Listing screen**, you can display any of the following 17 fields in either of two Variable Field columns:
 - ◊ **Fields of the Collection table:** Locality Code, Collection Method*, Site*, Source*, Host Specimen Code, Collection Record Date, Collection Record Changed Date, and Collection Record Changed By#.
 - ◊ **Fields of the Locality table:** District*, State/Province*, Country*, Elevation*, Latitude (in decimal degrees), Longitude (in decimal degrees), Alt Coordinate 1*, Alt Coordinate 3*, and Alt Coordinate 3*.
 - ◊ **Default fields:** [Collection] Method* and [Collection] Site*.
- **In the Locality Record Listing screen**, you can display any of the following 12 fields in any of four Variable Field columns:
 - ◊ **Fields of the Locality table:** District*, State/Province*, Country*, Elevation*, Latitude (in decimal degrees), Longitude (in decimal degrees), Alt Coordinate 1*, Alt Coordinate 2*, Alt Coordinate 3*, Locality Record Date, Locality Record Changed Date, and Locality Record Changed By#.
 - ◊ **Default fields:** [Locality] District*, [Locality] State/Province*, [Locality] Country*, and [Locality] Elevation*.
- **In the Species Record Listing screen**, you can display any of the following 21 fields in either of two Variable Field columns:
 - ◊ **Fields of the Species table:** Species Author, Subgenus*, Section*, Subspecies, Subspecies Author, Variety, Variety Author, Common Name*, Distribution*, Type Locality*, Type Depository*, Valid Sp Code, Species Record Date, Species Record Changed Date, and Species Record Changed By#.

- ◊ **Fields of the Genus table:** Family, Tribe*, Subfamily*, Genus Custom 1*, Genus Custom 2*, and Genus Custom 3*.
- ◊ **Default fields:** [Genus] Family and [Species] Subgenus*.

Viewing, Editing, Printing, or Deleting Individual Records from an Input Screen

To open an individual record from the Record Listing screen for any Core table, simply double-click the record (or use keyboard shortcuts to select and open the record; see “[Keyboard Shortcuts for Record Listing Screens](#)” later in this chapter).

The record for the genus *Geospiza* is being double-clicked in the example in the illustration in the previous section. The record appears in the Input (single-record) screen for the table.



With the record open in the Input screen, you can view the record, edit any field in the record and save the changes, duplicate (Carry) the record, print it, delete it, or access linked records in the parent table (the Family table, in the example) or the child table (Species, in the example).

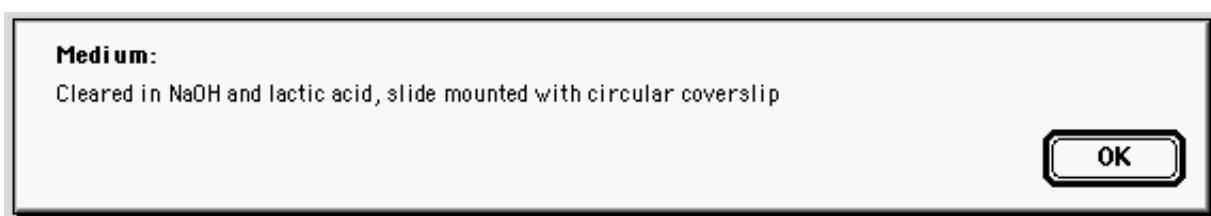
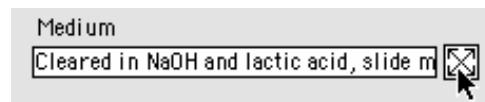
Some Input screens, like the Genus screen above, consist of a single page. Others, such as the Species input screen below, consist of several pages, accessed by a series of tabs. (You can use keyboard shortcuts to move between tabs in these screens. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7.)

Species Record

Classification	Subsp/Names	Synonymy	Dist/Types	Images	Aux Fields	Notes	Refs
geosfort							
Geospiza fortis Gould 1837							
Species Code	geosfort	Assign					
Genus	Geospiza						
Specific Name (Specific Epithet)	fortis						
Species Author (& Date)	Gould 1837	X					
Subgenus		()					
Section		X					
Synonymy	Valid Species Code geosfort						
A valid Species name with no synonyms in the database							
Record Number 1 of 1 Created May 14, 1996 Last changed Changed By							
Classification Family Fringillidae Order Passeriformes							
Show Genus Record Show Specimens (3) This Species record Save Print Carry Delete Cancel							
Navigate records 							

To View an Entry That Is Longer Than the Entry Area

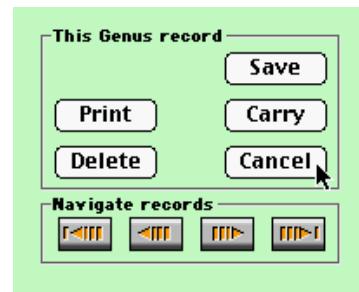
In Biota Input screens, the entry area for some fields are too short to display a very long entry in full. To view the entire entry, click the “zoom” icon placed just to the right of the entry area. Biota shows the full entry in a special window.



To Return to the Record Listing Screen

To dismiss a record displayed in an Input screen and return to the Record Listing screen, without making any changes in the record, click the “Cancel” button. Biota returns you to the Record Listing screen, with the record selected.

KEYBOARD SHORTCUT: Instead of clicking the “Cancel” button, simultaneously press the CTRL and ENTER keys (Windows) or the COMMAND (⌘) and RETURN keys (Mac OS).



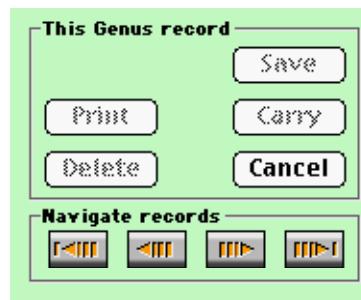
Editing and Saving Changes to the Record

To edit a field, click in the field and use standard editing techniques. Any changes you make can be saved by either of two methods:

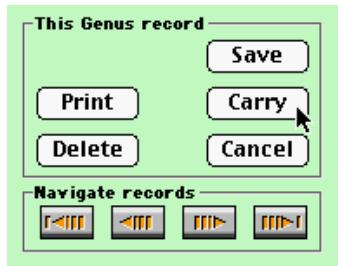
- **Either: Click the “Save” button.** In this case, Biota saves all changes and returns you to the Record Listing screen, with the same record selected.
- **Or: Click any of the Navigation buttons.** To accept any changes and move to another record in the current selection, click any button in the “Navigate Records” panel (the arrow buttons). This action automatically saves any changes.

KEYBOARD SHORTCUTS: Instead of clicking the “Save” button, simultaneously press the CTRL and S keys (Windows) or the COMMAND (⌘) and S keys (Mac OS). To move to the next record, press the CTRL and RIGHT ARROW keys (Windows) or the COMMAND (⌘) and RIGHT ARROW keys (Mac OS). To move to the previous record, press the CTRL and LEFT ARROW keys (Windows) or the COMMAND (⌘) and LEFT ARROW keys (Mac OS).

NOTE: If the “Save,” “Carry,” and “Delete” buttons are dimmed on the Input screen, it means you do not have Write privileges. The record is in Read-only mode. You must either click “Cancel” or a navigation button to dismiss the record (or use the keyboard equivalent).



Duplicating a Record Displayed in the Input Screen Using the “Carry” Button



Every Input screen includes a “Carry” button that allows you to make a new record using the current record as a template. Because, in many cases, only one or two fields need changing between a template record and a new one, this capability saves a great deal of effort.

1. **Click the “Carry” button in the Input screen.** A new record appears with the Key field (see “[Key Fields](#)” in Chapter 3) blank but all or most other fields (depending on the table) already filled in with the same information as the existing record. (The record below uses the *Geospiza* record as a template.)
2. **Enter a new value for the Key field.** You can also change any other fields you wish in the new record.
 - ***Either:*** Click the “Save” button to accept the new record and return to the Record Listing screen.
 - ***Or:*** Click the “Carry” button again to accept the new record and use it as a template for an additional new record.

In either case, if you have made any changes in the current record or it is a new record, the template record is saved first, automatically, when you click the “Carry” button.

Notes:

- a. A saved, existing record can also be used as a template. See “[Using an Existing Record as a Template for a New Record](#)” later in this chapter.
 - b. Auxiliary Fields and Notes can be carried or not, according to a setting in the “Other Settings” tab of the Preferences screen (Special menu). See “[Carrying Auxiliary Fields](#)” in Chapter 16 and “[Carrying Notes](#)” in Chapter 11.
-

KEYBOARD SHORTCUT: Instead of clicking the “Carry” button, simultaneously press the CTRL and K keys (Windows) or the COMMAND (⌘) and K keys (Mac OS).

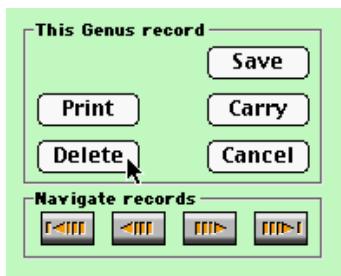
Printing a Single Record Displayed in an Input Screen

Click the “Print” button in the Input screen to print the information for the record shown in the Input screen, using the standard report format for the table. (See Chapter 14, “[Printing Reports](#)” for other printing options.)

KEYBOARD SHORTCUT: Instead of clicking the “Print” button, simultaneously press the CTRL and P keys (Windows) or the COMMAND (⌘) and P keys (Mac OS).

Deleting a Record Displayed in the Input Screen

- Click the “Delete” button.



- Confirm or Cancel the deletion. Unless the record is a new one that has not yet been saved, Biota presents you with one of two kinds of warnings.

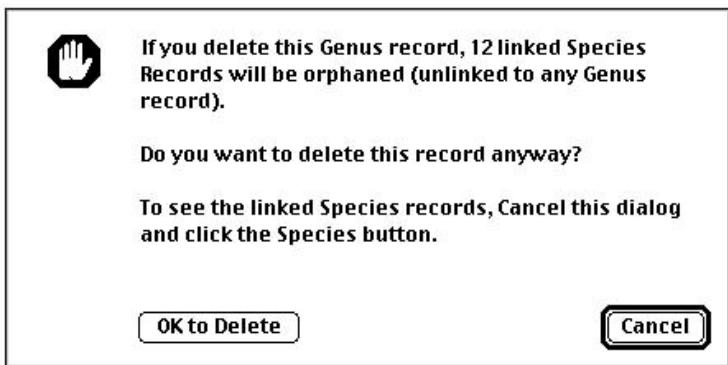
- For tables that have no linked Images, Auxiliary Fields, Notes, and/or References, such as the Genus table, Biota presents a simple warning.



- For tables that have associated Notes, Auxiliary Fields, or Image records (the Species, Specimen, Collection, Locality, and Loans tables), deleting a record automatically deletes any linked child records in Peripheral tables (Images, Auxiliary Fields, Notes, and/or Reference links, plus Determination History records linked to Specimen records). In such cases, Biota presents the warning below.



3. **Confirm or Cancel the orphaning of Core table child records.** If the record is linked to one or more child records in other Core tables (but not otherwise), Biota also posts the warning below, with the appropriate table names (Genus and Species, in this example). (For information on displaying linked records, as suggested in the warning, see “[Displaying Records With a Child Records Button](#)” later in this chapter.)



4. **Deleting a Personnel Record.** In the case of Personnel records, which may be linked to child records in several Core and Peripheral tables, the warning screen is more complex.



KEYBOARD SHORTCUT: For safety's sake, there is no keyboard shortcut for the “Delete” button.

Moving Up the Table Hierarchies from an Input Screen: Parent Record Buttons

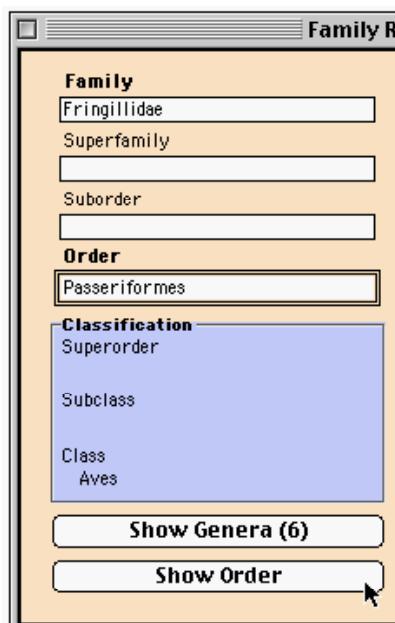
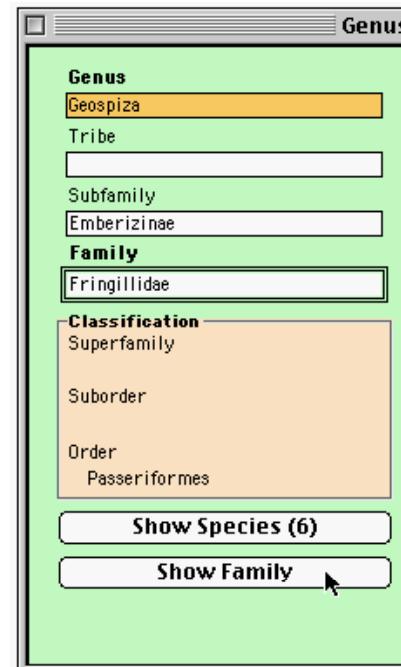
With an individual record open in the Input screen, you can display and edit the related parent record by clicking the “Show...” button with the name of the parent table. These buttons are referred to collectively as *Parent Records buttons*, although each button has its own name (e.g., “Show Family” in the Genus Input screen, “Show Locality” in the Collection Input screen). (See [Linking Fields: Parent and Child Records](#) in Chapter 3 for the definition of a parent table.)

Parent Record buttons are available on the Input screen for each level (rank) of the taxonomic hierarchy, with the exception of Kingdom, which has no parent table. The Specimen Input screen has Parent Record buttons for both Species and Collection, and the Collection Input screen has a Parent Record button for Locality. Locality has no parent table, so it has no Parent Record button.

Displaying Records with the Parent Record Button

For example, with the genus record for *Geospiza* open in the Genus Input screen (right), the principal fields from the linked Family record (*Fringillidae*) are shown in the “Classification” panel of the Genus Input screen. To see the full record for Family *Fringillidae*, click the “Family” button. (The Genus record remains open in its own window.)

The full record for the Family *Fringillidae* then appears in the Family Input screen (below). Information from the related Order record (for Order Passeriformes) appears in the “Classification” panel of the Family Input screen. Click the “Show Order” button to see the full record for the Order Passeriformes.



If you want, you can continue on up the taxonomic hierarchy by clicking Parent Record buttons. To return to the original record, click the “Cancel” button—or the “Save” button, if you have made changes.

KEYBOARD SHORTCUT: Instead of clicking a Parent Record button, simultaneously press the CTRL and UP ARROW keys (Windows) or the COMMAND (⌘) and UP ARROW keys (Mac OS). For the Specimen Input screen, those shortcuts apply to the “Show Species” button; for the “Show Collection” button simultaneously press the ALT and UP ARROW keys (Windows) or the OPTION (⌥) and UP ARROW keys (Mac OS)

Editing Records Displayed with the Parent Record Button

You can open a parent record using the Parent Record button, edit it, and save any changes by clicking the “Save” button in the Input screen for the record you edited.

Moving Down the Table Hierarchies From an Input Screen: Child Records Buttons

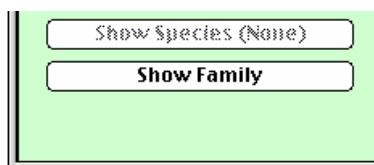
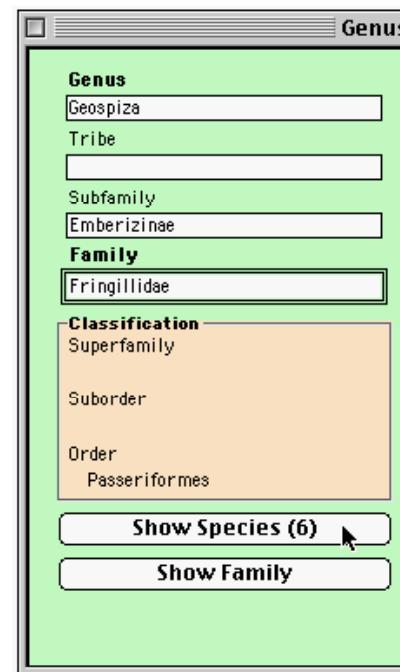
With an individual record open in the Input screen, you can display all related records in the next lower table in the hierarchy (child records) by clicking the “Show...” button with the name of the child table. In the example at the right, the “Show Species” button is being clicked. (See “[Linking Fields: Parent and Child Records](#)” in Chapter 3 for the definition of a child table.)

These buttons are referred to collectively as *Child Records buttons*, although each button has its own name. For example, the Child Records button in the Family Input screen is labeled Genera, whereas the Child Records button in the Locality Input screen is labeled Collections. (See Appendix A, “[Biota Tables, Fields, and Relational Links](#),” for table hierarchies.)

Child Records buttons are available on the Input screen for each level (rank) of the taxonomic hierarchy, as well as for the Locality and Collection Input screens. The Specimen table has no child tables (among the Core tables), so the Specimen Input screen has no Child Records button.

Biota displays a number next to each Child Records button, showing the number of child records for the parent record currently displayed. In the example above, the “Show Species” button indicates that 6 Species records are linked to the Genus record for Geospiza.

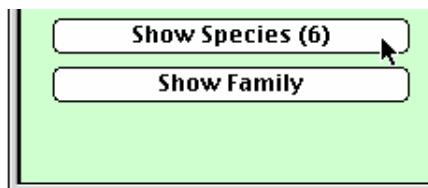
If there are no child records, the number displays zero and the Child Records button is disabled.



When you display child records using a Child Records button, they appear in an the standard Record Listing screen in a new window. Meanwhile, the parent record remains open in its own window. You can close the parent window if you want, and the Child Records window will remain open.

Displaying Records with a Child Records Button

For example, with the genus record for *Geospiza* open in the Genus Input screen, the “Show Species” button is enabled, and the number in the parentheses in the button text shows that there are six Species records linked to *Geospiza*.



If you click the “Show Species” button, the six species of *Geospiza* finches are displayed in the Species Record Listing screen.

Species Records							
Double click a Species to view or modify record				6 Records			
Species Code	Family	Genus	Specific Name, Subsp., Variety	Subgenus	Images	Aux	
geosconi	Fringillidae	Geospiza	conirostris		0	0	
geosdiff	Fringillidae	Geospiza	difficilis		0	0	
geosfort	Fringillidae	Geospiza	fortis		0	0	
geosfuli	Fringillidae	Geospiza	fuliginosa		0	0	
geosmagn	Fringillidae	Geospiza	magnirostris		0	0	
geosscan	Fringillidae	Geospiza	scandens		0	0	

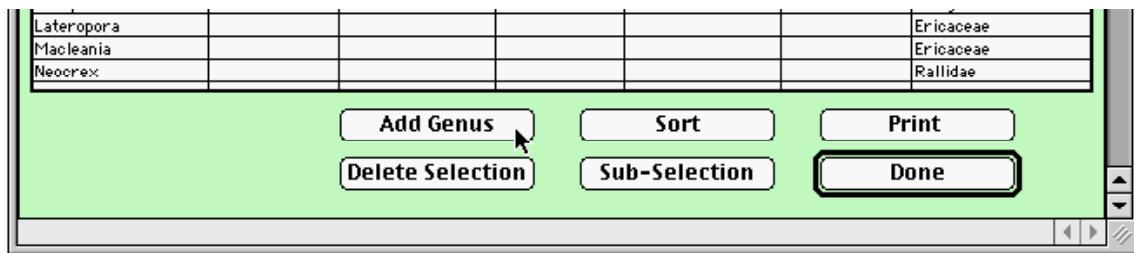
If you wish, you can now open and edit any of the child records listed to view or edit, or repeat the process by displaying the child records (Specimen records, in this example) for one of the Species displayed.

To return to the parent record (*Geospiza*, in the example), click the “Done” button on the child table Record Listing screen (above).

KEYBOARD SHORTCUT: Instead of clicking a Child Record button, simultaneously press the CTRL and DOWN ARROW keys (Windows) or the COMMAND (⌘) and DOWN ARROW keys (Mac OS).

Using the Add Record Button

The Add Record button at the base of the Record Listing screen for each Core table opens a new, blank record in the Input screen for the table. Although these buttons are referred to collectively as *Add Record buttons*, each button has its own name. For example, the Add Record button in the Genus Record Listing screen is labeled “Add Genus,” the Add Record button in the Collection Record Listing screen is labeled “Add Collection,” and so on for each Core table.



Once the Input screen is displayed by clicking an Add Record button, you can complete the new record. Click the “Save” button to accept the new record and return to the Record Listing screen, the “Carry” button to accept the new record and use it as a template for an additional new record, or Cancel to dismiss the Input screen without saving the new record.

In fact, adding a new record in this way is exactly like adding a new record using a command from the Input menu (see Chapter 11, “[Input—Table by Table](#)”), with one exception. With the Add Record approach, when you are done entering data in the record and click the “Save” button you are returned to the Record Listing screen, with the new record highlighted. To add another record, click the Add Record button again. (From the Input menu, the “Save” button accepts the record and presents a new, blank record.)

KEYBOARD SHORTCUT: Instead of clicking an Add Record button (for example, the “Add Genus” button illustrated above) in a Record Listing screen, simultaneously press the CTRL and J keys (Windows) or the COMMAND (⌘) and J keys (Mac OS).

Using an Existing Record as a Template for a New Record

Sometimes you need to create a new record that duplicates much of the information in an existing record listed in the Record Listing screen. You can use the existing record as a template for the new one.

1. **Double-click the existing record in the Record Listing screen.** The existing record opens in the Input screen. *Make no changes in the existing record.*
2. **Click the “Carry” button in the Input screen.** A new record appears, with the Key field blank, but with all, or most, other fields (depending on the table) already filled in with the same information as the existing record. (The record below uses the *Geospiza* record as a template.)

3. Enter a new value for the Key field. You can also change any other fields you wish in the new record.
 - **Either:** Click the “Save” button to accept the new record and return to the Record Listing screen.
 - **Or:** Click the “Carry” button again to accept the new record and use it as a template for an additional new record.

NOTE: As another variation, you can open an existing record, make changes in the existing record, then click Carry to accept the edited record and use it as a template for a new record.

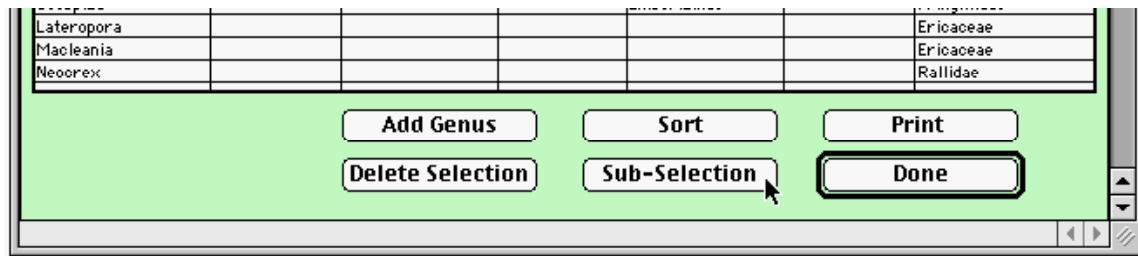
Creating a Sub-Selection of Records

Often, you will want to select one or more of the records displayed in a record Listing screen and dismiss the rest of the records. To do this, you use the “Sub-Selection” button at the bottom of the Record Listing screen.

1. Select the records that will form the new Sub-Selection.
 - **To select a single record,** click it once to highlight it.
 - **To select consecutive records,** click the first record of the group once to highlight it, then press and hold the SHIFT key and click the last record in the group.
 - **To select nonconsecutive records,** click the first record once to highlight it. Then press and hold the CTRL key (Windows) or the COMMAND (⌘) key (Macintosh) while single-clicking each additional record you want to select.

KEYBOARD SHORTCUTS: For information on keyboard shortcuts for selecting records from Record Listing screens, see “[Keyboard Shortcuts for Record Listing Screens](#)” later in this chapter.

2. Click the “Sub-Selection” button when all the records you want to include in the Sub-Selection are highlighted.



The Record Listing subsequently displays only the records in the Sub-Selection.

KEYBOARD SHORTCUT: Instead of clicking the “Sub-Selection” button, simultaneously press the CTRL and N keys (Windows) or the COMMAND (⌘) and N keys (Mac OS).

3. To designate the Sub-Selection as the current Record Set for the table, click the “Done” button, then the “OK” button in the standard Record Set option screen (see [“The Record Set Options Screen”](#) in Chapter 3).

Deleting a Group of Records from the Record Listing Screen

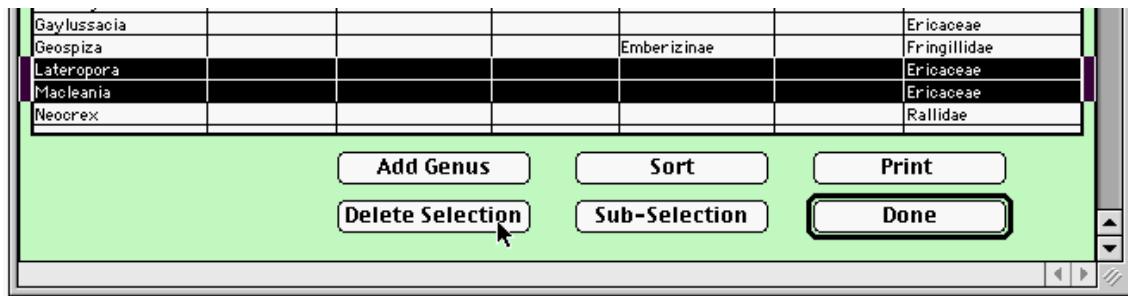
In the Record Listing screen, you can select records and delete them using the “Delete Selection” button.

NOTE: The database Administrator can set a limit on the number of records that can be deleted at each use of the “Delete Selection” button, to prevent accidental deletion of large numbers of records. See [“The ‘Admin Settings’ Tab”](#) in Appendix B.

1. Select the records that will form the new Sub-Selection.
 - To select a single record, click it once to highlight it.
 - To select consecutive records, click the first record of the group once to highlight it, then press and hold the SHIFT key and click the last record in the group.
 - To select nonconsecutive records, click the first record once to highlight it. Then press and hold the CTRL key (Windows) or the COMMAND (⌘) key (Macintosh) while single-clicking each additional record you want to select.

KEYBOARD SHORTCUTS: For information on keyboard shortcuts for selecting records from Record Listing screens, see [“Keyboard Shortcuts for Record Listing Screens”](#) later in this chapter.

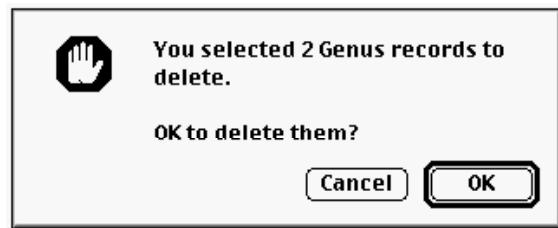
2. Click the “Delete Selection” button when all the records you want to delete are highlighted.



KEYBOARD SHORTCUT: For safety's sake, there is no keyboard shortcut for the “Delete Selection” button.

3. Confirm or Cancel the deletion. Biota displays two kinds of warnings.

- **For tables that have no linked Images, Auxiliary Fields, Notes, and/or References,** such as the Genus table, Biota presents a simple warning.
- **For tables that have associated Notes, Auxiliary Fields, or Image records** (the Species, Specimen, Collection, Locality, and Loans tables), deleting a selection of records automatically deletes any linked child records in Peripheral tables (Images, Auxiliary Fields, Notes, and/or Reference links, plus Determination History records linked to Specimen records). In such cases, Biota presents a warning like this.



4. Decide whether to orphan Core table child records. If the records to be deleted are linked to one or more child records in other Core tables (but not otherwise), Biota also posts the following warning, with the appropriate table names (Genus and Species, in this example).



If you see this warning, you can Cancel the deletion; choose to delete only those selected records that are not linked to any Core table child records; or delete all the selected records anyway, leaving some records orphaned.

NOTE: If you choose the second option (delete all selected records, even though some child records will be orphaned), you can find the orphaned records later using the “Find Orphan records” tool from the Find menu.

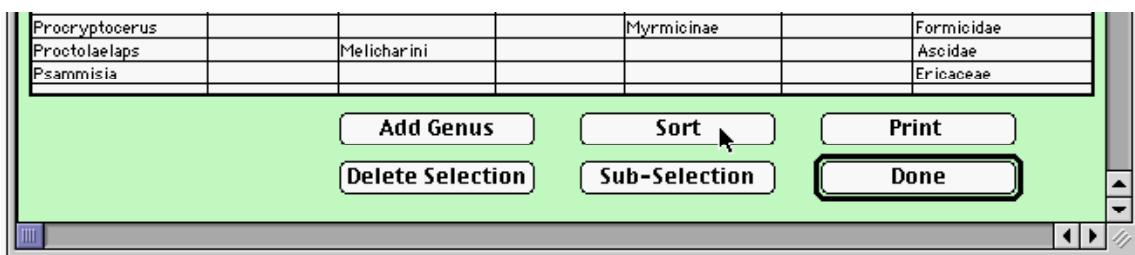
5. **Deleting Personnel records.** In the case of Personnel records, which may be linked to child records in several Core and Peripheral tables, the warning screen is more complex. Before deleting a group of Personnel records, you should consider whether you really intend to lose all the links listed in the warning screen.



Sorting Records in Record Listing Screens

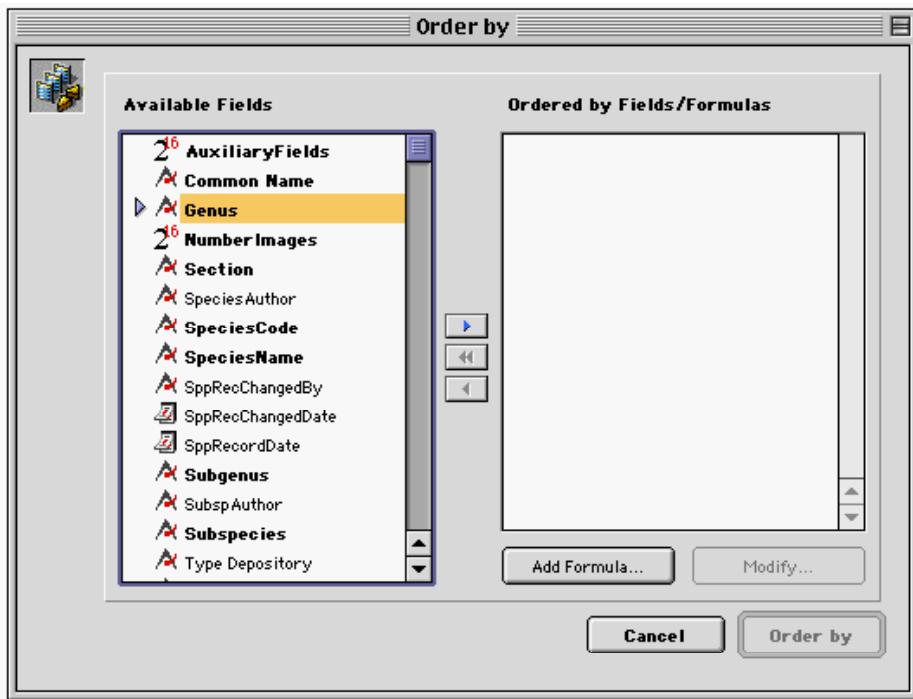
To sort the records displayed in a record Listing screen, you use the Sort Editor displayed by clicking the “Sort” button at the bottom of the Record Listing screen. The Species Record Listing screen will be used as an example in this section, but the procedures are the same for all Record Listing screens.

1. Click the “Sort” button at the bottom of the Record Listing screen.



KEYBOARD SHORTCUT: Instead of clicking the “Sort” button in a Record Listing screen, simultaneously press the CTRL and R keys (Windows) or the COMMAND (⌘) and R keys (Mac OS).

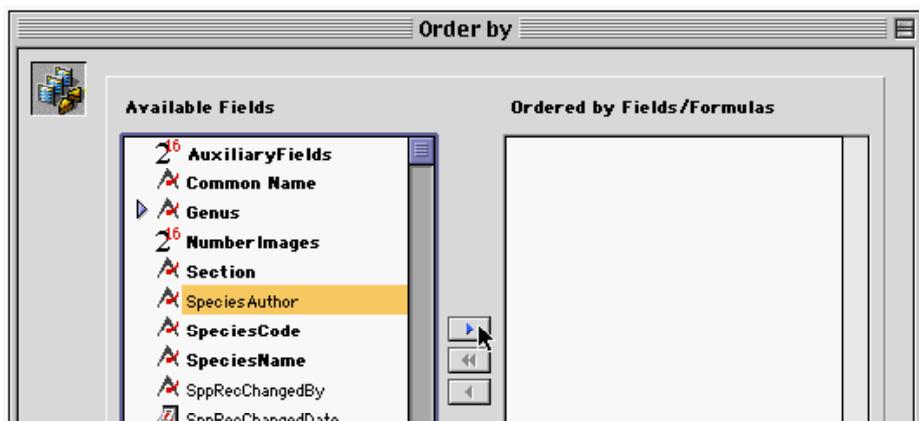
The Sort Editor (“Order by”) window appears.



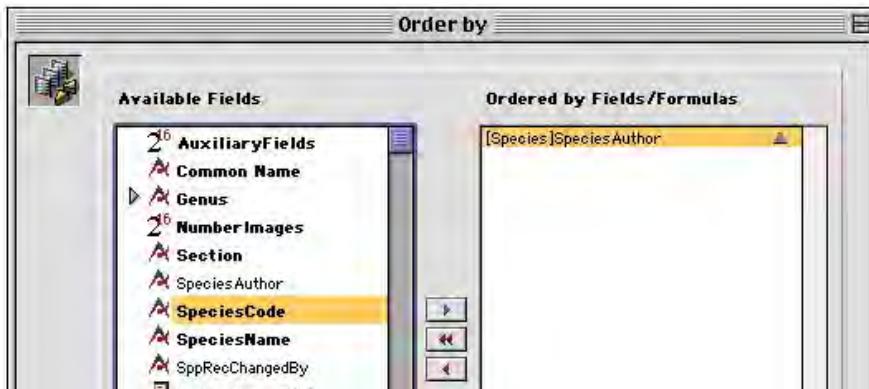
In the “Available Fields” panel on the left, you will see the names of all fields for the current table (the Species table, in the example). Field names in **boldfaced** type are indexed fields, which sort faster than non-indexed fields, but you can sort on any field. (Indexes take up space in data files and require processor time to maintain, so not all fields in Biota are indexed.)

Note: If you have defined any Core Field Aliases (see Chapter 18, “[Renaming Fields](#)”) the field aliases appear in the list instead of the default field names.

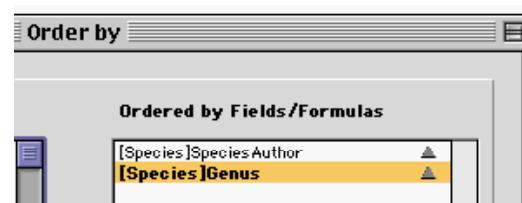
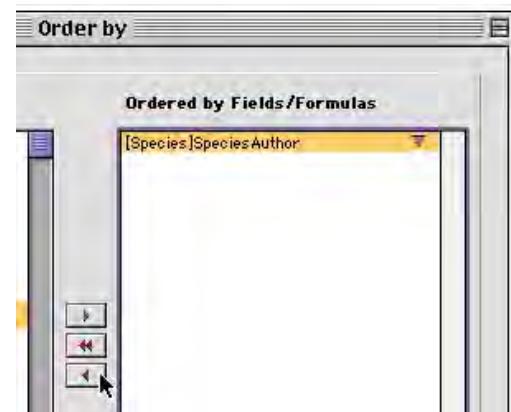
2. To sort on a field for the current table (Species, in the example), double-click a field name in the “Available Fields” panel, or select the field name and click the “insert” button (the blue, right-pointing triangle). The “Species Author” field is being selected in the example below.



The field name appears in the “Ordered by Fields/Formula” panel on the right, with an upward-pointing triangle to the right of the field name. This is the *sort direction indicator*. (Notice also that the “remove” button (the red, left-pointing triangle) and the “remove all” button (the red, left-pointing double triangle) are activated.

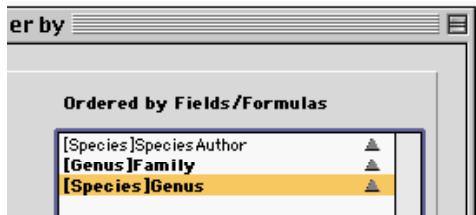


- **An upward sort direction indicator** (above) means a normal alphanumeric sort (0 to 9, then A to Z).
 - **A downward sort direction indicator** (below) means a reverse alphanumeric sort (Z to A, then 9 to 0).
3. **Changing the direction of a sort.** Click the sort direction indicator to toggle between normal and reverse sorts.
 4. **Removing a sort level.** If you make a mistake and want to remove a sort level from the list of sort criteria, select the sort level you want to remove (click once on it to highlight it), then click the “remove” button (the red, left-pointing triangle). To remove all fields at once, click the “remove all” button (the red, left-pointing double triangle).
 5. **Adding additional sort levels.** To add an additional level to the sort criteria, click another field name in the field name panel, as in Step 2. The sort proceeds hierarchically from the top of the list of sort criteria to the bottom. In the example below, Species records will be sorted alphabetically by Genus within those described by each Species Author.
 6. **Launching the Sort.** When all sort criteria are ready, click the “Order by” button at the bottom of the Sort Editor (“Order by”) window to launch the sort.



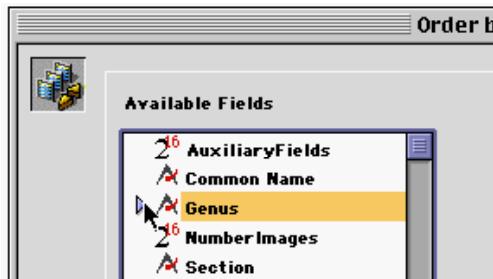
Using Fields from Related Tables for Sorting Records

You can use fields from related (linked) tables as sort criteria, as long as a child-parent relation exists between the current table (the table whose records you are sorting) and the table you use to add a sort criterion. For example, in sorting Species (child table) records, you can use fields from the Genus table (parent table).

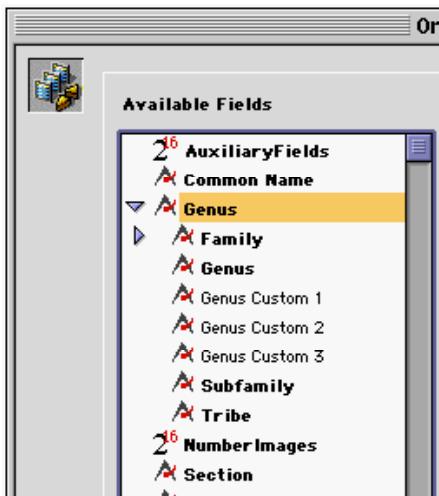


NOTE: This section assumes you are familiar with the previous section of this chapter, “[Sorting Records in Record Listing Screens](#).”

1. **Display the fields for the related (parent) table** by clicking on the list expansion icon (blue triangle) next to the name of the linking field in the current table. In the example below, the Sort Editor (“Order by”) screen has been displayed for the Species table, and the list expansion icon is being clicked for the Genus field in the “Available Fields” list.



The list of fields for the related table (the Genus table, in the example below) is displayed.



2. **Select a sort field from the related table.** Once the fields for the related table appear in the field list, you can add fields as sort criteria, using the same techniques described in the section “[Sorting Records in Record Listing Screens](#)” earlier in this chapter.
3. **Mixing sort criteria from different tables.** You can mix sort criteria from related tables. In the example below, Species records will be sorted alphabetically by Species Author (a field from the Species table), then within authors by Family (a field from the Genus table), then within Families by Genus (using the Genus field from the Species table).

NOTE: When you have a choice between using a linking field in a child table and Key field in a parent table as a sort criterion, the sort will be faster if you use the linking field in the child table. In the example above, the [Species] Genus field was added to the list instead of the [Genus] Genus field. It does not really matter which way you do it, however, and the difference in sort speed will not be noticeable unless there are many records.

Guidelines for Using Fields from Related Tables as Sort Criteria

It is up to you to ensure that a sort on a field in a related table makes sense. Here are a few guidelines:

- **You cannot sort the records in a parent table based on a field in a child table.** For example, you cannot sort Species records based on a field in the Specimens table. It makes no sense to sort Species records according to any field in the Specimens table, since there may be different values in Specimen fields for different specimens of the same Species.
- **You cannot sort the records of a table in one hierarchy (e.g., the taxonomic hierarchy) based on a field in the other hierarchy (the place hierarchy).** It makes no sense to sort Species records, for example, by the Locality Name field of the Locality table, since a species may have specimens from many localities.

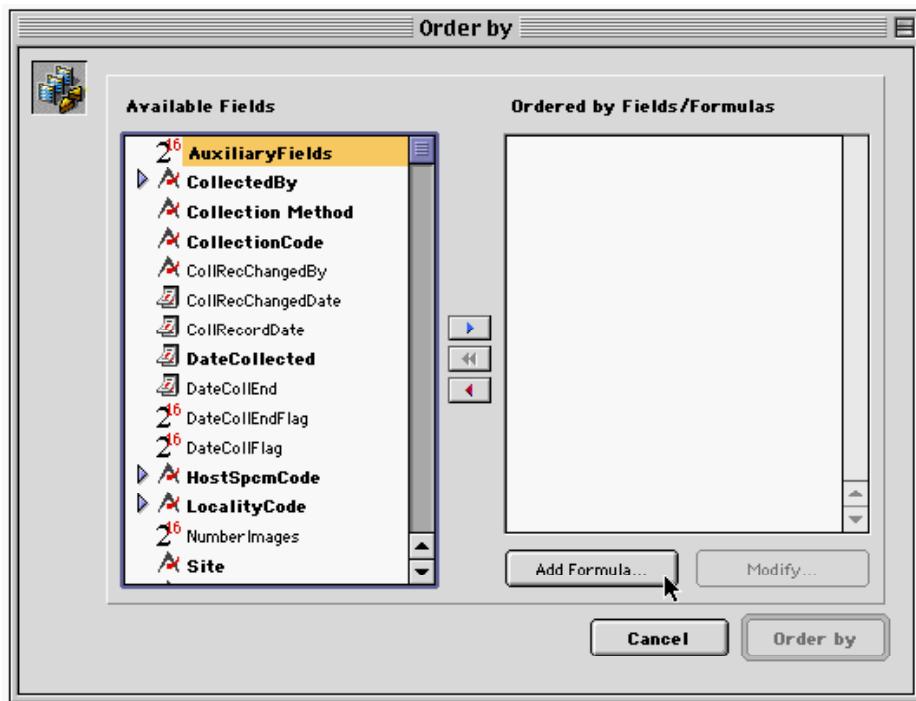
Consult Appendix A, “[Biota Tables, Fields, and Relational Links](#),” if you are unsure how Biota tables are linked.

Using Formulas to Sort Dates by Day, Month, or Year

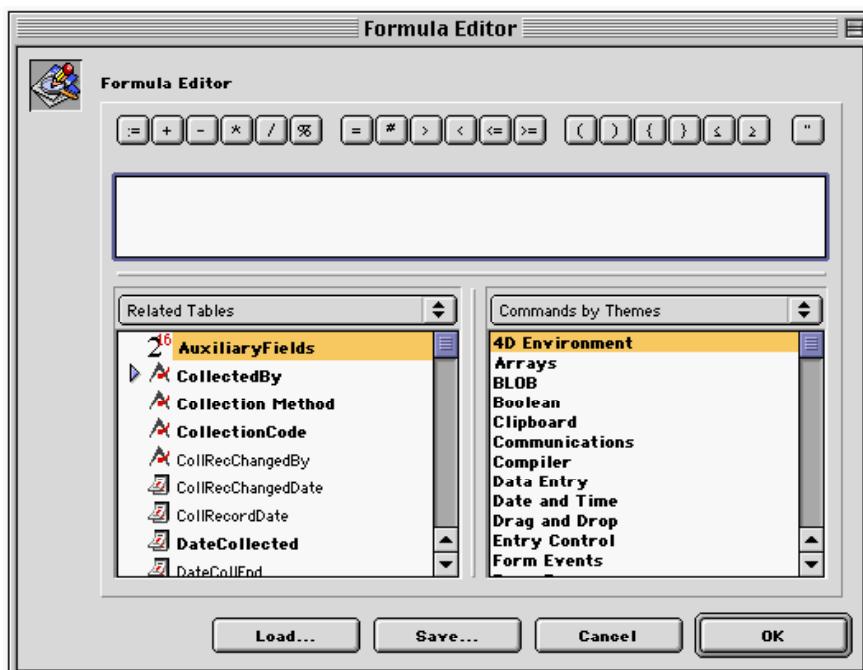
If you sort on a date field (e.g., [Collection] Date Collected) in the usual way (see “[Sorting Records in Record Listing Screens](#)” earlier in this chapter), Biota sorts records chronologically according to complete dates. Sometimes you may want to use partial dates to perform a sort. To study seasonal patterns, for example, you might want to sort by month, disregarding year and day of the month.

NOTE: This section assumes you are familiar with the previous section of this chapter, “[Sorting Records in Record Listing Screens](#).”

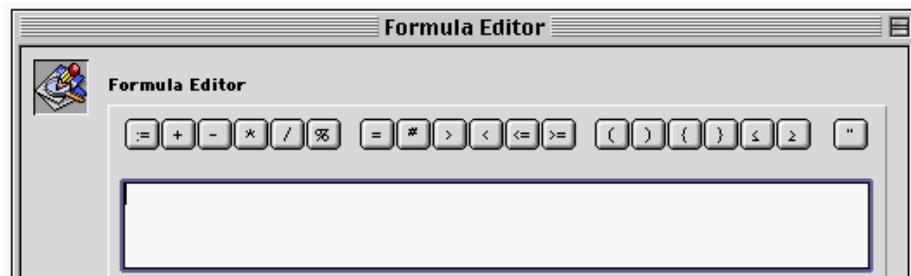
1. **Display the records to be sorted in the Record Listing screen.** Suppose you want to sort Collection records by month of collection, ignoring years and days.
2. **Click the “Sort” button at the bottom of the Record Listing screen.** The Sort Editor (“Order by”) screen appears.
3. **Click the “Add Formula” button near the bottom of the Sort Editor (“Order by”) screen.**



The 4D Formula Editor appears.



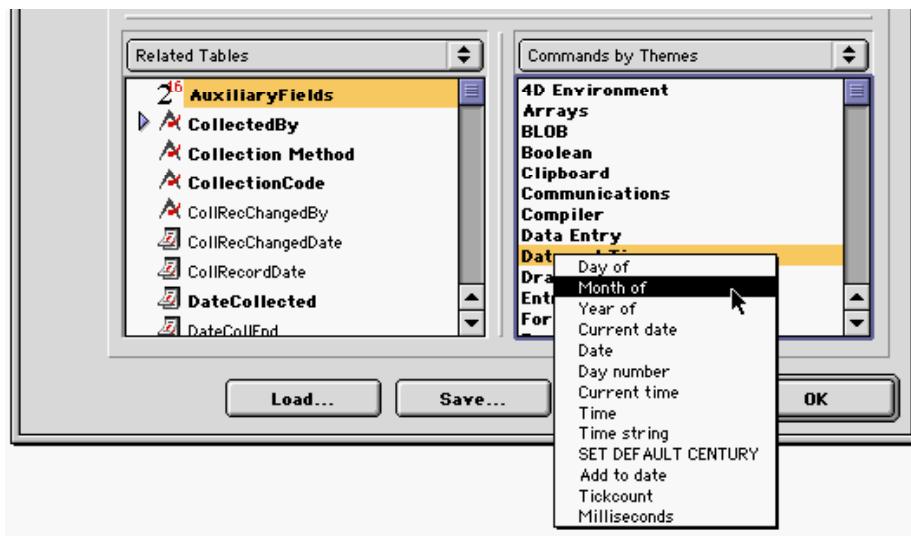
- You can re-size the Sort Editor (“Order by”) screen or the Formula Editor screen by dragging on the right and/or lower border.
- The upper panel of the Formula Editor is the formula entry area, where you construct the Sort (“Order by”) formula. You can type all entries in this area manually if you wish. In this example, we will construct the sort criterion: “Month of ([Collection] Date Collected).”



- To enter mathematical operators, you can use the row of buttons just above the formula entry panel.



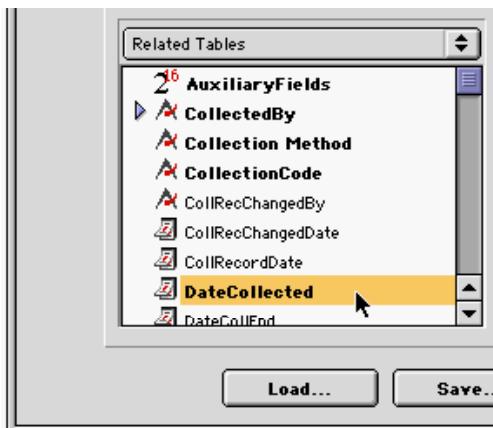
- The lower left panel, labeled “Related Tables,” lists the fields available for use in the constructed formula. The default list is identical to the “Available Fields” list in the main Sort Editor (“Order by”) screen, and it works the same way as that list for related tables. (See [“Using Fields from Related Tables for Sorting Records”](#) earlier in this chapter.)
- The lower right panel, labeled “Commands by Themes,” offers a series of command groups with boldfaced titles. If you click and hold down the mouse button on one of these boldfaced titles, a popup list of commands appears.



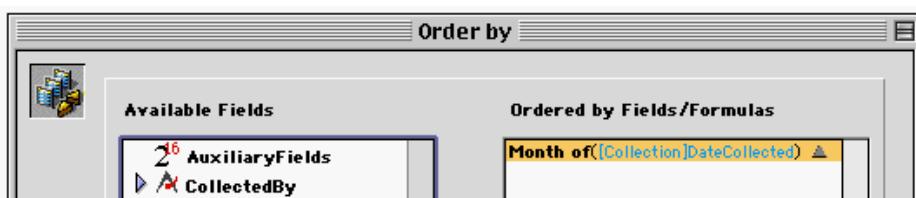
4. Find the boldfaced item “Date and Time” in the “Commands by Themes” panel. Click on the item and hold the mouse button down. A popup list of date and time functions appears.
5. Click “Month of,” “Day of,” or “Year of,” as required for the formula. The function will be entered in the formula entry area. In the example above, the “Date and Time” category is being clicked, and the “Month of” command is being selected with the mouse. The command appears in the formula entry area.



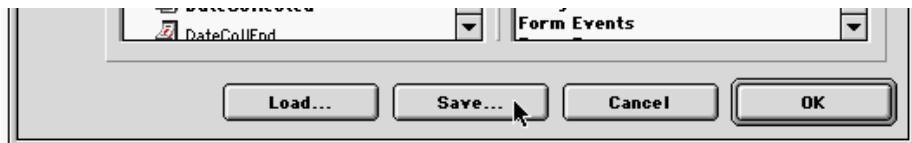
6. Enter a left parenthesis using an operator button, or type it on the keyboard.
7. In the “Related Tables” panel, showing fields available, click a date field. In the example, the [Collection] DateCollected field is being clicked.



8. Enter a right parenthesis using an operator button, or type it on the keyboard. In the example, the formula now reads: “Month of ([Collection] Date Collected).”
9. Click the “OK” button in the Formula Editor. The Formula Editor is dismissed and the Sort Editor (“Order by”) screen reappears with the formula entered in the “Ordered by Fields/Formulas” panel. (You cannot type it in directly in this area.)



10. If you need to edit a formula, select it in the “Ordered by Fields/Formulas” panel and click the “Modify” button below the panel.
11. When the formula is entered correctly, click the “Order by” button on the Sort Editor (“Order by”) screen.
12. Saving and loading formulas. Notice that the Formula Editor includes “Save” and “Load” buttons. If you use a complicated formula often, you might want to save it to a disk file and reload it when you need it.



CRITICAL WARNING: There are hundreds of other 4D commands and nearly 2000 Biota methods listed in the “Commands by Themes” list that appears in the Formula Editor. There are a few other functions that users familiar with 4D might use, but *under no circumstances attempt to use any of the italicized Biota methods in a formula. You may do irreparable damage to your data file if you do so.*



Using a Formula to Sort Numbers in an Alphanumeric Field

Sometime, you may choose to use an alphanumeric field for numerical data. (See Appendix A, “[Biota Tables, Fields, and Relational Links](#),” for information on Biota field types.) For example, a plant ecologist might re-name the [Specimen] Medium field *DBH* and use it to record the diameter at breast height (dbh) of living trees in a quadrat-based study.

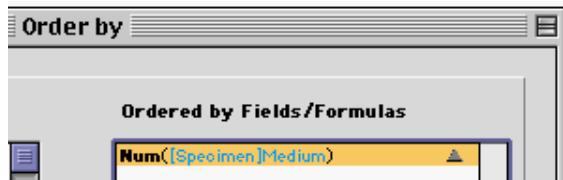
Using an alphanumeric field for numerical data causes no problems for data entry or display, but if you *sort* on an alphanumeric field, Biota sorts by ASCII code, left to right. This means that the numbers 1, 2, 3, 9, 10, 20, and 30 will sort in the order 1, 10, 2, 10, 3, 30, 9.

To sort then numerically, you must use the *Num* function in a sort formula. (The *Num* function ignores any non-numeric characters.)

NOTE: This section assumes you are familiar with the previous sections of this chapter, “[Sorting Records in Record Listing Screens](#)” and “[Using Formulas to Sort Dates by Day, Month, or Year](#).”

1. **Display the records to be sorted** in the Record Listing screen for the table. Suppose you want to sort Specimen records by numerical values in the [Specimen] Medium field, for example.
2. **Click the “Sort” button at the bottom of the Record Listing screen.** The Sort Editor (“Order by”) screen appears.
3. **Click the “Add Formula” button** at the bottom of the Sort Editor (“Order by”) window. The Formula Editor appears.
4. **Review the introduction to the Formula Editor** in the previous section (“[Using Formulas to Sort Dates by Day, Month, or Year](#)”), if necessary.
5. **Enter the formula *Num ([Field Name])*.** The easiest way to do this is to type *Num* in the formula entry area, add an opening parenthesis, click the appropriate field name in the “Related Tables” panel, then add the closing parenthesis to complete the formula.

In the illustration below, the sort criterion *Num([Specimen]Medium)* was entered in this way.



NOTE: Although any Biota Core field aliases you have set up (see Chapter 18, “[Renaming Fields](#)”) appear in place of internal field names in the “Related Tables” panel of the Formula Editor, when you double-click an alias to add a field to a formula, the equivalent internal field name is entered instead of the alias. For example, even though the field [Specimen] Medium had been re-named DBH, the formula uses the internal field name, as shown in the illustration, above.

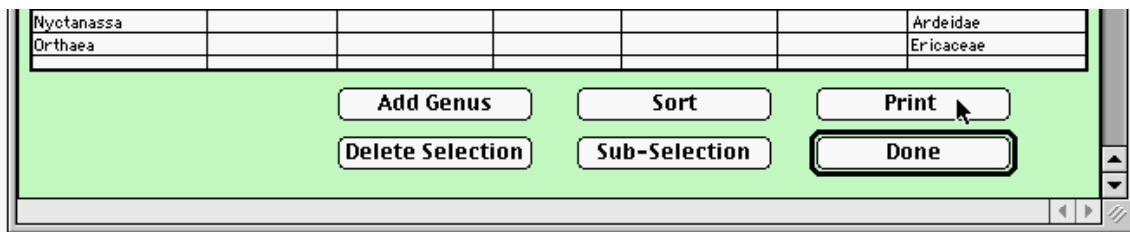
Printing Reports or Creating Text Files Based on Records in a Record Listing Screen

For each Core table and for the Determination History table, Biota offers a preformatted report that you can print, listing all records in the current Selection, including fields from related tables where appropriate (see “[Printing a Report Based on a Selection of Records](#)” in Chapter 14). Or, you can print the records using a custom report layout that you design yourself using the Quick Report Editor (see “[Designing and Printing Reports with the Quick Report Editor](#)” in Chapter 14). As a third option, you can use the Quick Report Editor to export information from the records and related tables to a text flatfile (see “[Exporting Custom Flatfiles](#)” in Chapter 27).

Printing a Report Based on Records in a record Listing Screen

1. **Display the records to be printed.**

2. Click the “Print” button at the bottom of the Record Listing screen.



Alternatively, you can select Print from the File menu while the records are displayed in the Record Listing screen.

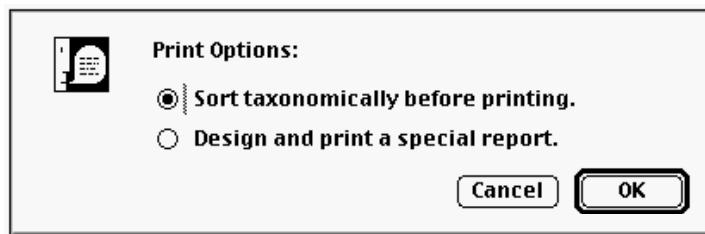
KEYBOARD SHORTCUT: Instead of clicking the “Print” button in a Record Listing screen, simultaneously press the CTRL and P keys (Windows) or the COMMAND (⌘) and P keys (Mac OS).

3. Choose a print option. A print option window appears offering two or three choices, depending on the table for which you are printing records. (The Determination History table has no options.) Three different option windows are illustrated below.

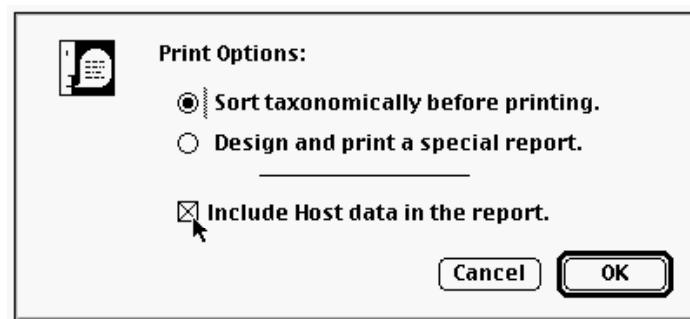


- **Sort by [Record] Code before printing.** Use this option to print a report with the records sorted by Record Code (Species Code, Specimen Code, Collection Code, or Locality Code). The Loans report can be sorted by Loan Code.
- **Print using the existing order.** If you have used the Sort tool to create a special order for the records that you want maintained in the report, choose this option.
- **Design and print a special report.** If you choose this option, Biota presents the 4th Dimension Quick Report Editor, which you can use to design, save, and/or load custom report formats that you create yourself (see “[Designing and Printing Reports with the Quick Report Editor](#)” in Chapter 14). The report will be based on the selection of records in the Record Listing screen when you clicked the “Print” button or selected Print from the File menu.

- **Sort taxonomically before printing.** For records from taxonomic tables (Species, Genus, Family, etc., and Specimen as well), this option prints the records for the table in alphabetical order within taxonomic levels (ranks) in a hierarchical report organized by rank (as in the table in the section “[The Relational Model](#)” in Chapter 2).



- **Include Host data in the report.** For the Specimen table, an additional option is offered. If the “Include Host data” checkbox is checked, the report will include, for each Specimen record, the Specimen Code of the Host for that specimen (see Chapter 24, “[Host-Guest Relations](#)”).



NOTE: This option is automatically checked if any Specimen records in the current selection have host data. Otherwise, it appears unchecked. In either case, you can override the setting manually. The host data checkbox is disabled when the “Design and print a special report” option is clicked.

4. Click the “OK” button in the print option screen.
 - If you choose the standard Biota report, see “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.
 - If you choose Design and Print a Special Report, see “[Designing and Printing Reports with the Quick Report Editor](#)” in Chapter 14

Exporting a Text Flatfile Based on Records in a Record Listing screen

1. Display the records to be exported to a text file.
2. Click the “Print” button at the bottom of the Record Listing screen.
Alternatively, you can select Print from the File menu.
3. When the print option screen appears, choose “Design and print a special report.” The option windows are illustrated in the previous section, “[Printing a](#)

[Report Based on Records in a Record Listing Screen.](#) Biota presents the Quick Report Editor.

4. Follow the instructions in the section “[Exporting Custom Flatfiles](#)” in Chapter 27.

Keyboard Shortcuts for Record Listing Screens

You can use keyboard shortcuts for most functions in Record Listing screens. Some are always available and others must be enabled in the Preferences screen. (See also “[Keyboard Shortcuts for Input Screen Tabs](#)” and “[Keyboard Shortcuts for Input Screen Buttons](#)” in Chapter 7, summarized in Appendix C, “[Keyboard Shortcuts](#).“)

Keyboard Shortcuts Always Available

The table below summarizes shortcuts that are always available in Records Listing screens. The following section of this chapter, “[Optional Keyboard Shortcuts](#),“ describes shortcuts available only if you enable them in the Shortcuts tab of the Preferences screen (Special menu).

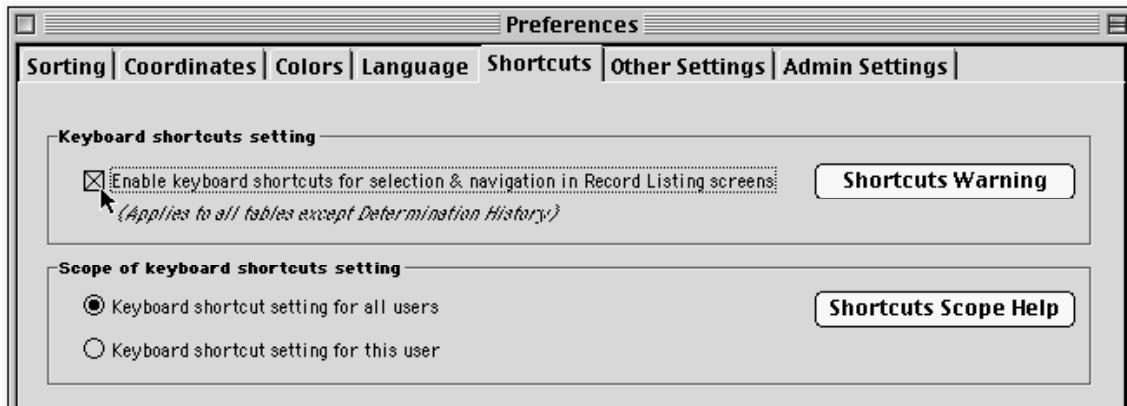
In the table below, shortcuts for on-screen buttons are indicated with a lavender background, whereas shortcuts that do not correspond to an onscreen button are indicated with a yellow background. Most of the button functions are described in previous sections of this chapter, but a few are detailed in other chapters:

- The “Aux Fields” button is described in Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).“
- The “Scroll” and “Page” (“Display Images”) buttons are described in Chapter 19, “[Images](#).“

FUNCTION	MAC OS	WINDOWS
“Done” button	RETURN	ENTER
“Print” button	COMMAND–P (⌘–P)	CTRL–P
“Sort” button	COMMAND–R (⌘–R)	CTRL–R
“Sub-Selection” button	COMMAND–N (⌘–N)	CTRL–N
Add Record button (e.g., “Add Species”)	COMMAND–J (⌘–J)	CTRL–J
“Aux Fields” button (Core fields screens)	COMMAND–M (⌘–M)	CTRL–M
“Core Fields” button (Auxiliary fields screens)	COMMAND–M (⌘–M)	CTRL–M
“Scroll” (Display Images) button	COMMAND–H (⌘–H)	CTRL–H
“Page” (Display Images) button	COMMAND–I (⌘–I)	CTRL–I
Close screen (with Record Set Query screen; same as “Done” button)	OPTION–W	ALT–W
Dismiss screen (bypassing the Record Set Query screen)	COMMAND–HYPHEN (⌘–HYPHEN)	CTRL–HYPHEN

Optional Keyboard Shortcuts

This section summarizes keyboard shortcuts for Record Listing screens that become available only if you enable them in the Shortcuts tab of the Preferences screen (Special menu), shown below. (See also Appendix B, “[Setting Preferences](#)”.)



- In the “Keyboard shortcuts setting” panel, you indicate whether the shortcuts in the table below are to be enabled (checkbox checked) or disabled (checkbox empty).
- In the “Scope of keyboard shortcuts settings” panel, you control the scope of the setting in the “Keyboard shortcuts setting” panel.
 - ◊ If you select the first option, “Keyboard settings for all users” (the default setting), the keyboard shortcuts setting is saved between Biota sessions and affects all users if you are running Biota4D under 4D Server.
 - ◊ If you select the second option, “Keyboard settings for this user,” you must reset your preferred keyboard shortcut setting each time Biota is launched, if it differs from the setting most recently saved under the first option. With the second option, any changes you make in the keyboard shortcuts setting will not affect other users under 4D Server.
- These optional shortcuts are not enabled when you first create a new Biota Data File, so if you want to use them you must specifically enable them.
- These shortcuts do not apply to the Record Listing screen for the Determination History table.

FUNCTION	MAC OS	WINDOWS
Next record	DOWN ARROW	DOWN ARROW
Previous record	UP ARROW	UP ARROW
Last record	PAGE DOWN	PAGE DOWN
First record	PAGE UP	PAGE UP
Select or deselect highlighted record	SPACE BAR	SPACE BAR
Display selected record(s) in the Input screen	SEMI-COLON (;)	SEMI-COLON (;)

WARNING: With the optional keyboard shortcuts for Record Listing screens enabled, if you use the mouse or another pointing device to select a record (single click) in the second or higher page of records in the Record Listing screen, the clicked record immediately scrolls to the top the display. (No scrolling occurs with the *first* page of records.)

For this reason, if you use a mouse or another pointing device to *open* a record from the Record Listing screen while the optional shortcuts are enabled, you must first select the record with *one* mouse-click, *wait* for the record to scroll to the top of the list, *then* double-click the record to open it in the Input screen. If you double-click a record without waiting for the scrolling to occur, the second click may open the wrong record. Using the semicolon key to open a selected record or records (details in the next section, “[Using the Optional Keyboard Shortcuts for Record Selection and Revision](#)”) avoids this problem entirely.

A warning regarding this behavior appears when you first enable the optional shortcuts and, as a reminder, each time Biota is launched while the optional shortcuts are enabled. Unfortunately, there is currently no way to alter this 4D behavior with programming.

Using the Optional Keyboard Shortcuts for Record Selection and Revision

With the optional keyboard shortcuts for Record Listing screens enabled (see the previous section, “[Optional Keyboard Shortcuts](#)”), you can select individual records or groups of records in the Record Listing screen for a table without using the mouse or other pointing device, then display the selected group of records in the record Input screen for the table.

- **To highlight a record**, use the up and down arrow keys to move one record at a time.
- **To select a highlighted record**, click the keyboard space bar. When you move the highlight to another record, the selected record remains highlighted.
- **To add another record to the highlighted selection**, move to that record and click the keyboard space bar. You can create a highlighted selection including any number of records, whether they are consecutive or on the screen or not.
- **To remove a record from the highlighted selection**, move to that record and click the keyboard space bar. No other record in the selection will be affected.
- **To display a highlighted record or a highlighted selection of records in the Input screen**, click the semicolon key on the keyboard. The highlighted record or the first record in a highlighted selection appears in the Input screen for the table.
- **The behavior of the navigation buttons** (“Navigate records”) in the Input screen depends on how many records you highlighted in the Record Listing screen before clicking the semicolon key to display the Input screen.
 - ◊ **If only one record was highlighted**, the navigation buttons operate just as they do when the optional keyboard shortcuts are disabled, and you open a record in the Input screen with a mouse double-click. The navigation buttons in the Input



screen access all the records in the selection of records in the Record Listing screen.

- ◊ If more than one record was highlighted, the navigation buttons in the Input screen access only the records that were highlighted in the Record Listing screen. In this case, other records in the full selection in the Record Listing screen are not accessible with the navigation buttons. This behavior is quite useful for viewing or editing a subset of the records in the current selection, without using the “Sub-Selection” button and thereby losing view of the rest of the full selection.

WARNING: With the optional keyboard shortcuts for Record Listing screens enabled (see the previous section, “[Optional Keyboard Shortcuts](#)”), if you use the mouse or another pointing device to select a record (single click) in the second or higher page of records in the Record Listing screen, the clicked record immediately scrolls to the top of the display. (No scrolling occurs with the *first* page of records.)

For this reason, if you use a mouse or another pointing device to *open* a record from the Record Listing screen while the optional shortcuts are enabled, you must first select the record with *one* mouse-click, *wait* for the record to scroll to the top of the list, *then* double-click the record to open it in the Input screen. If you double-click a record without waiting for the scrolling to occur, the second click may open the wrong record. Using the semicolon key to open a selected record or records (details above in this section) avoids this problem entirely.

A warning regarding this behavior appears when you first enable the optional shortcuts and, as a reminder, each time Biota is launched while the optional shortcuts are enabled. Unfortunately, there is currently no way to alter this 4D behavior with programming.

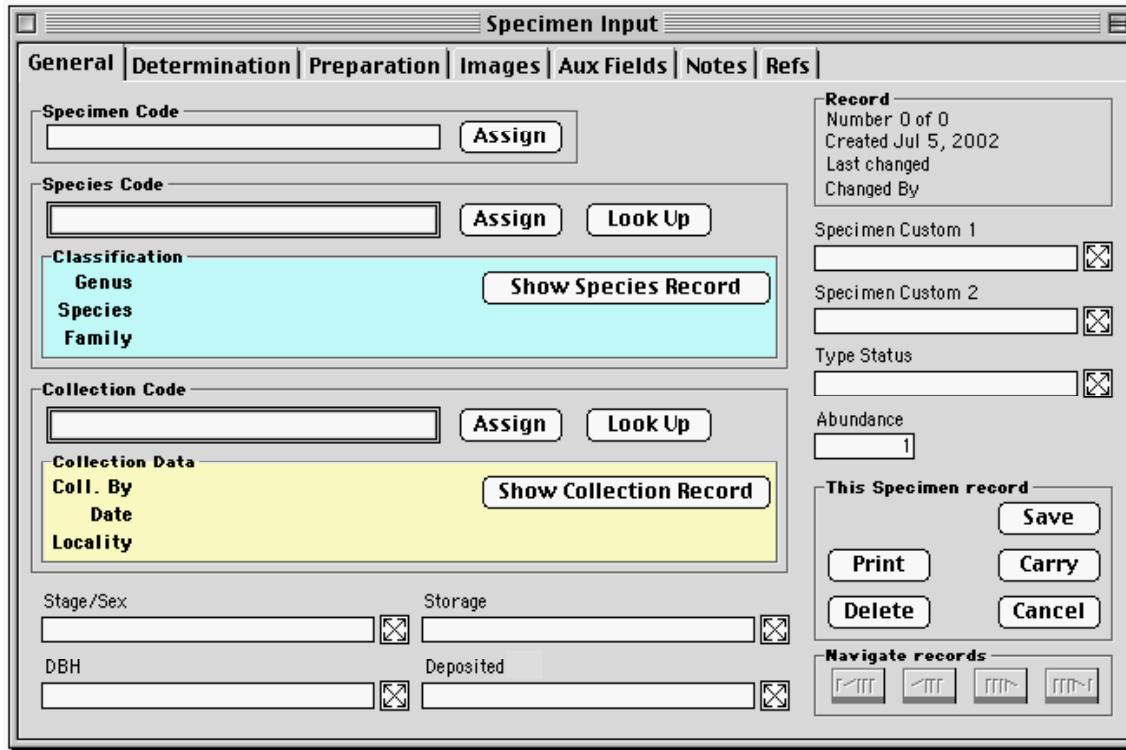
Chapter 11

Input—Table by Table

As much as possible, all of Biota's Input screens share the same features. These common elements are discussed in Chapter 7, “[Overview of Record Input Screens](#),” Chapter 8, “[Record Codes](#),” and Chapter 10, “[Working With Records in Record Listing and Input screens](#).” This chapter focuses on features restricted to one or a few Input screens.

Specimen Input

You can enter a new record in the Specimen Input screen by selecting Specimen from the Input menu or by clicking the “Add Specimen” button on the Specimen Record Listing screen. The Specimen Input screen has seven tabs. Once you have entered a Specimen Code, you can move to any tab. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move among the tabs.



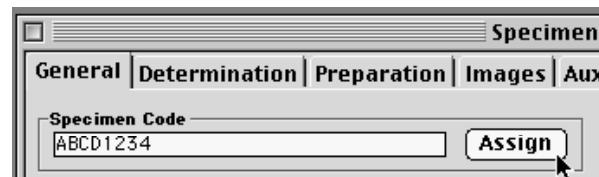
This section describes how to enter data in the General, Determination, and Preparation tabs of the Specimen Input screen.

- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”

- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

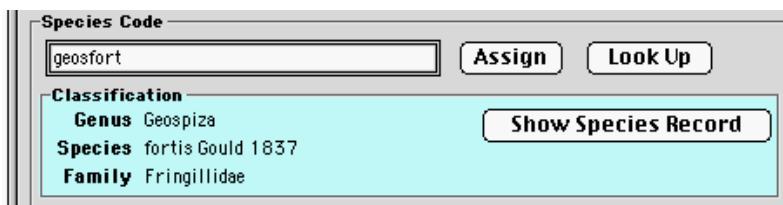
Entering Specimen Data: The “General” Tab

1. **Enter a Specimen Code.** You can enter the Specimen Code by typing it in the Specimen Code entry area, by using the adjacent “Assign” button (see “[Assigning New Record Codes Using an “Assign” button: Step by Step](#)” in Chapter 8), by setting up the Record Code Settings tool to enter it automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8, or by reading in a barcode (see Appendix K, “[Barcodes](#)”).



The Specimen Code may be up to 30 characters in length. Because Specimen Code is the Key field for the Specimen table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Specimen Code you enter must not duplicate the Specimen Code of any existing Specimen record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3). For help understanding how Specimen Codes work, see Chapter 8, “[Record Codes](#).”

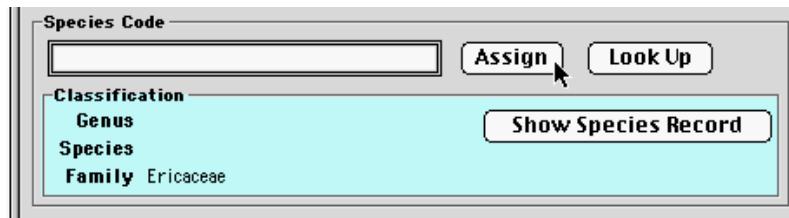
2. **Enter a Species Code.** The Species Code links this Specimen record with a record in the Species table (see “[Species Input](#)” later in this chapter). There are five *alternative* methods for entering a Species Code:



- **Method 1:** Enter a complete Species Code manually or with a barcode reader.
 - ◊ If a Species record exists with the Species Code you entered, the Classification panel displays the Genus, Species (specific name), and Family. The cursor moves on to the next entry area.

NOTE: Be sure to confirm that the correct Species record was found. If your entry uniquely matches the first part of a different Species Code, the wrong link will be made. See “[Overriding Wildcard Input for Linking Fields](#)” in Chapter 7.

- ◊ If no Species record exists with the Species Code you entered, Biota offers you the option of creating a new Species record “on the fly” (using the Species Code you entered) or accepting an orphan Specimen record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.
- **Method 2: Use the adjacent “Assign” button to create a new Species Code.** Biota offers you the option of creating a new Species record “on the fly,” with the Code you entered, or accepting an orphan Specimen record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.



- **Method 3:** Set up the Record Code Settings tool to enter a Species Code automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8)
- **Method 4: Enter the first letter or first few letters of a Species Code, then press TAB (wildcard lookup).** See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.
 - ◊ If only one existing Species Code matches the entry, Biota automatically completes the entry.
 - ◊ If more than one existing Species Code matches the entry, a scrollable list of matching Species Codes for existing Species records appears, from which you can choose the correct code by clicking it with the mouse.

Species Records

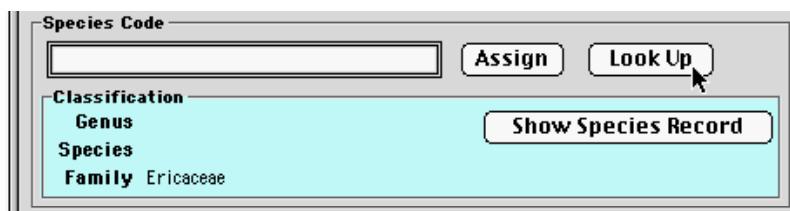
Click buttons to sort records

Species Code	Genus	Species Name
cactheli	Cactospiza	heliobates
cactpall	Cactospiza	pallida
camaparv	Camarhynchus	parvulus
camapaup	Camarhynchus	pauper
camapsit	Camarhynchus	psittacula
cavcomp	Cavendishia	complectens subsp. striata
cavouat	Cavendishia	ouatrecasasii?
cavforr	Cavendishia	ferreroi
cavgilg	Cavendishia	giliana
cavleuc	Cavendishia	leucantha
cavpalu	Cavendishia	palustris
cavpseud	Cavendishia	pseudospicata
cavsmilt	Cavendishia	smithii
cavtene	Cavendishia	tenella
cenoao	Centropogon	caoutchouc
ceneria	Centropogon	erianthus
cernodo	Ceratostema	nodosum
cerperu	Ceratostema	peruvianum
cerregi	Ceratostema	reginaldi
certoliv	Certhidea	olivacea

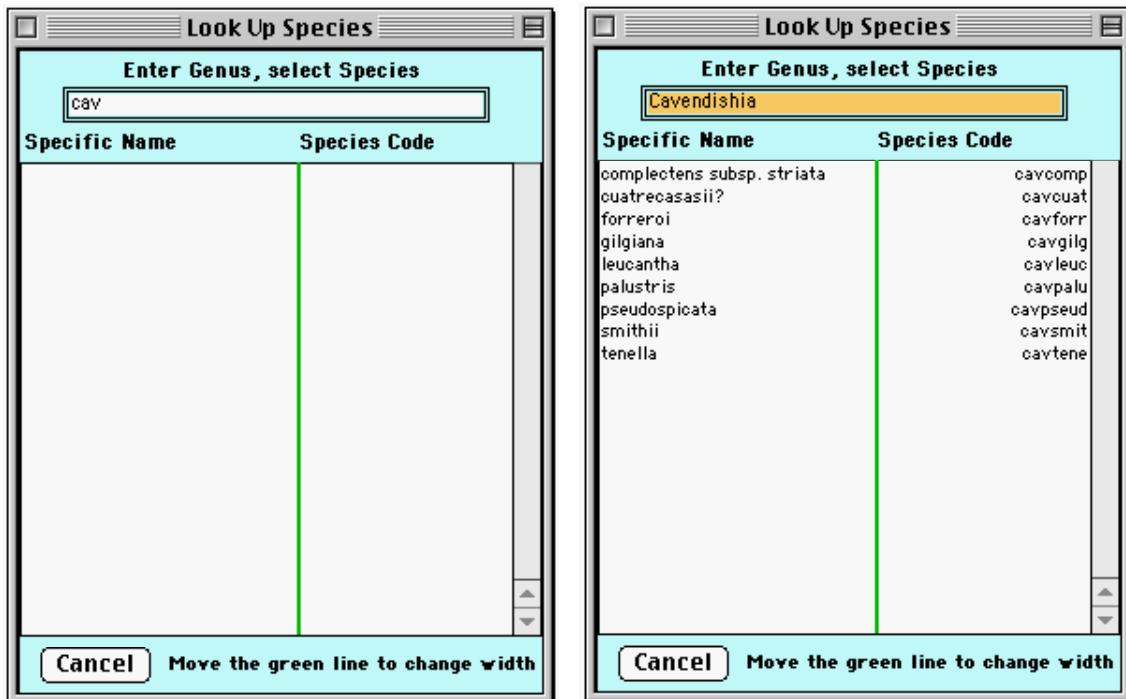
Move the green lines to change column width

Cancel

- ◊ If you enter the @ character (the wildcard character in Biota), and nothing else, all Species codes appears in the scrollable list.
- To sort the entries in the list by Genus or Species Name (specific name) or to re-sort by Species Code, click the sort buttons at the top of the screen. When you sort by Genus, records are sorted within Genus by Species Name. You can change the width of the columns by dragging the green vertical lines with the mouse.
- ◊ If no existing Species Code matches your entry, Biota offers you the option of creating a new Species record “on the fly,” with the Species Code you entered, or accepting an orphan Specimen record. See “[“On-the-Fly” Creation of Linked Records](#)” in Chapter 7 for details.
- **Method 5: Click the “Look Up” button** in the Species Code panel of the Specimen Input screen.



The Look Up Species window appears.



- a. Enter a Genus, or the first letter or letters of a Genus and press TAB. If a matching Genus record is found, all Species records for the Genus appear in the scrollable area of the Lookup window. If more than one match is found, a list of matches appears, from which you can select the correct Genus.

- b. If you find the Species you want, click it to enter the corresponding Species Code.
- c. To see the full Species record, once the Species Code has been entered, click the “Show Species Record” button in the Species Code panel of the Specimen Input screen.

Species Code
cavpalu Assign Look Up

Classification
Genus Cavendishia
Species palustris A.C. Smith
Family Ericaceae

Show Species Record

- 3. Enter a Collection Code. The Collection Code links this Specimen record with a record in the Collection table (see “[Collection Input](#)” later in this chapter). You can enter a Collection Code using any of five *alternative* techniques.

Collection Code
Assign Look Up

Collection Data
Coll. By
Date
Locality

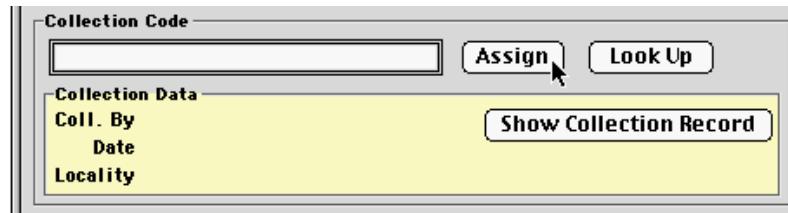
Show Collection Record

- **Method 1:** Enter a complete Collection Code manually.
 - ◊ If a Collection record exists with the Collection Code you entered, the “Collection Data” panel displays the Collector’s name (“Collected By”), the Date Collected (or date range), and the collection Locality (the Locality Name field of the Locality record linked to the Collection record). The cursor moves on to the next entry area.

Note: Be sure to confirm that the correct Collection record was found. If your entry uniquely matches the first part of a different Collection Code, the wrong link will be made. See “[Overriding Wildcard Input for Linking Fields](#)” in Chapter 7.

- ◊ If no Collection record exists with the Collection Code you entered, Biota offers you the option of creating a new Collection record “on the fly” (using the Collection Code you entered) or accepting an orphan Collection record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.

- **Method 2: Use the adjacent “Assign” button to create a new Collection Code.** Biota offers you the option of creating a new Collection record “on the fly,” with the Code you entered, or accepting an orphan Specimen record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.



- **Method 3:** Set up the Record Code Settings tool to enter a Collection Code automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8).
- **Method 4: Enter the first letter or first few letters of a Collection Code, then press TAB (wildcard lookup).** See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.
 - ◊ If only one existing Collection Code matches the entry, Biota automatically completes the entry.
 - ◊ If more than one existing Collection Code matches the entry, a scrollable list of matching Collection Codes for existing Collection records appears, from which you can choose the correct code by clicking it with the mouse.
 - ◊ If you enter the @ character (the wildcard character in Biota), and nothing else, all Collection codes appear in the scrollable list.

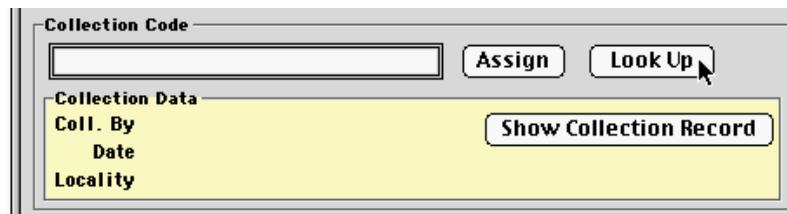
To sort the entries in the list by Collector (“Collected By”) or to re-sort by Collection Code, click the sort buttons at the top of the screen. You can change the width of the columns by dragging the green vertical lines with the mouse.

 - ◊ If no existing Collection Code matches your entry, Biota offers you the option of creating a new Collection record “on the fly,” with the Collection Code you entered, or accepting an orphan Specimen record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.

Collection Records	
Click buttons to sort records	
Collection Code	Collected By
JLL7017	J.L. Luteyn
JLL7017H	J.L. Luteyn
JLL7166	J.L. Luteyn
JLL7209	J.L. Luteyn
JLL7209H	J.L. Luteyn
JLL7269	J.L. Luteyn
JLL7269H	J.L. Luteyn
JLL7281H	J.L. Luteyn
JLL7629	J.L. Luteyn
JLL7629H	J.L. Luteyn

Cancel Move the green line to change width

- **Method 5: Click the “Look Up” button in the Collection Code panel of the Specimen Input screen.**



The Collections lookup options window appears.

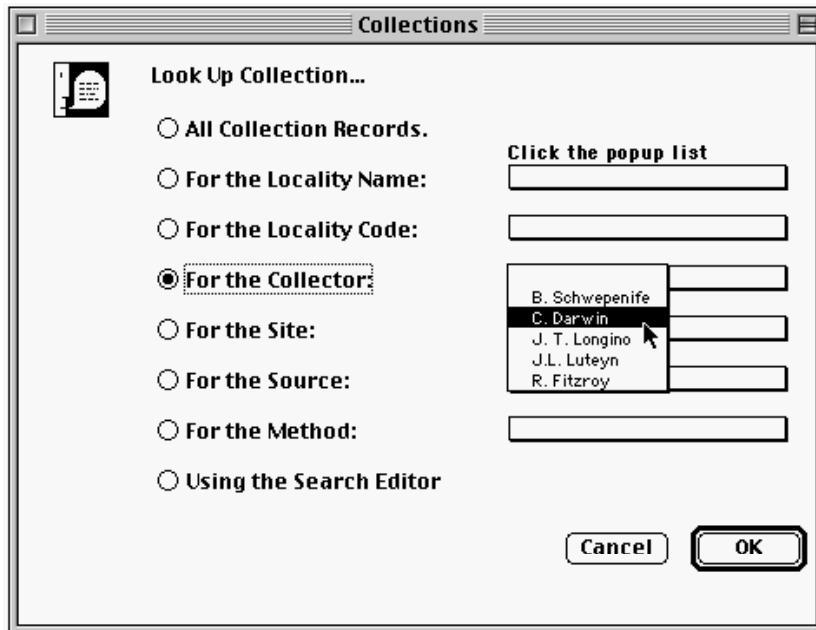


- Select a display option by clicking a button in the Collections lookup options window. You can display All Collection Records (not the best approach if there are hundreds or thousands of records) or restrict the choices displayed to a certain value for Locality Name, Locality Code, Collector (the “Collected By” field), Site, Source, or Method. Or, you can launch the Query Editor (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12) to find a record using ad hoc criteria.

NOTE: If you have defined an Alias for the Site, Source, or Method fields of the Collection table (see Chapter 18, “[Renaming Fields](#)”), the Alias appears in the corresponding button text in the Look Up Collection window in place of the Internal Field Name.

- If you select the Locality Name, Locality Code, Collector, Site, Source, or Method option, Biota creates a list of all unique values for the selected field.

- ◊ If there are only a few values, Biota displays the list in a popup list to the right of the selected button. Click and hold the popup to display the list of values, as shown below.



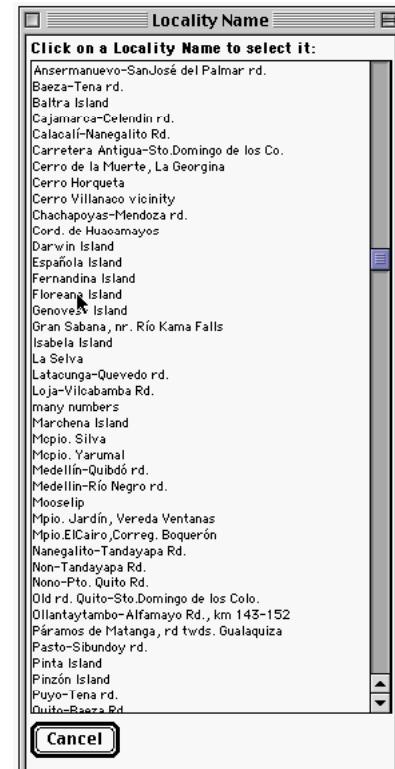
- ◊ If there are many values, Biota displays the list in a separate window with a scrollbar, as shown on the right.

- c. Select the value you want from the popup list or the scrolling list. Biota then shows the selected value in the popup area.

For the Collector:

C. Darwin

- d. Click the “OK” button in the Look Up Collection window. The Look Up Collection display screen appears, listing all Collection records that match the option and criteria you selected in steps a. and b. above (see the next page).



Look Up Collection

Sort using the buttons below, then select Collection							4 Records
Locality Code	Collector	Site	Source	Method	Date	Coll. Code	
Fernandina	C. Darwin			Shotgun	Sep 30, 1832	CD003	
Floreana	C. Darwin			Shotgun	Sep 24, 1832	CD002	
SanCristobal	C. Darwin			Shotgun	Sep 19, 1932	CD001	
Santiago	C. Darwin			Shotgun	Oct 9, 1832	CD004	

Try Again **Cancel**

- ◊ If there are many records in the display screen, you may first want to use the sort buttons at the top of each column to sort the records displayed by the values for that column.
 - ◊ If you want to try a different selection option or field value to display records, click the “Try Again” button at the bottom of the Look Up Collection selection screen.
- e. When you find the record you want in the Lookup Collection display screen, click it to enter its Collection Code in the Specimen Input screen.
 - f. To see the full Collection record, once the Collection Code has been entered, click the “Show Collection Record” button in the “Collection Data” panel.

Collection Code	<input type="text" value="CD002"/>	Assign	Look Up
Collection Data			
COLL. By	C. Darwin		
Date	Sep 24, 1832-Dec 21, 1833		
Locality	Floreana Island		
Show Collection Record			

4. Enter data for Stage/Sex, Medium, Storage, Deposited, Specimen Custom 1, Specimen Custom 2, and Type Status. Enter each value and press TAB key to advance to the next entry area.

Stage/Sex <input type="text" value="Adult male"/>	Storage <input type="text" value="Cabinet 22, Drawer 3"/>
Medium <input type="text" value="Skin"/>	Deposited <input type="text" value="MHN Quito"/>
Specimen Custom 1 <input type="text"/>	
Specimen Custom 2 <input type="text"/>	
Type Status <input type="text" value="Paratype"/>	

You can set any of the following options for each of these seven Specimen fields:

- **Aliases.** Each field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- **Field Value Defaults.** You can ask Biota to enter a particular value in each new record automatically using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for each field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

NOTES:

- a. The “Deposited” field in the Specimen table is used by the Specimen Loans system in Biota. If you intend to use the Loans system do not use this field for another purpose. See Chapter 21, “[Specimen Loan System](#)” for details.
 - b. The Medium field also appears on the Preparation tab of the Specimen Input screen. You can enter data in this field on either tab and the data will appear in both locations.
-

5. **Enter a value for Abundance.** Biota enters a “1” as the default for the Abundance field.
 - **If this record is for a single physical specimen,** leave the value at 1. Some Biota tools sum the values in this field for sets of specimen records, so a record representing a single physical specimen should read “1” for Abundance.
 - **If this record represents more than one physical specimen,** enter the total number it represents. If the record for one physical specimen represents n additional, unmounted specimens (a physical voucher), enter the value $n + 1$.

Entering Specimen Data: The “Determination” Tab

In the "Last Determined By" and "Date Last Determined" fields of the Specimen table, located in the Determination tab of the Specimen Input screen, Biota records the name of the last person to identify (determine) the physical specimen referenced by the Specimen record and the date the determination was made.

The Determination History for a Specimen record is also displayed in the Determination tab of the Specimen Input screen. If you enable Biota's Determination History system before any subsequent changes in determination are made, Biota records each change in determination, who made the change, when, and where (i.e., in the Specimen record itself or through changes in the linked Species or Genus record). For full information on the Determination History system, see Chapter 22, "[Determination Histories](#)."

NOTE: You can set Field Value Default entries for the entry areas “Last Determined By” and “Date Last Determined.” See “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17.

To enter determination data, take these steps.

1. **Enter the determiner's "Short Name" in the "Last Determined By" entry area** on the Determination tab. Because this field is linked to the Short Name field of the Personnel table, the entry area has a double border. You can use any of the techniques for entering data in linking fields described in Chapter 7, "[Overview of Record Input Screens](#)."
 - **If you know that the determiner has no existing record in the Personnel table**, enter a Short Name for the determiner in the "Last Determined By" entry area (e.g., Albert B. Smith or A. B. Smith) and press the TAB key. If the entry you

make does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Specimen record without creating a link to the Personnel table (a “Personnel-orphan” Specimen record) (see “[Entering Data in Linking Fields](#)” in Chapter 7).

NOTE: On Pin, Slide, Vial, and Herbarium labels, Biota uses the Short Name field for the collector’s name (see Chapter 15, “[Printing Labels](#)”). Although the Short Name may have up to 80 characters, it is best to make it substantially shorter (20-30 characters is a good guideline) if you intend to use Biota to produce specimen labels. Since determiners are very often also collectors and preparators, be sure to choose a version of the determiner’s name that is appropriate for collector’s names on labels—e.g., initials and last name, or first name and last name. You can also use a “Group Name” in the “Determined By” field, e.g., A. B. Smith & C. D. Jones (for help with Group Names, see “[Entering Personnel Data: The ‘Group’ Tab](#)” later in this chapter).

- If you think the determiner may already have a Personnel record, but you are not sure what Short Name the record carries, enter the @ character and press the TAB key. A scrollable list of all existing Personnel records appears (below), from which you can choose the correct record by clicking it. You can sort the records by Short Name, Last Name, or Institution by clicking the buttons above the columns.

Personnel Records		
Click buttons to sort records		
Short Name	Last Name	Institution
B. Schwenk	Schwenk	CSATS
C. Darwin	Darwin	H. M. S. Beagle
Colwell & Naeem	Colwell & Naeem	UConn & U Minn
E. Lindquist	Lindquist	Agriculture Canada
INBio	INBio	Instituto Nacional de Biodiversidad
J. T. Longino	Longino	The Evergreen State College
J.L. Luteyn	Luteyn	New York Botanical Garden
Luteyn Mites	Luteyn Mite Collections	University of Connecticut
NYBG	New York Botanical Garden	New York Botanical Garden
P. Naskrecki	Naskrecki	University of Connecticut
R. Colwell	Colwell	University of Connecticut
R. Fitzroy	Fitzroy	H. M. S. Beagle
S. Naeem	Naeem	University of Minnesota
UConn	University of Connecticut	University of Connecticut

- If you know the Short Name for the determiner’s existing Personnel record, enter the first letter, the first few letters of the Short Name, or the full Short Name, and press the TAB key. If a single match is found, Biota completes the name and

the cursor moves into the next field. If more than one match is found, a choice list like the one above appears, with all matches shown.

If the “Last Determined By” entry you make does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Specimen record without creating a link to the Personnel table (a “Personnel-orphan” Specimen record) (see “[Entering Data in Linking Fields](#)” in Chapter 7).

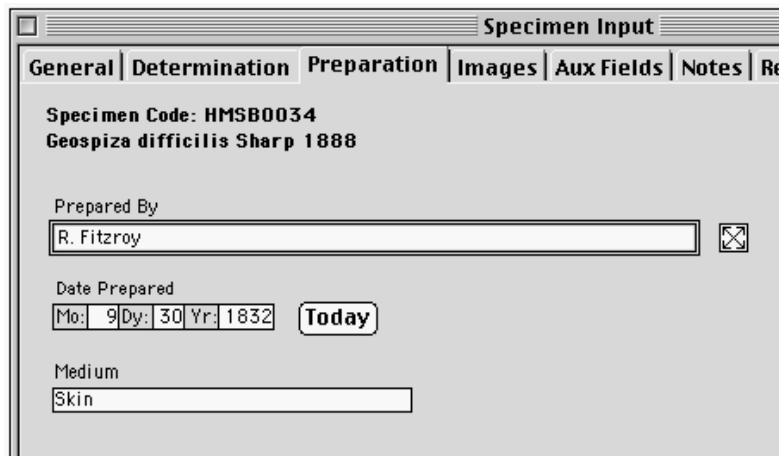
Note: If you are working with historical specimens, you may not want to create a Personnel record for every Determiner, Preparator, or Collector—some of whom may be long deceased and their particulars unknown.

2. Enter the “Date Last Determined.” You can enter either a full date or a partial date. See “[Dates](#)” in Chapter 9 for details on entering dates, date formats (International vs. U.S.), partial dates, and how Biota handles dates in the Data File.

Note: If you have enabled the Determination History system and you change the determination of a Specimen record in any way, Biota prompts you to complete the “Last Determined By” and “Date Last Determined” fields of the Specimen record. For full information on the Determination History system, see Chapter 22, “[Determination Histories](#).”

Entering Specimen Data: The “Preparation” Tab

The Preparation tab of the Specimen Input screen records the name of the preparator of the physical specimen represented by the Specimen record, together with the date the specimen was prepared (the “Date Prepared” field). For step-by-step help entering data in these two fields, refer to the instructions for the “Last Determined By” and “Date Last Determined” fields of the Determination tab (see “[Entering Specimen Data: The ‘Determination’ Tab](#)” earlier in this chapter).



In addition, the Medium field appears on the Preparation tab to record how the specimen was prepared (e.g., “ethanol,” “exsiccatum,” “liquid nitrogen”) or what part of the

specimen was prepared or preserved (e.g., “fruits,” “skin,” “skull,” “liver tissue,” “amplified DNA”).

You can set any of the following options for the Medium field:

- **Alias.** The Medium field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- **Field Value Default.** You can ask Biota to enter a particular value in the Medium field for each new record automatically using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Entry Choice List.** You can enable an Entry Choice List (pick list) for the Medium field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

NOTE: The Medium field also appears on the Preparation tab of the Specimen input screen. You can enter data in this field on either tab and the data will appear in both locations.

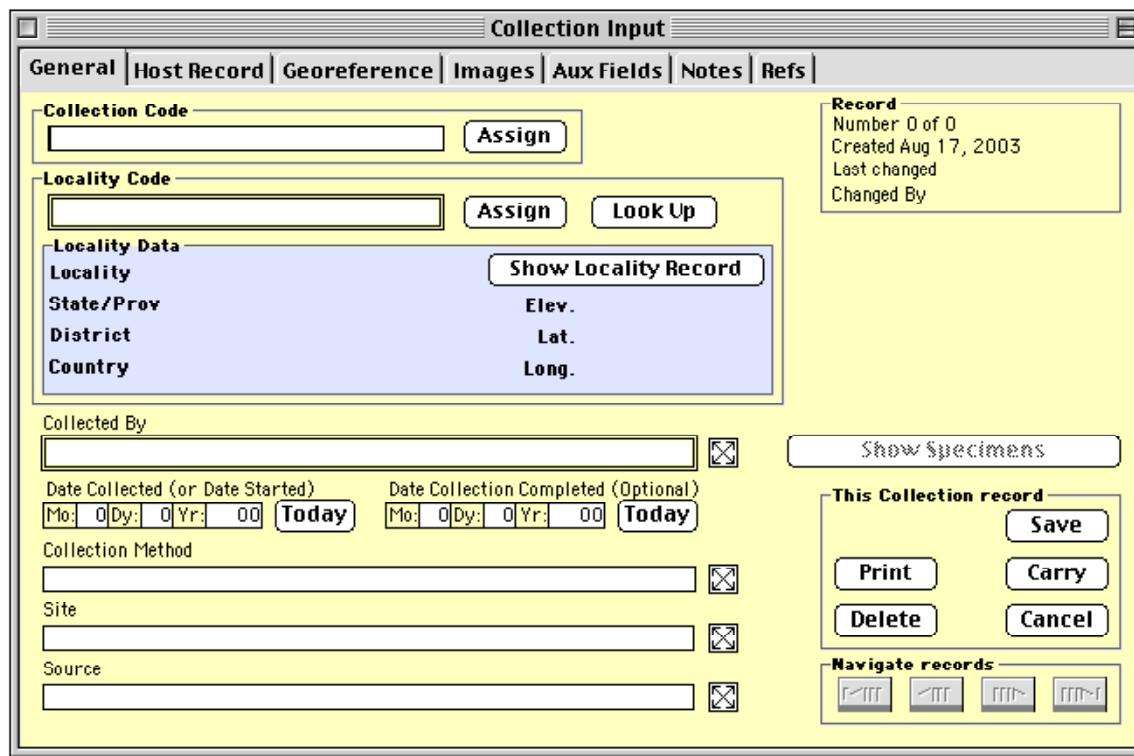
Entering Specimen Data: The “Images,” “Aux Fields,” “Notes,” and “Refs” Tabs

Information on entering and working with data in these tabs appears elsewhere in the Manual. Follow the links below:

- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Collection Input

You can enter a new record in the Collection Input screen by selecting Collection from the Input menu, by clicking the “Add Collection” button on the Collection Record Listing screen, or “on the fly” from the Specimen Input screen. The Collection Input screen has seven tabs. Once you have entered a Collection Code, you can move to any tab. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move among the tabs.

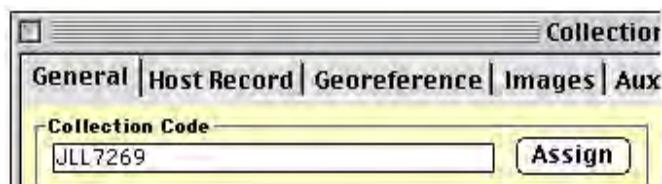


This section describes how to enter data in the General tab of the Collection Input screen. For other tabs, follow the links below:

- **Host Record tab.** For information on creating host record links in the “Host Record” tab, see Chapter 24, “[Host-Guest Relations](#).”
- **Georeference tab.** For information on entering and working with spatial coordinates in the Georeference tab, see “[Spatial Coordinates](#)” in Chapter 9.
- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Entering Collection Data: The “General” Tab

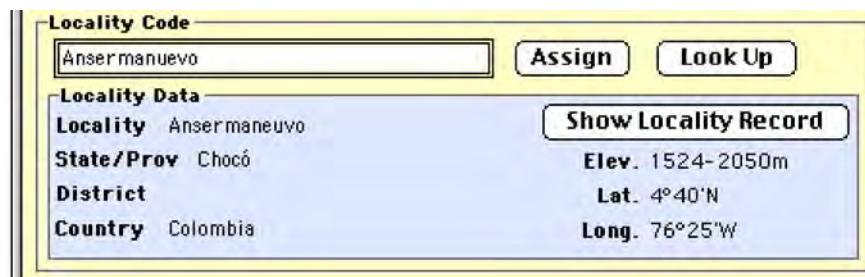
1. **Enter a Collection Code.** You can enter the Collection Code by typing it in the Collection Code entry area or by using the adjacent “Assign” button (see “[Assigning New Record Codes Using an “Assign” button: Step by Step](#)” in Chapter 8).



The Collection Code may be up to 30 characters in length. Because Collection Code is the Key field for the Collection table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Collection Code you enter must not duplicate the Collection Code of any existing Collection record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3). For help understanding how Collection Codes work, see Chapter 8, “[Record Codes](#).”

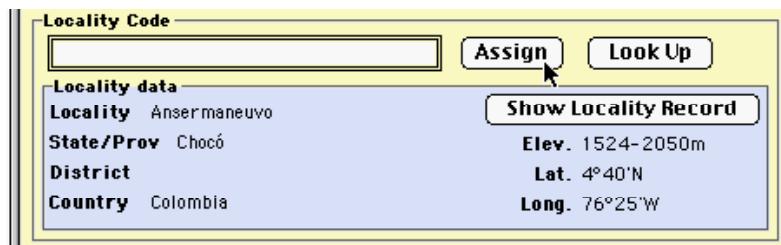
NOTE: If you are creating a Collection record “on the fly” while working on a Specimen record (see [Step 3 of “Entering Specimen Data: The ‘General’ Tab”](#) earlier in this chapter), the Collection Code you entered in the Specimen Input screen is already displayed and the cursor is in the next field (Locality Code).

2. **Enter a Locality Code.** The Locality Code links this Collection record with a record in the Locality table (see “[Locality Input](#)” later in this chapter). You can enter a Locality Code using any of five *alternative* techniques.
 - **Method 1:** Enter a complete Locality Code manually.
 - ◊ If a Locality record exists with the Locality Code you entered, the “Locality data” panel displays the Locality Name and five other fields from the related Locality record, and the cursor moves on to the next entry area.



NOTE: Be sure to confirm that the correct Locality record was found. If your entry uniquely matches the first part of a different Locality Code, the wrong link will be made. See “[Overriding Wildcard Input for Linking Fields](#)” in Chapter 7.

- ◊ If no Locality record exists with the Locality Code you entered, Biota offers you the option of creating a new Locality record “on the fly” (using the Locality Code you entered) or accepting an orphan Locality record. See “[On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.
- **Method 2: Use the adjacent “Assign” button to create a new Locality Code.** Biota offers you the option of creating a new Locality record “on the fly,” with the Code you entered, or accepting an orphan Collection record. See “[On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.



- **Method 3:** Set up the Record Code Settings tool to enter a Locality Code automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8).
- **Method 4: Enter the first letter or first few letters of a Locality Code, then press TAB (wildcard lookup).** See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.
 - ◊ If only one Locality Code matches the entry, Biota automatically completes the entry.
 - ◊ If more than one existing Locality Code matches the entry, a scrollable list of matching Codes for existing Locality records appears, from which you can choose the correct code by clicking it with the mouse.

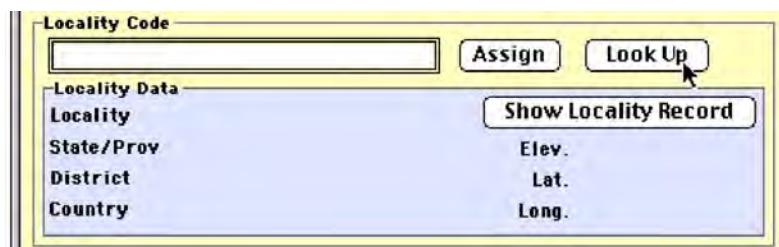
Locality Records

Click buttons to sort records

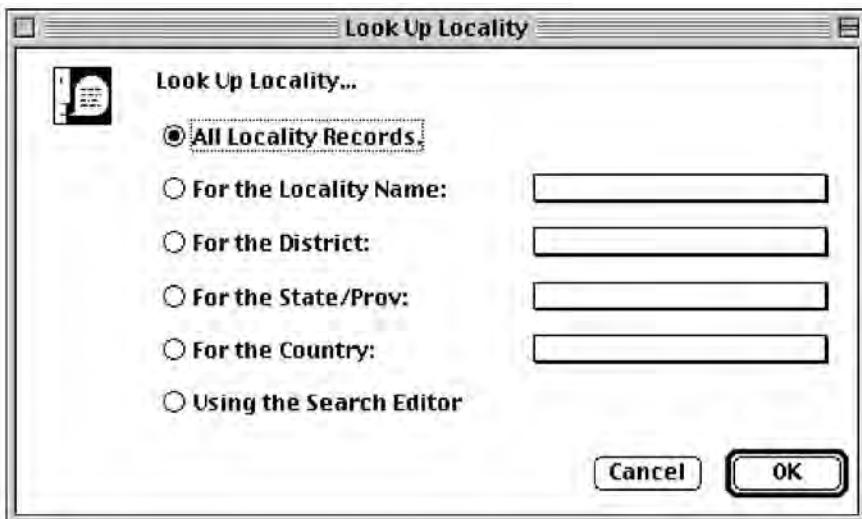
Locality Code	Locality Name
Salcedo-Napo rd.	Salcedo-Napo rd.
SanCristobal	San Cristóbal Island
Santiago	Santiago Island
StaCruz	Santa Cruz Island
Sto. Domingo rd.	Carretera Antigua-Sto.Domingo de los Cocos, 19 km SW Estación Culcabamba

Cancel Move the green line to change column width

- ◊ If you enter the @ character (the wildcard character in Biota), and nothing else, all Locality codes appear in the scrollable list.
- To sort the entries in the list by Locality Name or re-sort by Locality Code, click the sort buttons at the top of the screen. You can change the width of the columns by dragging the green vertical lines with the mouse.
- ◊ If no existing Locality Code matches your entry, Biota offers you the option of creating a new Locality record “on the fly,” with the Locality Code you entered, or accepting an orphan Collection record. See “[“On-the-Fly” Creation of Linked Records](#)” in Chapter 7 for details.
- **Method 5: Click the “Look Up” button** in the Locality Code panel of the Collection Input screen.



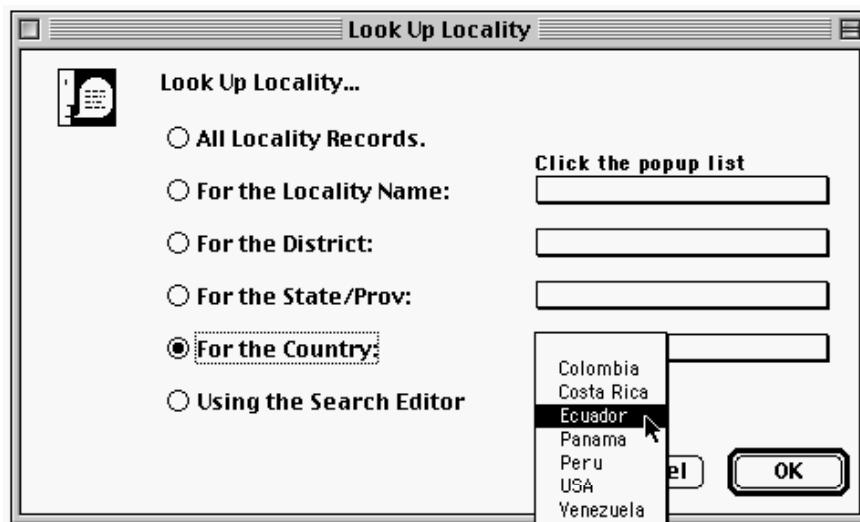
The Look Up Locality window appears.



- a. Select a display option by clicking a button in the Look Up Locality window. You can display All Locality Records (an inefficient approach if there are many Locality records in the database) or restrict the choices displayed to a certain value for Locality Name, State/Province, or Country. Or, you can launch the Query Editor (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12) to find a record using ad hoc criteria.

NOTE: If you have defined an Alias for the Locality Name, District, State/Province, or Country fields of the Locality table (see Chapter 18, “[Renaming Fields](#)”), the Alias appears in the corresponding button text in the Look Up Locality window in place of the Internal Field Name.

- b. **If you select the Locality Name, District, State/Province, or Country option,** Biota creates a list of all unique values for the selected field.
 - ◊ **If there are only a few values,** Biota displays the list in a popup list to the right of the selected button. Click and hold the popup to display the list of values, as shown below.



- ◊ **If there are many values,** Biota displays the list in a separate window with a scrollbar, as shown on the right.
- c. **Select the value you want** from the popup list or the scrolling list. Biota then shows the selected value in the popup area.
- d. **Click the “OK” button in the Look Up**



Locality window. The Look Up Locality selection screen appears, listing all Locality records that match the option and criteria you selected in steps **a.** and **b.** above.

- ◊ **If there are many records in the display screen,** you may first want to use the sort buttons at the top of each column to sort the records displayed by the values for that column.



Look Up Locality				
Sort using the buttons below, then select Locality				
Locality Name	District	State/Prov	Country	Loc. Code
62-75km W Tulcán		Carchi	Ecuador	Tulcán
7-9km NE Pindilíg tow. Rivera		Cañar	Ecuador	Pindilíg
Baeza-Tena rd.		Napo-Pastaza	Ecuador	Baeza-Tena rd.
Baltra Island		Galápagos Islands	Ecuador	Baltra
Calacalí-Nanegalito Rd.		Pichincha	Ecuador	Calacalí-Nanegal
Carretera Antigua-Sto.Domingo de los Cocos		Pichincha	Ecuador	Sto. Domingo rd.
Cerro Villanaco vicinity		Loja	Ecuador	Cerro Villanaco
Cord. de Huacamayos		Napo	Ecuador	Huacamayos
Darwin Island		Galápagos Islands	Ecuador	Darwin
Española Island		Galápagos Islands	Ecuador	Espanola
Fernandina Island		Galápagos Islands	Ecuador	Fernandina
Floreana Island		Galápagos Islands	Ecuador	Floreana
Genovesa Island		Galápagos Islands	Ecuador	Genovesa
Isabela Island		Galápagos Islands	Ecuador	Isabela
Latacunga-Quevedo rd.		Cotopaxi	Ecuador	Latacunga
Loja-Vilcabamba Rd.		Loja	Ecuador	Loja-Vilca
Marchena Island		Galápagos Islands	Ecuador	Marchena
Nanegalito-Tandayapa Rd.		Pichincha	Ecuador	Nanegalito
Nono-Tandayapa Rd.		Pichincha	Ecuador	Nono-Tandayapa
Nono-Pto. Quito Rd.		Pichincha	Ecuador	Nono-Pto. Quito
Old rd. Quito-Sto.Domingo de los Colos.		Pichincha	Ecuador	Quito-Sto.D. old

Try Again**Cancel**

◊ If you want to try a different selection option or field value to display records, click the “Try Again” button at the bottom of the Look Up Locality selection screen.

- When you find the record you want in the Lookup Locality display screen, click it to enter its Locality Code in the Collection Input screen.
- To see the full Locality record, once the Locality Code has been entered, click the “Show Locality Record” button in the “Locality Data” panel.

Locality Code	<input type="text" value="Fernandina"/>	Assign	Look Up								
Locality data	<table border="1"> <tr> <td>Locality Fernandina Island</td> <td>Show Locality Record</td> </tr> <tr> <td>State/Prov Galápagos Islands</td> <td>Elev.</td> </tr> <tr> <td>District</td> <td>Lat. 0°26'S</td> </tr> <tr> <td>Country Ecuador</td> <td>Long. 91°30'W</td> </tr> </table>			Locality Fernandina Island	Show Locality Record	State/Prov Galápagos Islands	Elev.	District	Lat. 0°26'S	Country Ecuador	Long. 91°30'W
Locality Fernandina Island	Show Locality Record										
State/Prov Galápagos Islands	Elev.										
District	Lat. 0°26'S										
Country Ecuador	Long. 91°30'W										

3. Enter information on the collector and date(s) of collection.

NOTE: You can ask Biota to enter a particular value in each new record automatically for the entry areas Collected By, Date Collected, and Date Collection Complete using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).

- Enter the collector’s “Short Name” in the “Collected By” entry area on the General tab. Because this field is linked to the Short Name field of the Personnel table, the entry area has a double border. You can use any of the techniques for entering data in linking fields described in Chapter 7, “[Overview of Record Input Screens](#).”

Collected By	<input type="text" value="J.L. Luteyn"/>	<input type="button" value="X"/>
Date Collected (or Date Started)	Mo: 4 Dy: 19 Yr: 1979	Date Collection Completed (Optional)
	<input type="button" value="Today"/>	Mo: 4 Dy: 21 Yr: 1979
	<input type="button" value="Today"/>	

- ◊ If you know that the Collector has no existing record in the Personnel table, enter a Short Name for the Collector (e.g., Albert B. Smith or A. B. Smith) and press the TAB key. If the entry you make in the “Collected By” entry area does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Collection record without creating a link to the Personnel table (a “Personnel-orphan” Collection record) (see [“Entering Data in Linking Fields”](#) in Chapter 7).

NOTE: On Pin, Slide, Vial, and Herbarium labels, Biota uses the Short Name field for the collector’s name (see Chapter 15, [“Printing Labels”](#)). Although the Short Name may have up to 80 characters, it is best to make it substantially shorter (20-30 characters is a good guideline) if you intend to use Biota to produce specimen labels. Choose a version of the collector’s name that is appropriate for specimen labels—e.g., initials and last name, or first name and last name. You can also use a “Group Name” in the “Collected By” field—e.g., A. B. Smith & C. D. Jones (for help with Group Names, see [“Entering Personnel Data: The ‘Group’ Tab”](#) later in this chapter).

- ◊ If you think the collector may already have a Personnel record, but you are not sure what Short Name the record carries, enter the @ character and press the TAB key. A scrollable list of all existing Personnel records appears (next page), from which you can choose the correct record by clicking it. You can sort the records by Short Name, Last Name, or Institution by clicking the buttons above the columns.

Personnel Records

Click buttons to sort records

Short Name	Last Name	Institution
B. Schwepenife	Schwepenife	CSATS
C. Darwin	Darwin	H. M. S. Beagle
Colwell & Naeem	Colwell & Naeem	UConn & U Minn
E. Lindquist	Lindquist	Agriculture Canada
INBio	INBio	Instituto Nacional de Biodiversidad
J. T. Longino	Longino	The Evergreen State College
J.L. Luteyn	Luteyn	New York Botanical Garden
Luteyn Mites	Luteyn Mite Collections	University of Connecticut
NYBG	New York Botanical Garden	New York Botanical Garden
P. Naskrecki	Naskrecki	University of Connecticut
R. Colwell	Colwell	University of Connecticut
R. Fitzroy	Fitzroy	H. M. S. Beagle
S. Naeem	Naeem	University of Minnesota
UConn	University of Connecticut	University of Connecticut

Cancel Move the green lines to change column width

- ◊ If you know the Short Name for the Collector's existing Personnel record, enter the first letter, the first few letters of the Short Name, or the full Short Name, and press the TAB key. If a single match is found, Biota completes the name and the cursor moves into the next field. If more than one match is found, a choice list like the one above appears, with all matches shown.

If the entry you make in the “Collected By” entry area does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Collection record without creating a link to the Personnel table (a “Personnel-orphan” Collection record) (see “[Entering Data in Linking Fields](#)” in Chapter 7).

NOTE: If you are working with historical Collections, you may not want to create a Personnel record for every Collector—some of whom may be long deceased and their particulars unknown.

- b. **Enter date(s) of collection.** To enter a single collection date, use the “Date Collected” entry area and leave the “Date Collection Completed” entry area blank (“TAB through” it). To enter a Date Range, use both areas. You can enter either a full date, a Month-Year date, or a Year-only date in either date entry area.

NOTE: See “Dates” in Chapter 9 for full details on entering dates, date formats (International vs. U.S.), Collection Date ranges, partial dates, and how Biota handles dates in the Data File.

4. **Enter data for Collection Method, Site, and Source.** Each field accommodates entries up to 80 characters in length. Enter each value and press the TAB key to advance to the next entry area.

Collection Method
Manual extraction from FAA-preserved flowers

Site
Second growth montane wet forest

Source
Collections of J. L. Luteyn, NYBG

You can set any of the following options for each of these three Collection fields:

- **Aliases.** Each field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- **Field Value Defaults.** You can ask Biota to enter a particular value in each new record automatically using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for each field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

Entering Collection Data: The “Host Record,” “Georeference,” “Images,” “Aux Fields,” “Notes,” and “Refs” Tabs

Information on entering and working with data in these tabs appears elsewhere in the Manual. Follow the links below:

- **Host Record tab.** For information on creating host record links in the “Host Record” tab, see Chapter 24, “[Host-Guest Relations](#).”
- **Georeference tab.** For information on entering and working with spatial coordinates in the Georeference tab, see “[Spatial Coordinates](#)” in Chapter 9.
- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Specimen and Collection Combined Input

Biota's structure (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) allows you to link any number of Specimen records to a single Collection record (a many-to-one relation). This approach makes sense when a collector, collecting expedition, inventory, or quadrat-based study gathers two or more distinct specimens, each requiring a separate Specimen record, that nonetheless share the same Collection data.

Historical specimens in museum or herbarium collections, however, are often unique with regard to collection data, each produced by a distinct collecting event (as far as a particular museum or herbarium is concerned). For this reason, many museum databases simply treat all collecting-event data (often including locality data as well) as specimen attributes (fields in a specimen table). With such a design, however, any many-to-one relationships between specimens and collecting events or between collecting events and localities, for specimens produced by contemporary collecting protocols, are either lost or must be recovered by laborious, text-based searches.

Biota allows you to freely mix records for unique historical specimens with Specimen records that bear many-to-one-structured collecting event and locality data. The “Input Specimen and Collection” tool speeds data entry for specimens (each with unique Collection data) by automatically creating a linked Collection record for each Specimen record. This approach preserves the option to later link additional Specimen records to automatically-generate Collection records, if appropriate.

Specimen and Collection Combined Input: How It Works

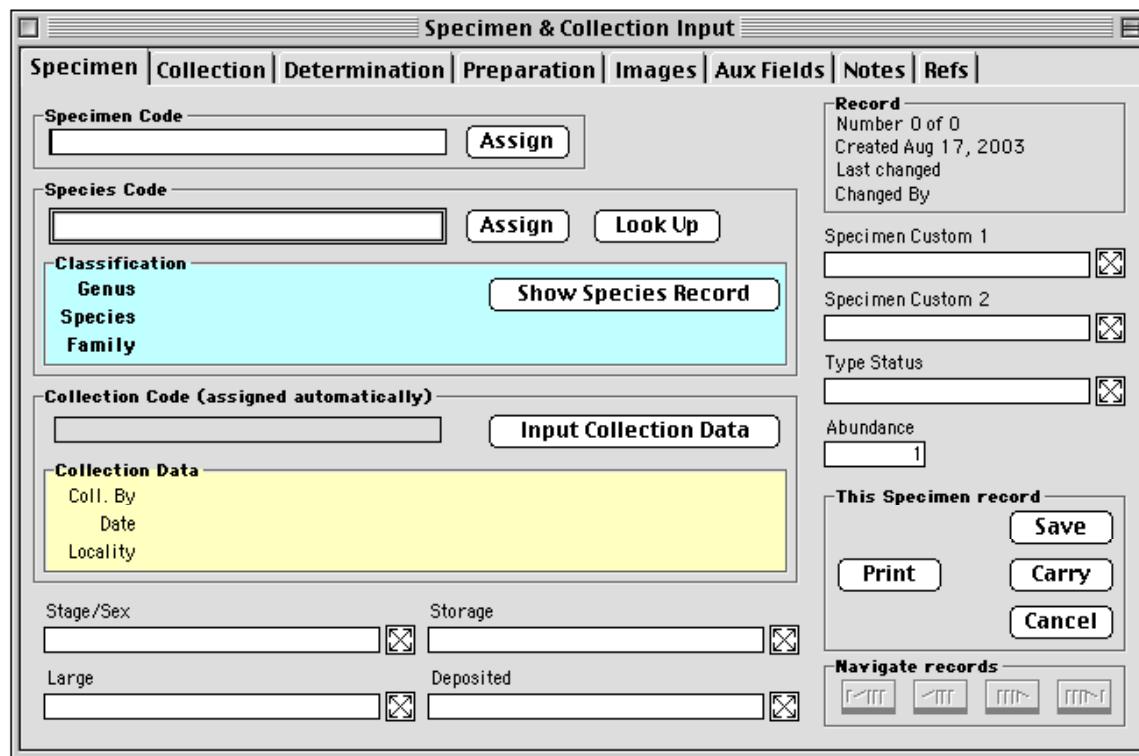
- **Automatic creation of a linked Collection record.** When you choose “Specimen and Collection” from the Input menu, Biota creates a Specimen record (initially blank), just as if you had selected “Specimen” from the Input menu. As soon as you enter a valid Specimen Code manually, a linked Collection record is automatically created, bearing a Collection Code identical to the Specimen Code for the linked Specimen record. (Record Codes need not be unique if in different tables.)
- **Option to create Record Codes automatically.** Alternatively, you can set up the Record Code Settings tool to enter, automatically, a Specimen Code using one prefix and a Collection Code for the linked Collection record, using a different prefix (see Chapter 8, “[Record Codes](#)”). Or, you can enter Specimen codes manually and set up the Record Code Settings tool to enter Collection codes, automatically, with a prefix of your choice.
- **Save or Carry both records.** When you click the “Save” button in the “Specimen and Collection” Input screen, both records are saved. If you click Carry, a new Specimen record is created, but it is automatically linked to the Collection record created for the *previous* Specimen record. In addition, the same fields are duplicated that the “Carry” button copies in the Input Specimen and Input Collection screens.
- **Locality record.** The “Input Specimen and Collection” screen does not automatically create a Locality record linked to the automatically-created Collection record. You must either create the Locality record “on the fly” from the Collection tab of the “Input Specimen and Collection” screen, link the automatically-created Collection record to an existing Locality record, or leave the Collection record unlinked to any Locality record (“orphaned”). The next section provides details.
- **An input tool only.** The “Input Specimen and Collection” screen is strictly an input tool. When you finish a session of record entry using this screen, click the “Cancel”

button to dismiss the screen and display the newly created Specimen records in the standard Specimen Record Listing Screen. If you double-click one of the records in this screen, it appears in the standard Specimen input screen, not the Input Specimen and Collection screen. To enter additional records using the Input Specimen and Collection screen, you must select “Specimen and Collection” from the Input menu.

- **Based on the Specimen Input screen.** The “Input Specimen and Collection” screen is identical in overall design to the Specimen Input Screen. The only differences are the automatic entry of the Collection Code for the automatically-created, linked Collection record, and the addition of a Collection tab for entering data in the fields of the linked Collection record. The Collection tab duplicates the General tab of the Collection Input screen.

Specimen and Collection Combined Input: Tabs of the Input Screen

You can enter a new Specimen record and a linked Collection record by selecting “Specimen and Collection” from the Input menu. The “Specimen and Collection Input” screen has eight tabs. Once you have entered a Specimen Code, you can move to any tab. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move among the tabs.



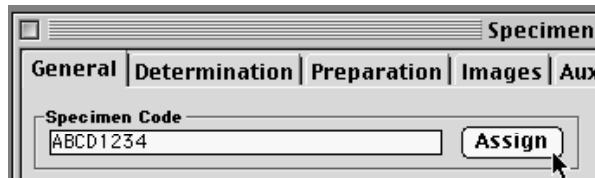
This section describes or refers you to descriptions of how to enter data in the General, Collection, Determination, and Preparation tabs of the Specimen Input screen.

- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”

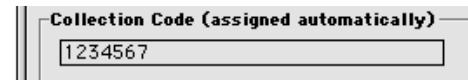
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Specimen and Collection Combined Input: The General Tab

1. **Enter a Specimen Code.** You can enter the Specimen Code by typing it in the Specimen Code entry area, by using the adjacent “Assign” button (see “[Assigning New Record Codes Using an ‘Assign’ button: Step by Step](#)” in Chapter 8), by setting up the Record Code Settings tool to enter it automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8, or by scanning in a barcode (see Appendix K, “[Barcodes](#)”).

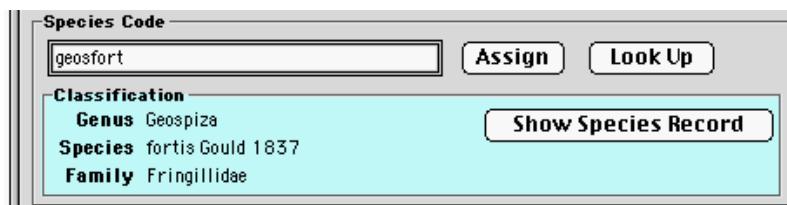


Once a Specimen Code has been entered, Biota automatically creates a linked Collection record. Unless you have set up the Record Code Settings tool to enter Collection Codes automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8), the Collection Code in the linked Collection record duplicates the Specimen Code. Biota displays the Collection Code in the “Collection Code” panel of the “General” tab.

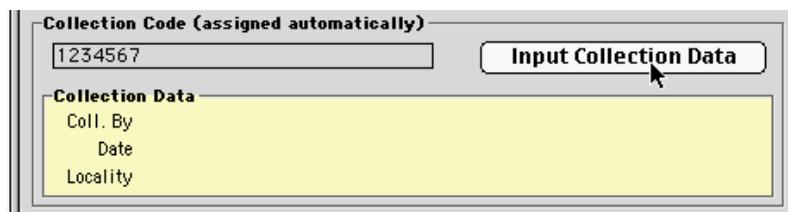


Note: The Specimen Code may be up to 30 characters in length. Because Specimen Code is the Key field for the Specimen table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Specimen Code you enter must not duplicate the Specimen Code of any existing Specimen record. Likewise, the Collection Code for the automatically created Collection record must not duplicate the Collection Code of any existing Collection record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3). For help understanding how Record Codes work, see Chapter 8, “[Record Codes](#).”

2. **Enter a Species Code.** The Species Code links this Specimen record with a record in the Species table (see “[Species Input](#)” later in this chapter). There are five *alternative* methods for entering a Species Code. For details, refer to [Step 2 in the section “Entering Specimen Data: The ‘General’ Tab,”](#) earlier in this chapter.



3. If you wish to enter data for the linked Collection record now, click the “Input Collection Data” button in the Collection Code panel to move to the Collection tab of the combined “Specimen and Collection Input” screen. (Remember, the Collection Code had been entered automatically.) Alternatively, you can first complete the General tab (Specimen fields), then move to the Collection tab.



4. Enter data for Stage/Sex, Medium, Storage, Deposited, Specimen Custom 1, Specimen Custom 2, and Type Status. Enter each value and press the TAB key to advance to the next entry area.

You can set any of the following options for each of these seven Specimen fields:

- **Aliases.** Each field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- **Field Value Defaults.** You can ask Biota to enter a particular value in each new record automatically using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for each field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

NOTES:

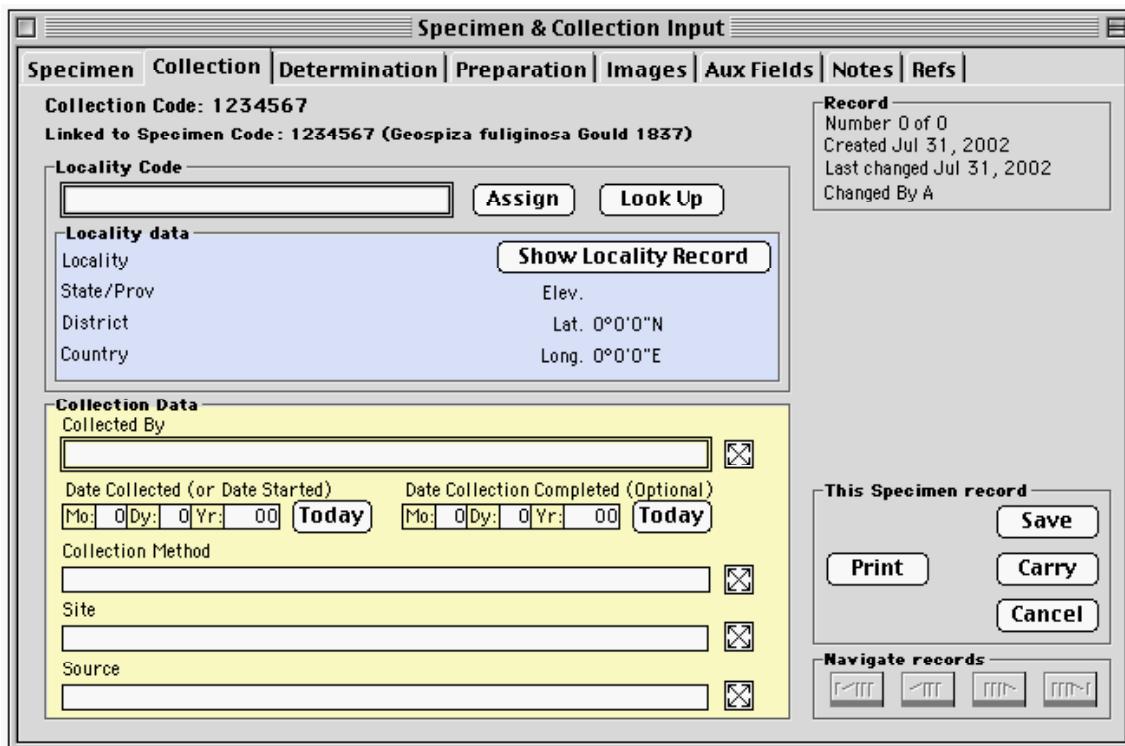
- The “>” field in the Specimen table is used by the Specimen Loans system in Biota. If you intend to use the Loans system do not use this field for another purpose. See Chapter 21, “[Specimen Loan System](#)” for details.
 - The Medium field also appears on the Preparation tab of the “Specimen and Collection Input” screen. You can enter data in this field on either tab and the data will appear in both locations.
5. **Enter a value for Abundance.** Biota enters a “1” as the default for the Abundance field.
- **If this record is for a single physical specimen,** leave the value at 1. Some Biota tools sum the values in this field for sets of specimen records, so a record representing a single physical specimen should read “1” for Abundance.

- If this record represents more than one physical specimen, enter the total number it represents. If the record for one physical specimen represents n additional, unmounted specimens (a physical voucher), enter the value $n + 1$.

Specimen and Collection Combined Input: The Collection Tab

The Collection tab of the combined “Specimen and Collection Input” screen shows the Collection Code already entered at the top of the screen. Otherwise, the Collection tab is identical in function and layout to the General tab of the “Collection Input” screen.

For full instruction on entering data in the Collection tab, refer to the section “[Entering Collection Data: The ‘General’ Tab](#)” earlier in this chapter, and begin with Step 2 in that section.



Specimen and Collection Combined Input: The “Determination,” “Preparation,” “Images,” “Aux Fields,” “Notes,” and “Refs” Tabs

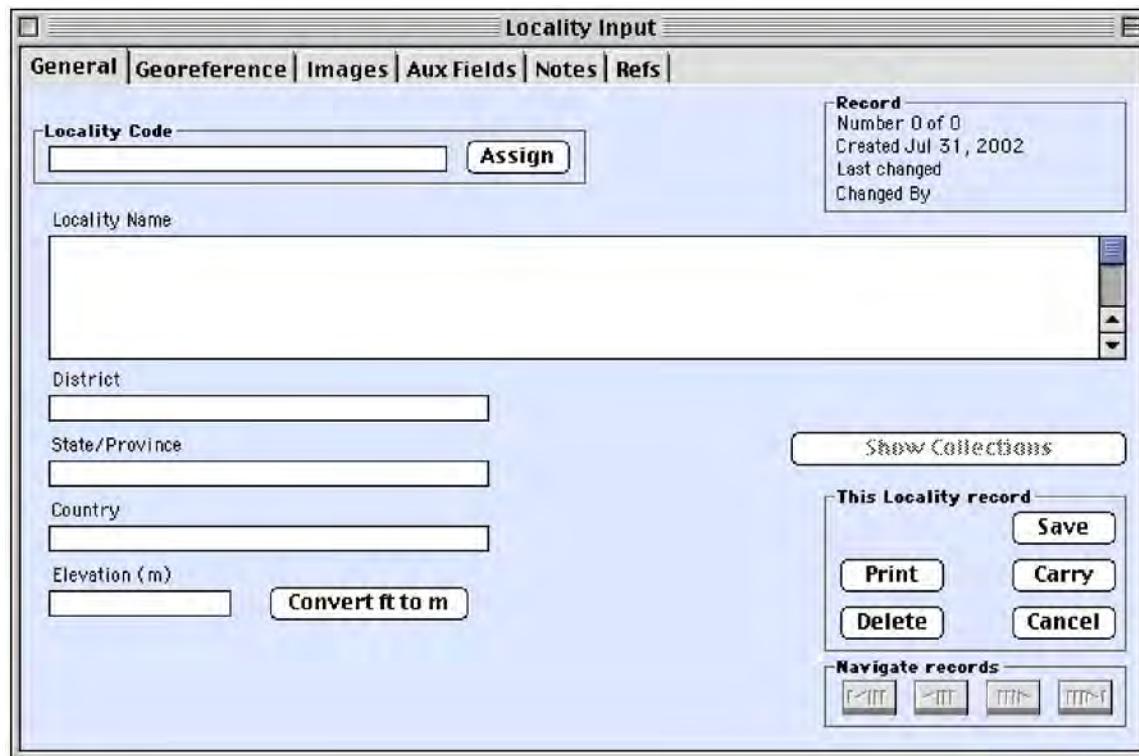
Information on entering and working with data in these tabs appears elsewhere in the Manual. Follow the links below.

- **Determination tab.** For information on entering and working with the field “Last Determined By” and “Date Last Determined,” see “[Entering Specimen Data: The ‘Determination’ Tab](#)” earlier in this chapter. (Because the combined “Specimen and Collection Input” screen is for data entry only, the Determination History panel does not appear on the Determination tab of this screen.)
- **Preparation tab.** For information on entering and working with the “Prepared By” field on the Preparation tab, see “[Entering Specimen Data: The ‘Preparation’ Tab](#)” earlier in this chapter.

- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Locality Input

You can enter a new record in the Locality Input screen by selecting Locality from the Input menu, by clicking the “Add Locality” button on the Locality Record Listing screen, or by creating a new Locality record “on the fly” from the Collection Input screen. The Locality Input screen has six tabs. Once you have entered a Locality Code, you can move to any tab. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move among the tabs.



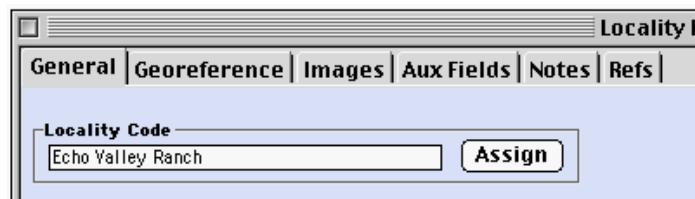
This section describes how to enter data in the General tab of the Collection Input screen. For other tabs, follow the links below.

- **Georeference tab.** For information on entering and working with spatial coordinates in the Georeference tab, see “[Spatial Coordinates](#)” in Chapter 9.
- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”

- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Entering Locality Data: The “General” Tab

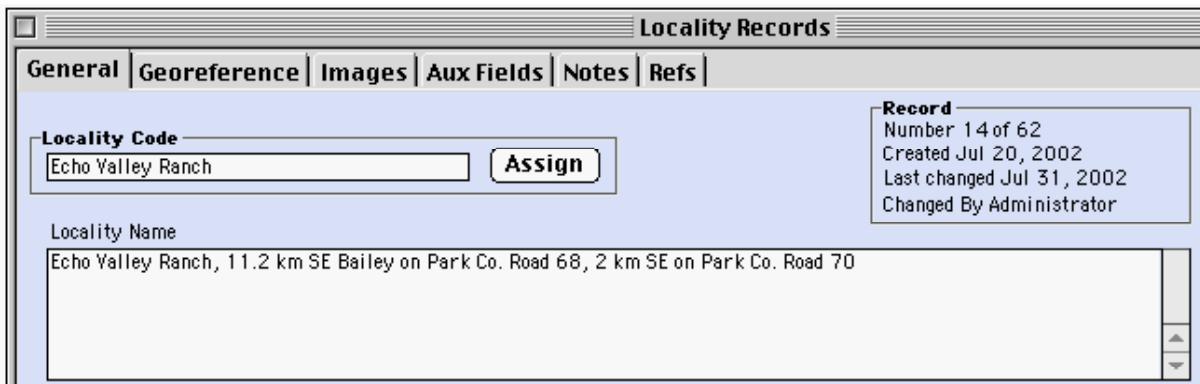
1. **Enter a Locality Code.** You can enter the Locality Code by typing it in the Locality Code entry area or by using the adjacent “Assign” button (see “[Assigning New Record Codes Using an “Assign” button: Step by Step](#)” in Chapter 8).



The Locality Code may be up to 30 characters in length. Because Locality Code is the Key field for the Locality table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Locality Code you enter must not duplicate the Locality Code of any existing Locality record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3). For help understanding how Locality Codes work, see Chapter 8, “[Record Codes](#).”

NOTE: If you are creating a Locality record “on the fly” while working on a Collection record (see [Step 3 of “Entering Collection Data: The ‘General’ Tab”](#) earlier in this chapter), the Locality Code you entered in the Collection Input screen is already displayed and the cursor is in the next field (Locality Name).

2. **Enter Locality Name.** The Locality Name may be very long, if necessary—up to 32,000 characters in length (the standard length of a “text” field in 4th Dimension). Where possible, this entry might be an official geographical place name from a geographical authority list or gazetteer. The Locality Code (Step 1 above), on the other hand, can be any unique alphanumeric value, but in the absence of official locality codes (which do exist in some countries), you may find it convenient to make it either the same as Locality Name (if no more than 30 characters in length), or an abridgement of the Locality Name.



NOTE: Text fields in 4th Dimension, such as Locality Name, cannot be sorted or indexed. (Indexing is an internal way of making sorts and queries faster.) Therefore, Biota automatically and invisibly maintains a parallel “indexing field” for Locality Name, called “Locality Name Index.” For each Locality record, Locality Name Index contains the first 80 characters of the Locality Name field (80 characters is the longest indexable field length in 4th Dimension). When you use the Sort Editor, use the Locality Name Index to sort (Locality Name is not even listed). When you use the Query Editor, you may search on either field, but the search will be faster if you use Locality Name Index.

3. Enter District, State/Province, Country, and Elevation.

You can set any of the following options for each of these four Locality fields—as well as for the Locality Name field (step 2 above):

- **Aliases.** Each field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”). For example, you might want to rename the District field *County* or the Elevation field *Depth*.
- **Field Value Defaults.** You can ask Biota to enter a particular value in each new record automatically using the “Field Value Defaults” tool from the Special menu (see “[Setting Default Entries: Field Value Defaults](#)” in Chapter 17).
- **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for each field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

District	Park County
State/Province	Colorado
Country	USA
Elevation (m)	8000-8100 ft
	Convert ft to m

NOTES ON THE ELEVATION FIELD:

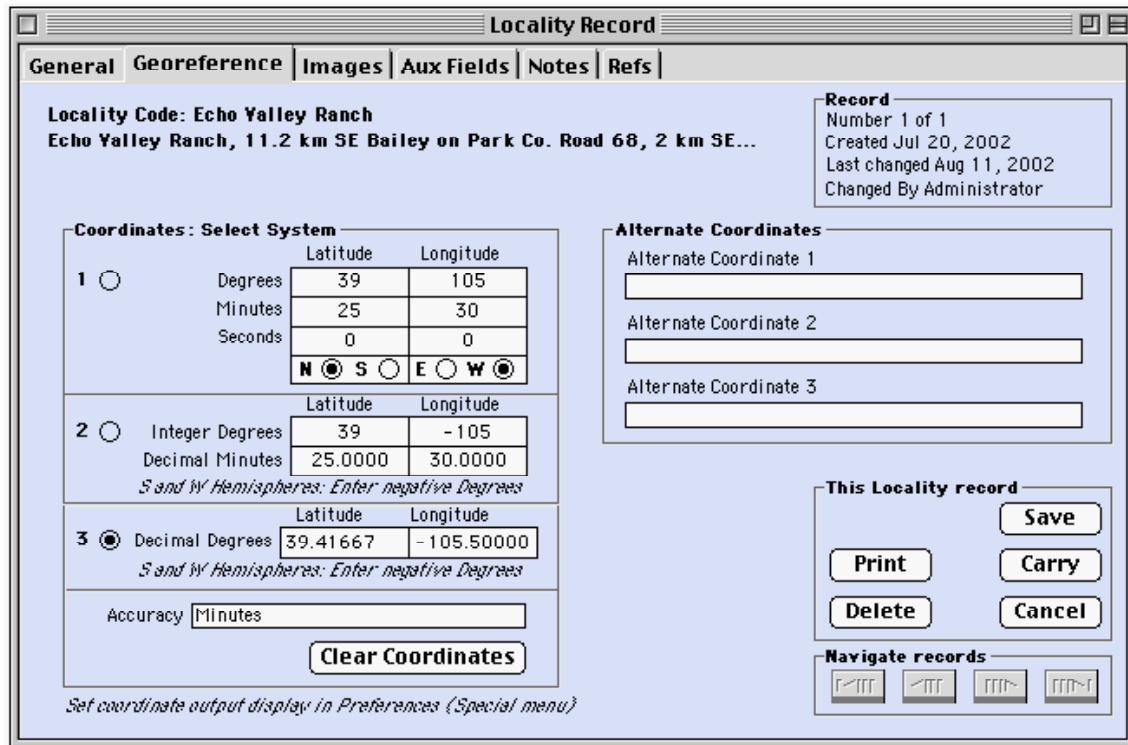
- a. **The [Locality] Elevation field is an alphanumeric**, not a numeric, field. This design allows elevation ranges (as illustrated above) and non-metric units (e.g., feet) to be included in the entry.
- b. **If you enter a numeral, with no units**, Biota assumes that the elevation is in meters, when printing Specimen locality labels, and automatically appends “m” to the elevation (see Chapter 15, “[Printing Labels](#)”). Or, you can include “m” in the field entry itself, if you wish.
- c. **If you enter elevations or depths in feet instead of meters**, be sure to include the abbreviation “f” or “ft” (or anything with the letter “f” in it). In this case, Biota prints the value on locality labels just as you entered it, without adding “m.” If all your elevation data are in feet and you do not intend to convert the values to meters, you may want to change the default name for the [Locality] Elevation field from “Elevation (m)” to “Elevation (ft)” (see Chapter 18, “[Renaming Fields](#)”).
- d. **If the elevation entry is in feet and you wish to convert it to meters**, click the “Convert ft to m” button. The abbreviation “f” or “ft” (or anything with the

letter “f” in it) must be present in the field, or the button does nothing and presents an explanatory message.

- **If the entry is a single value**, with or without a minus sign, it is directly converted to meters and “m” is appended.
- **If the entry is a range**, of the form “8000-8100 ft” or “8000 to 8100 ft,” the range is converted to meters, in the same format (“2438-2469 m” or (“2438 to 2469 m”)
- **If the entry is a range, and either value includes a minus sign**, you must use the “to” format (e.g., “-200 to -50 ft”) for the range to be converted properly.

Entering Locality Data: Entering Latitude and Longitude in the “Georeference” Tab

This section assumes you have already read the section “[Spatial Coordinates](#)” in Chapter 9, which provides an overview of georeference options in Biota, including settings in the Coordinates panel of the Preferences screen (Special menu).



1. Enter Coordinates: Latitude and Longitude.

Biota stores Latitude and Longitude data in units of decimal degrees—the standard system used in Geographic Information Systems (GIS) work. Nonetheless, Biota offers three unit systems for the entry and display of latitude and longitude values in the Locality table. You can enter data using any of the three systems and freely use different systems for different records in the same data file. As you make an entry in any of the systems, Biota instantly translates the value into the other two and

displays all three versions in the Coordinates panel of the Georeference tab in the Locality input screen.

NOTE: Biota validates entries for the Latitude and Longitude fields of the Locality table. Latitude may not be less than -90 nor greater than +90, and Longitude may not be less than -180 nor greater than +180, or the equivalents in degree/minutes/seconds.

- a. **System 1: Degrees/Minutes/Seconds (DMS).** This is the traditional system found in most gazetteers and atlases—but see the important warning, in the section “[Latitude and Longitude \(Locality Table\)](#),” in Chapter 9.
 - i. Click the “1” button in the Coordinates panel to select System 1.
 - ii. Enter Degrees, Minutes, and Seconds of Latitude, pressing TAB after each entry.
 - iii. Continue with Degrees, Minutes, and Seconds of Longitude.
 - iv. Click the hemisphere buttons (N or S, E or W) if necessary. (The default Hemispheres are N and W, reflecting Biota’s heritage.)
- b. **System 2: Integer Degrees, Decimal Minutes.** This is the system used by many Geographical Positioning System (GPS) instruments.
 - i. Click the “2” button in the Coordinates panel to select System 2.
 - ii. Enter Integer Degrees and Decimal Minutes of Latitude, pressing TAB after each entry.
The Integer Degree value must be negative for Latitudes in the Southern Hemisphere.
 - iii. Continue with Integer Degrees and Decimal Minutes of Longitude. The Integer Degree value must be negative for Longitudes in the Western Hemisphere.

Coordinates : Select System		Latitude	Longitude
1 <input checked="" type="radio"/>		39	105
Degrees	25	30	
Minutes	0	0	
Seconds			
	<input checked="" type="radio"/> N <input type="radio"/> S	<input type="radio"/> E <input checked="" type="radio"/> W	<input checked="" type="radio"/> W <input type="radio"/> E

		Latitude	Longitude
2 <input checked="" type="radio"/>	Integer Degrees	39	-105
	Decimal Minutes	25.0000	30.0000
S and W Hemispheres: Enter negative Degrees			

WARNING: Beware! Some gazetteers list Latitude and Longitude values in DMS, but use a *format* that looks like Integer Degrees with Decimal Minutes, e.g., 24° 48.39 actually means 24° 48' 39" in these gazetteers. The easiest way to detect this deceptive format is to see if you can find any values in the gazetteer to the right of the "decimal point" that exceed 59. If not, those values are Seconds, not the decimal part of true Decimal Minutes.

c. **System 3: Integer Degrees, Decimal Minutes.** This is the system used in Geographical Information Systems (GIS).

- i. Click the “3” button in the Coordinates panel to select System 3.
- ii. Enter Decimal Degrees of Latitude and press TAB. The value must be negative for Latitudes in the Southern Hemisphere.
- iii. Enter Decimal Degrees of Longitude. The value must be negative for Longitudes in the Western Hemisphere.
- d. Enter a code or description for the Accuracy of the Coordinates, once the Coordinates have been entered.
- e. To clear all Coordinate entry areas, click the “Clear Coordinates” button at the bottom of the Coordinates panel.

	Latitude	Longitude
3 <input checked="" type="radio"/> Decimal Degrees	39.41667	-105.50000
S and N Hemispheres: Enter negative Degrees		

Accuracy	Minutes
Clear Coordinates	

Set coordinate output display in Preferences (Special menu)

NOTE: You can tell Biota to display, print, and export only Degrees, Minutes, and Hemisphere for an individual record by entering the value “Minutes” (or “Minutos,” for the Spanish interface) in the Lat Long Accuracy field. (Do not enter the quotation marks.) See “[Setting Latitude and Longitude Display Resolution for Individual Locality Records](#)” in Chapter 9 for details.

Entering Locality Data: Entering Alternate Coordinates in the “Georeference” Tab

Please refer to the section “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9 for full details on using Alternate Coordinate systems (e.g., UTM or Lambert coordinates, or the U.S. Township-Range-Section system), translating alternate systems to latitude and longitude, and Alternate Coordinate display settings in the Coordinates panel of the Preferences screen (Special menu).

Entering Locality Data: The “Images,” “Aux Fields,” “Notes,” and “Refs” Tabs

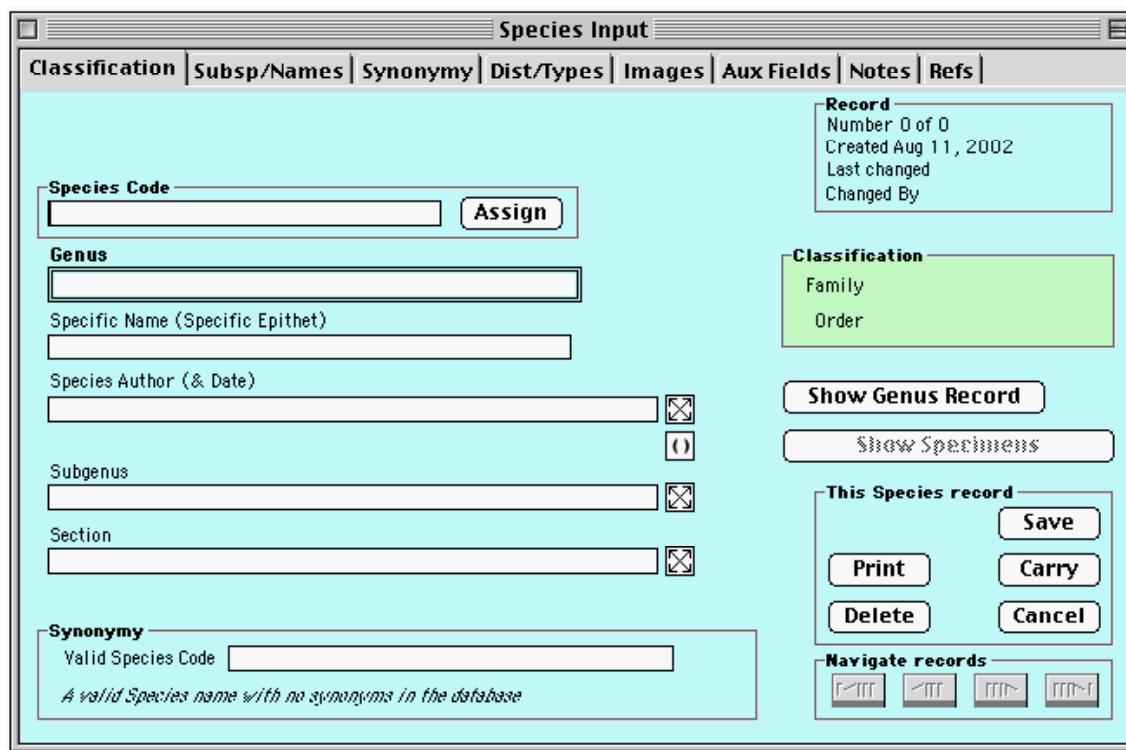
Information on entering and working with data in these tabs appears elsewhere in the Manual. Follow the links below:

- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.

- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Species Input

You can enter a new record in the Species Input screen by selecting Species from the Input menu, by clicking the “Add Species” button on the Species Record Listing screen, or “on the fly” from the Specimen Input screen. The Species Input screen has eight tabs. Once you have entered a Species Code, you can move to any tab. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move among the tabs.



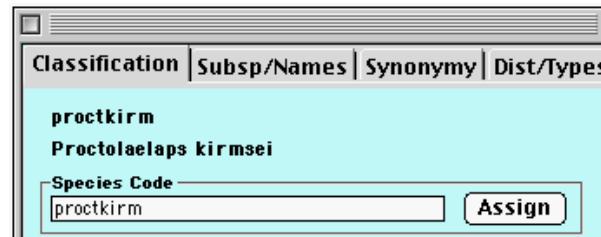
This section describes how to enter data in the Classification, Subsp/Names, and Dist/Types tabs of the Species Input screen. For other tabs, follow the links below:

- **Synonymy tab.** For information on designating a Species record as a synonym of another Species record, or to learn how to display the synonyms of a valid Species record, see Chapter 23, “[Synonymy System](#).”
- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Entering Species Data: The “Classification” Tab

- Enter a Species Code.** You can enter the Species Code by typing it in the Species Code entry area, by using the adjacent “Assign” button (see “[Assigning New Record Codes Using an ‘Assign’ button: Step by Step](#)” in Chapter 8), by setting up the Record Code Settings tool to enter it automatically (see “[Assigning New Record Codes Automatically During Data Entry](#)” in Chapter 8, or by reading in a barcode (see Appendix K, “[Barcodes](#)”).

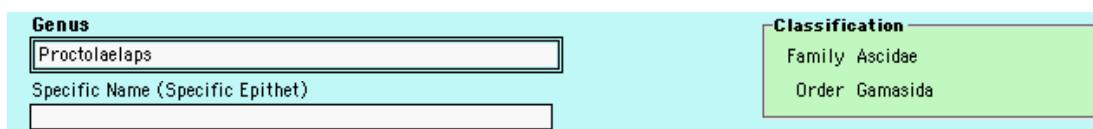
The Species Code may be up to 30 characters in length. Because Species Code is the Key field for the Species table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Species Code you enter must not duplicate the Species Code of any existing Species record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3). For help understanding how Species Codes work, see Chapter 8, “[Record Codes](#).”



NOTE: If you are creating a Species record “on the fly” while working on a Specimen record (see [Step 2 of “Entering Specimen Data: The ‘General’ Tab”](#) earlier in this chapter), the Species Code you entered in the Specimen Input screen is already displayed and the cursor is in the next field (Genus).

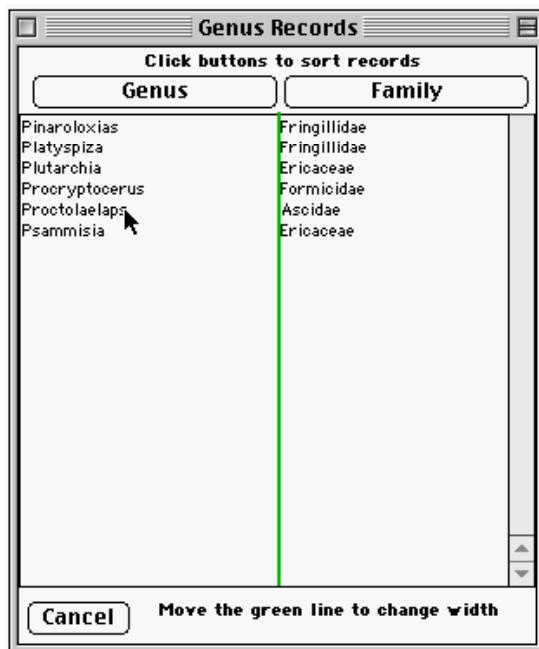
- Enter the Genus.** The Genus entry links this Species record with a record in the Genus table (see “[Genus, Family, Order, Class, Phylum, and Kingdom Input](#)” later in this chapter). You can enter a Genus using either of two methods for entering data in linking fields, as described in the section “[Entering Data in Linking Fields](#)” in Chapter 7.

- **Method 1: Enter the full Genus name manually.**
 - ◊ If a Genus record exists with the Genus name you entered, the “Classification” panel to the right of the Genus entry area displays the Family name from the linked Genus record and the Order name from the linked Family record, if any. The cursor moves on to the next entry area (Specific Name).



NOTE: Be sure to confirm that the correct Genus record was found. If your entry uniquely matches the first part of a different Genus name, the wrong link will be made. See “[Overriding Wildcard Input for Linking Fields](#)” in Chapter 7.

- ◊ If no Genus record exists with the Genus name you entered, Biota offers you the option of creating a new Genus record “on the fly” (using the Genus name you entered) or accepting an orphan Species record. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.
- Method 2: Enter the first letter or first few letters of a Genus name, then press TAB (wildcard lookup). See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.
 - ◊ If only one Genus record matches the entry, Biota automatically completes the entry.
 - ◊ If more than one existing Genus record matches the entry, a scrollable list of matching Genus names for existing Genus records appears, from which you can choose the correct record by clicking it with the mouse. (If you enter the @ character, and nothing else, all Genus records appear in the scrollable list.)



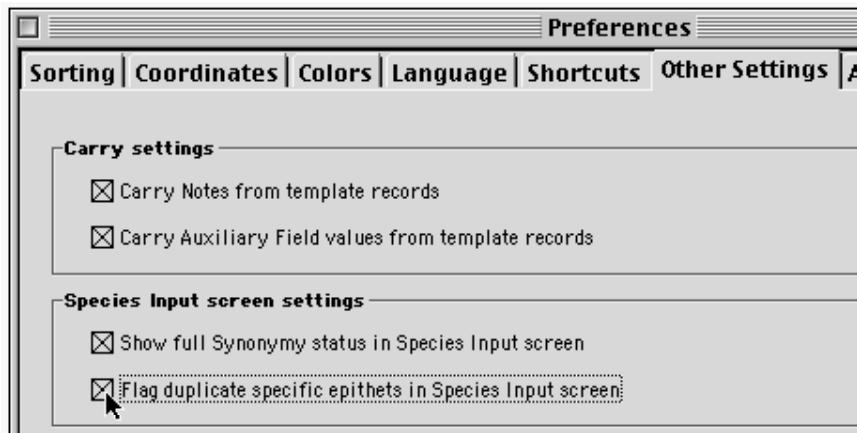
NOTE: In two special circumstances, you might need to create a new Genus record that legitimately duplicates an existing Genus name: (1) when genera in two kingdoms have the same name and (2) when you want to record a generic synonym. See “[A Special Problem for Genera: Legitimate Duplicate Generic Names](#)” later in this chapter, if either case arises.

3. Enter Specific Name (Specific Epithet).

- **Entry Choice List.** You can enable an Entry Choice List (pick list) for the Specific Name field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).
- **Duplicate Specific Name checking.** When you enter a Specific Name (the Species Name field of the Species table), you can set Biota to check

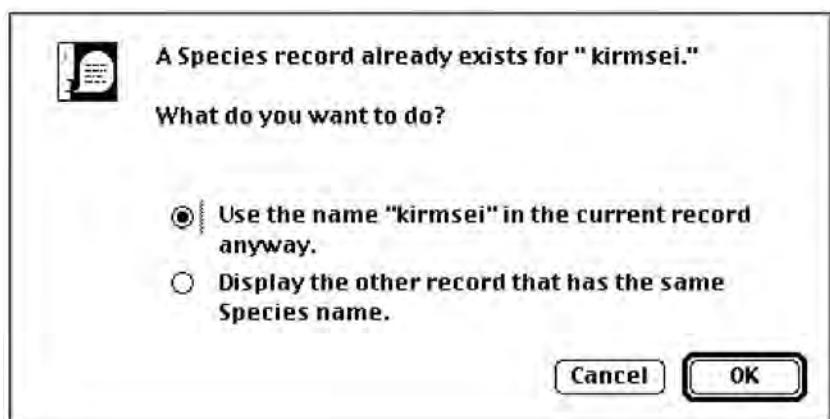
automatically for identical Species Name entries in existing records, *disregarding Genus*. The purpose of this check is to prevent the accidental creation of two or more Species records for the same species (albeit with distinct Species Codes). The reason for disregarding Genus is to take into account changed or alternative generic concepts.

To enable or disable checking for duplicate Specific Name values, choose Preferences from the Special menu. Go to the “Other Settings” tab and find the “Species Input screen settings” panel. Check or uncheck the setting for “Flag duplicate specific epithets in Species Input screen.”



Here is how it works, with duplicate Specific Name checking enabled:

- **If the Specific Name you entered is unique among Species records in the database**, Biota automatically accepts your entry and moves on to the next entry area (Species Author).
- **If the Specific Name you entered is any variation on *sp.***, Biota accepts your entry whether or not it is unique. Entries in this category include:
 - ◊ *sp* without any additional characters.
 - ◊ *sp* followed by a period or a space character, alone or followed by any additional characters, including numbers (e.g., *sp* 1, *sp*. 3, *sp. nov.*).
 - ◊ *n. sp* alone or followed by any additional characters.
- **If Biota finds another Species record with the same Species Name you entered**, an option window appears, shown below. (If more than one match is found, the message gives the number of matches.)

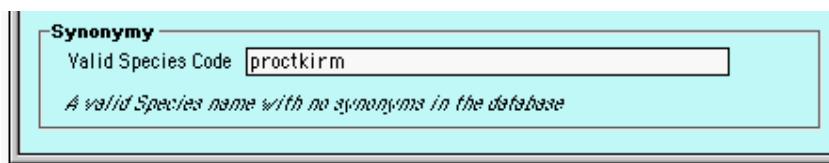


- ◊ If you select the first option (the default), Biota accepts your entry and moves on to the next entry area (Species Author).
 - ◊ If you select the second option, Biota accepts your entry and moves on to the next entry area, but a new window opens showing the existing Species record (or records) that shares the same Species Name value. Based on this information, it is then up to you whether to modify the Species record you are working on, delete it, or save it as is.
 - ◊ If you click Cancel in the option window, the entry you made in the Specific Name entry area is cleared.
4. **Enter Species Author (and Date).** The Species Author field is an ordinary alphanumeric field (up to 80 characters), not linked to the Personnel table. The date (usually only the year), if you include one, is part of the entry in the Species Author field and can therefore be in any format, without reference to the Biota date formats described in the section “[Dates](#)” in Chapter 9.

- **Entry Choice List.** You can enable an Entry Choice List (a pick list or authority list) for the Species Author field using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17). A Choice List can speed up data entry when certain authors (and dates) apply to many Species records. However, if you are entering a list of species that share the same entry in the Species Author field, using the “Carry” button (see “[Duplicating a Record Displayed in the Input Screen Using the ‘Carry’ Button](#)” in Chapter 10) may be more efficient than using an Entry Choice List.
- **The parenthesis button.** To place left and right parentheses around an entry in the Species Author entry area, click the parenthesis button to the right and just below the entry area.

5. **Enter Subgenus and Section.** In Biota’s structure, Subgenus and Section are attributes (field) of the Species table. See “[Intermediate Taxonomic Levels \(Subtaxa and Supertaxa\)](#)” in Chapter 9 for details on how Biota handles Intermediate Taxonomic levels (ranks).
- **Aliases.** Each of the fields Subgenus and Section can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
 - **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for the Subgenus and/or Section fields using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

6. Note the **Valid Species Code and synonymy status summary** in the Synonymy panel at the bottom of the Classification tab. In a new record, the Valid Species Code is automatically entered when you enter the Species Code and matches it exactly. The synonymy status summary normally reads “A valid Species name with no synonyms in the database.” (The only exception would be in the unusual case that synonyms are already present.)



If you synonymize this Species record with another Species record, the Valid Species Code is changed to the Species Code for the senior synonym. See Chapter 23, "[Synonymy System](#)" for details on the Synonymy panel of the Classification tab, as well as the Synonymy tab itself.

Entering Species Data: The “Subsp/Names” Tab

The “Subsp/Names” tab records information on infra-specific classification and common names for the taxon represented by the Species record. The rationale for including

The screenshot shows the "Species Input" window with the "Subsp/Names" tab selected. The main area displays the taxon identification "SPP000250" and the full scientific name "Metrioptera roeseli Hagenbach roeseli Hagenbach diluta Charpentier". Below this, there are fields for "Subspecies, Variety, & Common Names". The "Subspecific Epithet" field contains "roeseli", and the "Subspecies Author (& Date)" field contains "Hagenbach". The "Variety or Cultivar" field contains "diluta", and the "Variety Author (& Date)" field contains "Charpentier". The "Common Name" field contains "Roesel's Bush-cricket". To the right of the main area, there is a "Record" panel showing "Number 82 of 83", "Created Aug 16, 2002", "Last changed Aug 16, 2002", and "Changed By Administrator". At the bottom right, there are buttons for "Save", "Print", "Delete", "Carry", and "Cancel". Below these buttons is a "This Species record" section with four icons. At the very bottom, there is a "Navigate records" section with four icons.

infraspecific taxa—subspecies, varieties, cultivars, and the like—as attributes of the Species table requires some explanation. Like other nonobligatory taxonomic ranks (e.g., Subfamilies, Tribes, and Superorders) infraspecific taxa are defined for some parent taxa (for some species, in this case) but not for others. By the logic presented in

the section on “[Intermediate Taxonomic Levels](#)” in Chapter 9, infraspecific rank ought, therefore, to be an attribute of Specimen records, not Species records, in a hierarchical table structure like Biota’s, just as Subfamily membership is considered an attribute of a Genus.

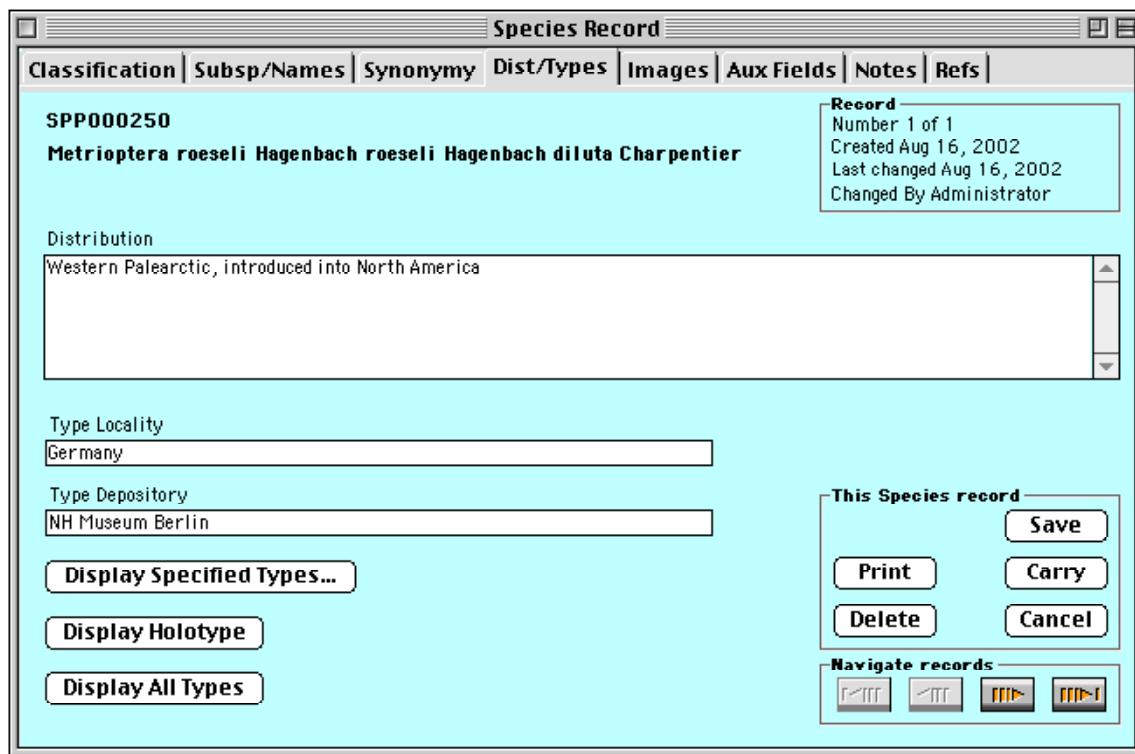
On the other hand, Specimen records are unique. They represent concrete entities—physical specimens or material derived from them—whereas records in the Species, Genus, Family, and higher taxon tables represent taxonomic concepts. In effect, *records in the Species table in Biota represent the lowest taxonomic concepts to which Specimen records can be assigned*, whether that level is in fact considered a species or an infraspecific taxon. This structure permits Specimen determinations to be represented by links to Species records, a key design feature of Biota’s structure, and essential to its functioning.

For species that have infraspecific taxa, a separate record in Biota’s Species table is required for each infraspecific taxon at the lowest level defined. For example, for a species that has two subspecies, each in turn split into three recognized varieties, six Species records would be required—one for each of the six varieties. Each of the six records would also record the subspecies and species to which the variety belongs.

- **Field lengths.** The Subspecies Author, Variety Author, and Common Name fields each allow up to 80 characters. The Subspecies and Variety fields each allow up to 40 characters.
- **Entry Choice List.** You can enable an Entry Choice List (a pick list or authority list) for the Subspecies Author, Variety Author, and Common Name fields using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).
- **The parenthesis button.** To place left and right parentheses around an entry in the Subspecies Author or Variety Author entry area, click the parenthesis button to the right of the entry area.
- **Alias.** The Common Name field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).

Entering Species Data: The “Dist/Types” Tab

The “Dist/Types” tab of the Species Input screen records information on the geographical Distribution of the taxon represented by the Species record, the Type Locality for the species, and the Type Depository (the institution in which the holotype is deposited).



- Field lengths.** The Distribution field is a text field, allowing up to 32,000 characters. The Type Locality and Type Depository fields each allow up to 80 characters.
- Entry Choice Lists.** You can enable an Entry Choice List (a pick list or authority list) for the Distribution, Type Locality, and Type Depository fields using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

NOTE: If you use an Entry Choice List to enter data in the Distribution field, each entry is limited to no more than 80 characters. You can always enter a larger number of characters manually for individual records.

- Aliases.** The Distribution, Type Locality, and Type Depository fields can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- The “Display All Types” button.** If you click this button, Biota finds and displays all Specimen records linked to this Species record for which the [Specimen] Type Status field contains either the string “type” (English) or “tipo” (Spanish), with or without other characters, disregarding case (upper or lower). Thus, all Specimen

records for this Species with “type,” “holotype,” “paratype,” “syntype,” etc., (or their Spanish equivalents) in the Type Status field will be found.

WARNING: For Specimen records that do *not* represent types of any kind, do *not* enter “Not a type,” “Non-type,” or any other entry containing the string “type” (or “tipo”) in the Type Status field, or Biota will find and display them when you click the “Display All Types” button.

- **The “Display Holotype” button.** If you click this button, Biota finds and displays all Specimen records linked to this Species record for which the [Specimen] Type Status field reads (precisely) “holotype” (English) or “holotipo” (Spanish), disregarding case (upper or lower). Presumably, there is at most one such record, but if there are more, Biota displays them.
- **The “Display Specified Types” button.** If you click this button, Biota presents a request screen.
 1. **Enter the category of types you wish to find** for this Species record by typing in the entry area in the request window.
(The entry may be either singular or plural. Biota strips terminal “s” before the search.)
 2. **Click the “OK” button** in the request window. Biota finds and displays all Specimen records linked to this Species record for which the [Specimen] Type Status field contains exactly the string you entered (in singular form), disregarding case (upper or lower).
- **For all three buttons,** any Specimen records found are displayed in the Specimen Record Listing screen in a separate window, leaving the Species Input and screen unchanged (although it may be hidden behind the Specimen Record Listing screen).



Entering Species Data: Display, Printing, and Export of Infraspecific Taxon, Distribution, and Type Information

- **In Record Listing screens and preformatted printed reports** that display Species information, the Species field displays Species Name (epithet), Subspecies (if any), and Variety (if any). If both Subspecies and Variety names are present, they are not likely to be fully displayed due to space limitations in Record Listing screens, but all fields are fully visible in the Species Input screen. In preformatted printed reports (e.g., the Species report, see Chapter 14, “[Printing Reports](#)”), sufficient space is available for long Genus-Species-Subspecies-Variety tetratomials.
- **On pin, vial, and slide determination labels**, full trinomials or tetratomials appear, where appropriate, followed by the author field for the *lowest* level included (e.g., *Metrioptera roeseli* subsp. *roeseli* var. *diluta* Charpentier). Authors for higher levels are not included. See Chapter 15, “[Printing Labels](#).”
- **On herbarium labels** (following botanical convention), the Author fields for *all* levels (species and below) are included (e.g., *Beta vulgaris* Linnaeus subsp. *nivea* Jones var. *odorata* Lopez). See “[Herbarium Specimen Labels](#)” in Chapter 15.

- In the Create Web Pages sequence, a window entitled “Select Options and Fields for Species Records” offers the option to treat subspecific authors in either the “pin-vial-slide label” format or the “herbarium label” format, as described above. In addition, checkboxes allow you to include Common Name, Distribution, Type Locality, and/or Type Depository for each Species. See Chapter 33, “[Exporting Static Web Pages](#).”
- If the Determination History option is enabled (see Chapter 22, “[Determination Histories](#)”), Biota creates a Determination History record for each linked Specimen when you add or update any infraspecific taxon fields (Subspecies, Subspecies Author, Variety, or Variety Author) in a Species record.
- To display infraspecific taxonomic, distribution, or type fields in the Species Record Listing screen, see “[Changing the Fields Displayed in an Record Listing screen](#)” in Chapter 10.

Entering Species Data: The “Synonymy,” “Images,” “Aux Fields,” “Notes,” and “Refs” Tabs

Information on entering and working with data in these tabs appears elsewhere in the Manual. Follow the links below:

- **Synonymy tab.** For information establishing and managing species synonymies, see Chapter 23, “[Synonymy System](#).”
- **Images tab.** For information on entering and working with Specimen Images in the Images tab, see Chapter 19, “[Images](#).”
- **Aux Fields tab.** For information on entering Specimen Auxiliary Field data in the Aux Fields tab, see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **Notes tab.** For information on entering Specimen Notes in the Notes tab, see “[Notes Input](#)” later in this chapter.
- **Refs tab.** For information on creating links to References in the Refs tab, see Chapter 20, “[References](#).”

Genus, Family, Order, Class, Phylum, and Kingdom Input

Data entry in the higher taxon (Genus, Family, Order, Class, Phylum, and Kingdom) Input screens is virtually identical for all levels. You can enter a new record in one of these screens by selecting the level from the Input menu, by clicking the Add Record (Add Genus, Add Family, etc.) button on the Record Listing screen for that level, or “on the fly” from the Input screen of a child table (for example, you can create a Genus records “on the fly” from the Species Input screen).

Differences Among the Higher Taxon Input Screens

The Input screens for Genus, Family, and Order are identical in layout. The illustration below shows the Genus Input screen as an example.

The Genus Input screen offers input areas for two intermediate taxon fields—Tribe and Subfamily—and for three Custom fields—Genus Custom 1 through 3. Likewise, the Family and Order Input screens also have entry areas for two intermediate taxon levels (Superfamily and Suborder in the Family Input screen; Superorder and Subclass in the

Order Input screen) and three Custom fields (labeled Family Custom 1–3 and Order Custom 1–3).

Genus Input

Genus	Genus Custom 1
<input type="text"/>	<input type="text"/>
Tribe	Genus Custom 2
<input type="text"/>	<input type="text"/>
Subfamily	Genus Custom 3
<input type="text"/>	<input type="text"/>
Family	
<input type="text"/>	
Classification	
Superfamily	
Suborder	
Order	
Show Species	
Show Family	
This Genus record <input type="button" value="Save"/> <input type="button" value="Carry"/> <input type="button" value="Print"/> <input type="button" value="Delete"/> <input type="button" value="Cancel"/>	
Navigate records <input type="button" value="◀◀"/> <input type="button" value="◀"/> <input type="button" value="▶"/> <input type="button" value="▶▶"/>	

The Input screens for Class and Phylum differ from this design by offering only a single intermediate taxon field (Subphylum in the Class Input screen and Subkingdom in the Phylum Input screen) and two Custom fields, instead of three. The Class Input screen is shown below as an example.

Class Input

Class	Class Custom 1
<input type="text"/>	<input type="text"/>
Subphylum	Class Custom 2
<input type="text"/>	<input type="text"/>
Phylum/Division	
<input type="text"/>	
Classification	
Subkingdom	
Kingdom	
Show Orders	
Show Phylum	
This Class record <input type="button" value="Save"/> <input type="button" value="Carry"/> <input type="button" value="Print"/> <input type="button" value="Delete"/> <input type="button" value="Cancel"/>	
Navigate records <input type="button" value="◀◀"/> <input type="button" value="◀"/> <input type="button" value="▶"/> <input type="button" value="▶▶"/>	

The Input screen for the Kingdom table, which has no parent table, is simplified by the lack of the Classification panel at the lower left, but is otherwise like the Class and Phylum Input screens. (The single intermediate taxon level is Superkingdom.)

- **Field lengths.** You can enter up to 40 characters in each field of the higher taxon tables.
- **Entry Choice Lists.** You can enable an Entry Choice List (a pick list or authority list) for the Tribe, Subfamily, and the Custom fields in the Genus table; the Superfamily, Suborder, and Custom fields in the Family table; and the Superorder, Subclass, and Custom fields in the Order table. You enable or disable the lists using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).
- **Aliases.** With the exception of Key fields (e.g., Genus in the Genus table, Family in the Family table) and Linking fields (e.g., Family in the Genus table, Order in the Family table), all fields in the higher taxon tables can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).

A Special Problem for Genera: Legitimate Duplicate Generic Names

The Genus field of each Genus record must contain a unique value within a Biota Data File. There are two cases in which Biota’s use of generic names as the Key field (see “[Key Fields](#)” in Chapter 3) for the Genus table may cause problems.

First, although the rules of nomenclature require unique names for Genera within Kingdoms, the rules do not require unique generic names among Kingdoms, and a number of cases exist in which the same name is legitimately used in two Kingdoms. For example, *Ammophila* and *Dryas* are each valid genera of both plants and animals. The uniqueness problem arises only if you need to use both names in the same Biota Data File. Aside from general cross-Kingdom databases, host-parasite or herbivore-plant databases provide potential examples.

Second, if you create Genus records to record generic junior synonyms, you will need to handle duplicate names in the Genus field.

In these cases, you need to create two (or more) Genus records, with distinct values in the Genus field. For synonyms within a Kingdom, appending the genus author in the Genus field makes sense. For valid genera in different Kingdoms, you can add an asterisk (*) or a pound (number or hash) sign (#) to distinguish the two records (e.g., *Dryas* and *Dryas** or *Dryas#* and *Dryas**). Or, you could add an explanatory suffix: *Dryas-Plant* and *Dryas-Butterfly*.

Note: Biota looks for the characters * and # in Genus names when printing determination labels and deletes the characters from the printed version (see Chapter 15, “[Printing Labels](#)”).

Entering Data in a Higher Taxon Input Screen: Step by Step

1. **Enter the taxon name** (a Genus name, in this example), which may be up to 40 characters in length. Because Genus is the Key field for the Genus table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Genus you enter must not duplicate the Genus of any existing Genus record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3).

NOTE: If you are creating a Genus (or other higher taxon) record “on the fly” while working on a Species (or other lower taxon) record, the Genus name you entered in the Species Input screen is already displayed and the cursor is in the next field (Tribe, in the Genus Input screen).

2. Enter intermediate taxon name or names (Tribe and Subfamily, in the Genus Input screen).

You can enable an Entry Choice List (a pick list or authority list) for each intermediate taxon field in the Genus, Family and Order tables, using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).

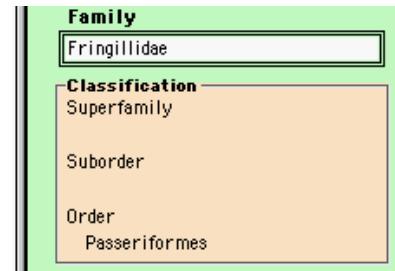
Each intermediate taxon field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).

3. Enter the parent taxon name (the Family name, in the Genus Input screen). You can enter the parent taxon name using either of two methods for entering data in linking fields, as described in the section “[Entering Data in Linking Fields](#)” in Chapter 7.

NOTE: This step does not apply to the Kingdom Input screen, since the Kingdom table has no parent.

- **Method 1: Enter the full parent taxon name manually.**

- ◊ If a parent taxon record exists with the name you entered, the “Classification” panel in the lower left corner or the Input screen displays the higher classification of the parent taxon from the linked taxon record (Superfamily, Suborder, and Order, in the case of the Genus input screen). The cursor moves on to the next entry area. The example here show the Classification panel of the Genus Input screen



NOTE: Be sure to confirm that the correct parent taxon record was found. If your entry uniquely matches the first part of a different parent taxon name, the wrong link will be made. See “[Overriding Wildcard Input for Linking Fields](#)” in Chapter 7.

- ◊ If no parent taxon record exists with the name you entered, Biota offers you the option of creating a new parent taxon record “on the fly” (using the name you entered) or accepting an orphan record. See “[‘On-the-Fly’ Creation of Linked Records](#)” in Chapter 7 for details.
- **Method 2: Enter the first letter or first few letters of a parent taxon name, then press TAB** (wildcard lookup). See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7.

- ◊ If only one parent taxon record matches the entry, Biota automatically completes the entry.
 - ◊ If more than one existing parent taxon record matches the entry, a scrollable list of matching names for existing parent taxon records appears, from which you can choose the correct record by clicking it with the mouse. (If you enter the @ character, and nothing else, all records for the parent table appear in the scrollable list.)
- 4. Enter data for the Custom fields.**
- You can enable an Entry Choice List (a pick list or authority list) for each Custom field in the Genus, Family and Order tables, using the “Entry Choice Lists” tool in the Special menu (see “[Using Entry Choice Lists](#)” in Chapter 17).
- Each Custom field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).
- 5. Save or Carry the record.**

Personnel Input

Through relational links, Biota uses records in the Personnel table to register the names of Specimen collectors, preparators, determiners, and loan borrowers; Biota Project managers and teams; and authors of Specimen, Species, Collection, Locality, and Loan Notes (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). By means of the recursive Group system (see below), you can build multi-level Personnel hierarchies.

But Personnel records need not be linked to other records. You can also use the Personnel table as an address book for colleagues and institutions you contact frequently, if you wish.

The Personnel table holds four kinds of records:

- **Individual Personnel records.** An Individual Personnel record generally registers information for one person, but you can also create an Individual record in the Personnel table to record contact information for an institution, organization, or company.
- **Group Personnel records.** A Group record in the Personnel table links together a set of Individual Personnel records, a set of Group Personnel records (to build a Personnel hierarchy), or a mixture of Individual and Group Personnel records. For example, a collecting team needs a Group record linking the Individual Personnel records of its members, so that all names in the group are linked to the appropriate Collection records (see “[Entering Collection Data: The ‘General’ Tab](#)” earlier in this chapter). Or, you might link all the individual records for your contacts at a museum or herbarium to a Group record for the institution. (You can transform an Individual record for an institution into a Group record at any time, see “[Entering Personnel Data: The ‘Group’ Tab](#),” later in this chapter.)
- **Project-linked Personnel records.** In Biota, a single Data File can accommodate any number of Projects, each of which is defined by a different record in the Project table (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”). Each Project record may be linked (one-to-one) to a single Personnel record that provides contact information for the Project.
- **Project-linked, Group Personnel records.** A Project-linked Personnel record can be a Group record, allowing any number of Individual or ordinary Group Personnel records to be linked to identify a group of people associated with the Project.

You can enter a new Personnel record by selecting Personnel from the Input menu; by clicking the Add Record button on the Personnel Record Listing screen; or “on the fly” from the Project, Specimen, Collection, or Notes Input screens. This section describes how to enter data in the General, Group, and Note tabs of the Personnel Input screen.

The screenshot shows the 'Personnel Input' window with the 'General' tab selected. At the top left is a toolbar with buttons for 'General', 'Create Group', and 'Create Note'. Below the toolbar is a 'Short Name, Group Name or Project Name' input field containing 'J. T. Longino'. To the right of this field are three checkboxes: 'Group Name', 'Project Name', and 'Show Project Record'. To the right of the input field is a 'Record' panel displaying the following information: Number 0 of 0, Created Aug 17, 2002, Last changed, and Changed By. Below the input field are several text entry fields: 'Last Name' (empty), 'First Names' (empty), 'Title' (empty), 'Institution' (empty), 'Address Line 1' (empty), 'Address Line 2' (empty), 'Address Line 3' (empty), 'City' (empty), 'State/Prov/Zip' (empty), and 'Country' (empty). To the right of these fields are 'VoicePhone 1' (empty), 'VoicePhone 2' (empty), 'FaxPhone' (empty), and 'E-mail' (empty). On the far right is a 'This Personnel record' group containing four buttons: 'Save', 'Print', 'Delete', and 'Cancel'. Below this group is a 'Navigate records' group with four navigation icons.

Entering Personnel Data: The “General” Tab

1. Enter a Short Name, Group Name, or Project Name (the Short Name field, collectively). You can enter the Short Name for a Personnel record by typing it in the entry area.

The screenshot shows the 'Personnel Records' window with the 'General' tab selected. At the top left is a toolbar with buttons for 'General', 'Create Group', and 'Edit Note'. Below the toolbar is a 'Short Name, Group Name or Project Name' input field containing 'J. T. Longino'. To the right of this field are three checkboxes: 'Group Name', 'Project Name', and 'Show Project Record'.

The Name may be up to 80 characters in length. Because Short name is the Key field for the Personnel table, it is an obligatory entry, which must be made first. All remaining entry areas are optional. The Short Name you enter must not duplicate the Short Name of any existing Personnel record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3).

NOTE: If you are creating a Personnel record “on the fly” while working on a Species, Specimen, Collection, Locality, Loan, or Project record, the Short Name you entered in the linking field entry area is already displayed.

What should you assign for a Short Name? The Short Name you assign appears in Specimen records in the Prepared By and Determined By fields, in Collection records in the Collected By field, in Project records as the Project Short Name, in Loan records as Borrower, and in Notes records in the Note By field.

On Pin, Slide, Vial, and Herbarium labels, Biota uses the Short Name field for the collector’s name (see Chapter 15, “[Printing Labels](#)”). Although the Short Name may have up to 80 characters, it is best to make it substantially shorter (20-30 characters is a good guideline) if you are entering the name of a collector (or potential collector) and you intend to use Biota to produce specimen labels. Choose a version of the collector’s name that is appropriate for specimen labels—e.g., initials and last name, or first name and last name. You can also use a “Group Name” in the “Collected By” field—e.g., A. B. Smith & C. D. Jones (for help with Group Names, see “[Entering Personnel Data: The ‘Group’ Tab](#)” later in this chapter).

2. **If the record is to be a Group Personnel record**, check the Group checkbox in the Short Name entry panel, then follow the instructions in the next section of this chapter, “[Entering Personnel Data: The ‘Group’ Tab](#).”

The screenshot shows a software interface for entering personnel names. At the top, there's a label "Short Name, Group Name or Project Name". Below it is a text input field containing the text "Longino & Fisher". To the right of the input field is a small "X" icon. Below the input field are two checkboxes: "Group Name" (which is checked) and "Project Name" (which is unchecked). To the right of these checkboxes is a button labeled "Show Project Record". A cursor arrow is pointing towards the "Show Project Record" button.

NOTE: You create a Project-linked Personnel record “on the fly” during creation of Project record. When you open a Project-linked Personnel record in the Project Input screen, the “Project Name” box is automatically checked and the “Show Project Record” button is enabled. If you click this button, the linked Project record is displayed in the Project Input screen in a separate window.

This screenshot shows the same input panel as the previous one, but with different data. The text input field now contains "Luteyn Mites". The "Group Name" checkbox is unchecked, and the "Project Name" checkbox is checked. The "Show Project Record" button is visible and has a cursor arrow pointing towards it.

To ensure proper linking values, you cannot create a Project-linked Personnel record directly in the Personnel input screen. See Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”

3. **Complete the rest of the Personnel record.** None of the remaining fields is mandatory. For a Group record, you may wish to leave them all blank.
4. **Accept or Carry the Personnel record.** The “Carry” button is particularly useful for entering a series of records for people who share an address. See “[Duplicating a](#)

[Record Displayed in the Input Screen Using the ‘Carry’ Button](#) in Chapter 10 for information on how the “Carry” button works.

Entering Personnel Data: The “Group” Tab

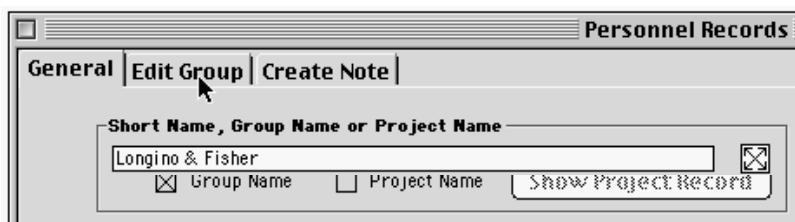
A Group record in the Personnel table links together a set of Individual Personnel records, a set of Group Personnel records (to build a Personnel hierarchy), or a mixture of Individual and Group Personnel records. (see the introduction to [Personnel Input](#), earlier in this chapter). Once you have created a Group record, you use the tools in the Group tab to establish the membership of the Group.

1. **Create a Personnel record.** See the previous section, “[Entering Personnel Data: The ‘General’ Tab](#).”

What should you assign for a Group Short Name? If you use a Group record to link members of an institution, project team, or other organization, choose a Short Name for the Group that best identifies the organization. If you use a Group record to identify a group of individuals who were jointly responsible for collecting, preparing, or determining certain specimens or for writing a Note, form the Short Name just as you want it to appear on collection labels; in the Collected By field of Collection records; in the Prepared By and Determined By fields of Specimen records; or in the Note By field of Notes records. On herbarium labels, a Group Record is used to create a list of collectors from the linked Individual records (see “[Herbarium Specimen Labels](#)” in Chapter 15).

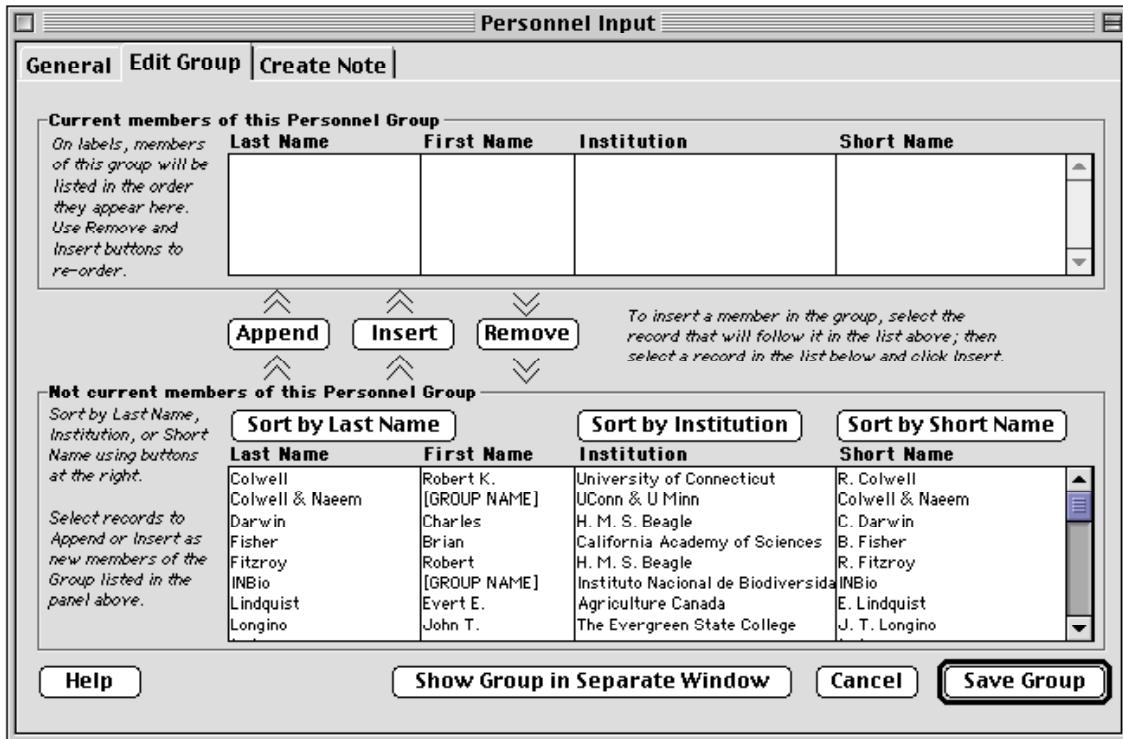
2. **Click the Group Name checkbox** to declare this a Group record.

When you check the Group name box, the Group tab label changes from “Create Group” to “Edit Group.” If you click the Group tab without first checking the Group checkbox, Biota asks if you want to create a group, then checks the box for you if you reply affirmatively.



3. **Click the “Edit Group” tab.** A query window appears.





4. Click the “OK” button in the query window to proceed. The Group Editor appears.

The Group Editor screen has two scrollable panels. For a new Group record, the lower panel (labeled “Not current members of this Personnel Group”) initially displays all Personnel records, including other Group Personnel records and Project-Linked Personnel records.

You can sort the records in the lower panel by Last Name, Institution or Short Name using the buttons just above it.

The upper panel (labeled “Current members of this Personnel Group”), initially blank in a new Group record, shows the members of the new Group once you form it.

5. Use the “Append,” “Insert,” and “Remove” buttons in the Group Editor window to establish and order the members of the Group in the upper panel.

- **“Append” button.** To enter the first Individual record or to add an Individual to the end of the “Current members” list in the upper panel, click the record you want in the lower panel to select it, then click the “Append” button. Notice that the record is “moved” to the upper panel—it is no longer listed in the lower panel.

Personnel																													
Up Create Note																													
of this Personnel Group																													
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Sort by Last Name <table border="1"> <thead> <tr> <th>Last Name</th> <th>First Name</th> <th>In</th> </tr> </thead> <tbody> <tr><td>Colwell</td><td>Robert K.</td><td>Uni</td></tr> <tr><td>Colwell & Naeem</td><td></td><td>UCc</td></tr> <tr><td>Darwin</td><td>Charles</td><td>H. I</td></tr> <tr><td>Fisher</td><td>Brian</td><td>Cal</td></tr> <tr><td>Fitzroy</td><td>Robert</td><td>H. I</td></tr> <tr><td>INBio</td><td></td><td>Inst</td></tr> <tr><td>Lindquist</td><td>Evert E.</td><td>Agr</td></tr> <tr><td>Longino</td><td>John T.</td><td>The</td></tr> </tbody> </table>			Last Name	First Name	In	Colwell	Robert K.	Uni	Colwell & Naeem		UCc	Darwin	Charles	H. I	Fisher	Brian	Cal	Fitzroy	Robert	H. I	INBio		Inst	Lindquist	Evert E.	Agr	Longino	John T.	The
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INBio		Ins																											
Lindquist	Evert E.	Ag																											
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- **“Insert” button.** To place an Individual record between two records already listed in the upper panel, click the record in the upper panel that you want to follow the record to be inserted. Click the record in the lower panel that you want to insert, then click the “Insert” button.
- **“Remove” button.** To remove an Individual record from the Group list in the upper panel, click the record in the upper panel to highlight it, then click the “Remove” button. Notice that the record now appears in the lower panel.

6. Click the “Save Group” button in the Group

Editor tab to record the Group’s composition and the order of its members. The General tab reappears with the Group record displayed. Notice that both the Group tab continues to read “Edit Group.” You can change the Group composition in the future using this tab.



7. Complete additional fields (or none) in the Personnel record for this Group. For an organizational Group record, you might record the address and contact information for the organization. For a Group record that links specimen collectors, preparators, or determiners, you would probably leave the rest of the record blank or possibly make an entry in the Notes tab with details of the collaboration.

8. Save the Group Personnel record.

Entering Personnel Data: The “Notes” Tab

Each Personnel record can include a single Personnel Note, up to 32,000 characters in length.

- To create a Personnel Note, click the Note tab (which reads “Create Note” when none is yet present), enter the Note text, and click the “Save” button for the record to save it.
- To edit an existing Personnel Note, click the Note tab (which reads “Edit Note” when note text is already in the record), edit the Note text, and click the “Save” button for the record to save it.

Displaying, Changing, or Reordering Group Membership for an Existing Group Personnel Record

1. Display the Group Personnel record in the Personnel Input screen.
2. Click the Group tab, which reads “Edit Group” for a Group Record.
 - To display the members of the Group, click the “Show Group in Separate Window” button at the bottom of the Group tab.



The records are displayed in a new window in the Personnel Record Listing screen. Any number of Groups can be displayed simultaneously, each in its own window. The original Personnel Record Listing screen from which you launched the Group Record Listing screen(s) remains open also.

- To change or reorder Group membership, use the “Append,” “Insert,” and “Remove” buttons in the Group Editor. When you are done, click the “Save Group” button in the Group Editor window to record the changes and return to the General tab.
2. Save the Group Personnel record, if you made any changes.

Notes Input

You can attach an unlimited number of Notes to each record in the Species, Specimen, Collection, Locality, and Loans tables.

For each of these tables, a special Notes table (linked as a child table to the Species, Specimen, Collection, Locality, or Loans table) accommodates these Notes records (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

This structure means you can import and export Notes records in the same way you would any other records, using the Import (see Chapter 28, “[Importing Data](#)”) and Export Editors (see Chapter 27, “[Exporting Data](#)”). In addition, the special Export Notes tool exports certain fields from each parent record, along with full records for each Note (see “[Exporting Notes](#)” in Chapter 27).

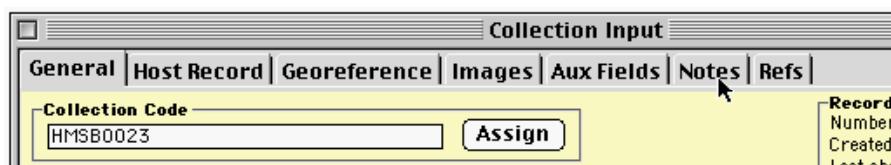
When you create a new record in the Species, Specimen, Collection, Locality, or Loans table, it has no Notes. When you delete a record from one of these five tables (or click the “Cancel” button for a new record not yet saved), any associated Notes you have created for it are deleted automatically (after Biota’s warning and your confirmation), since they would otherwise be “orphaned.”

The Personnel and Project tables accommodate notes in a simpler way. Each Personnel or Project record has a Notes *field*. This means you can enter or update just one note for each Personnel or Project record. The note can be up to 32,000 characters long. See “[Entering Personnel Data: The ‘Notes’ Tab](#)” earlier in this chapter, and “[Entering Project Data: The ‘General’ Tab](#)” in Chapter 16.

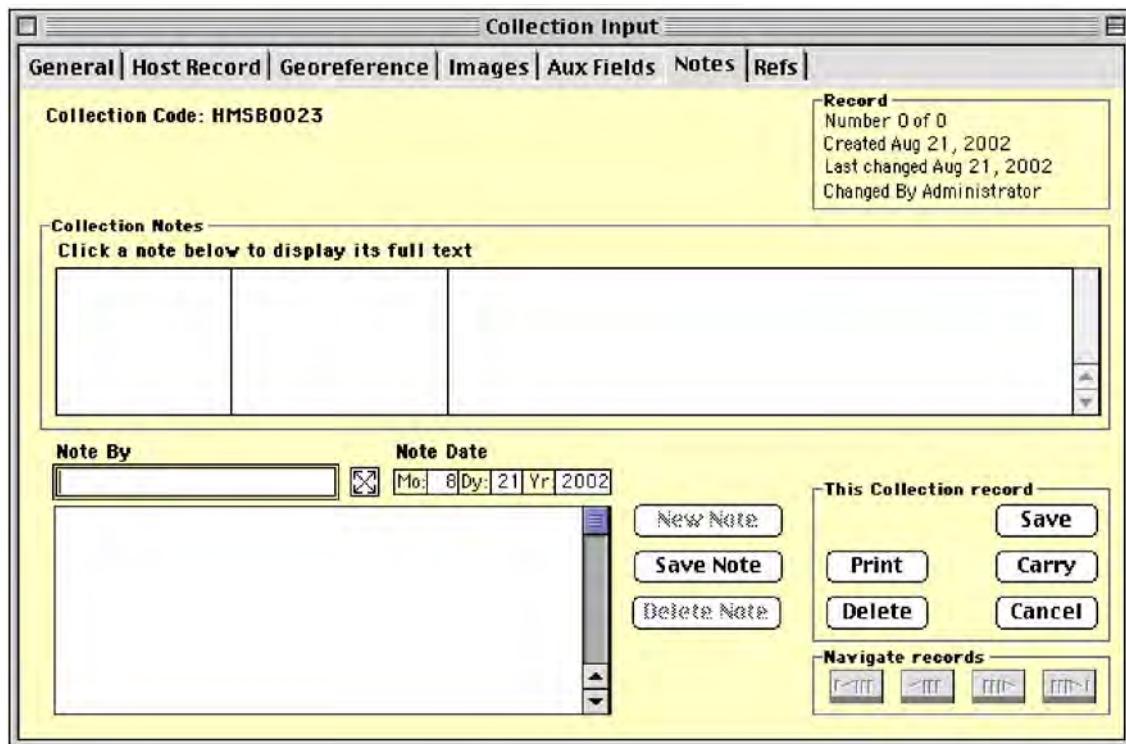
Entering a New Note in the Note Tab (Species, Specimen, Collection, Locality, and Loans)

This section uses Collection Notes screens as an example, but all procedures are identical and all screens analogous for Locality, Specimen, Species, and Loans Notes.

1. Click the Notes tab in the Collection, Locality, Specimen, Species, or Loan Input Screen. (You must first enter a valid Record Code.)



The Notes tab appears, with the insertion point (blinking cursor) in the Note By entry area and today's date (the date set in your computer's internal clock) appearing in the Note Date entry area. The “Save Note” button is enabled.

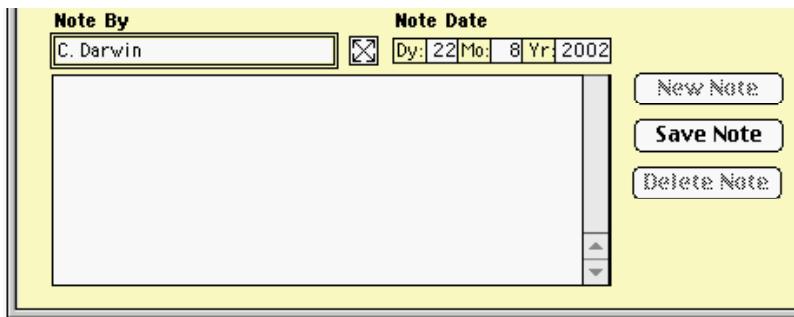


The Notes tab is used not only for creating new Notes and for displaying and editing existing individual Notes, but also for listing Notes, in the same way a Record

Listing screen lists records for Core tables. See “[Viewing, Editing, or Deleting a Note](#)” later in this chapter.

2. Enter the Note author's Short Name in the “Note By” entry area.

Because this field is linked to the Short Name field of the Personnel table, the entry area has a double border.



For step-by-step help entering a Short Name, refer to the instructions for the “Last Determined By” field of the Specimen Input screen’s Determination tab (see [Step 1 of “Entering Specimen Data: The ‘Determination’ Tab”](#) earlier in this chapter).

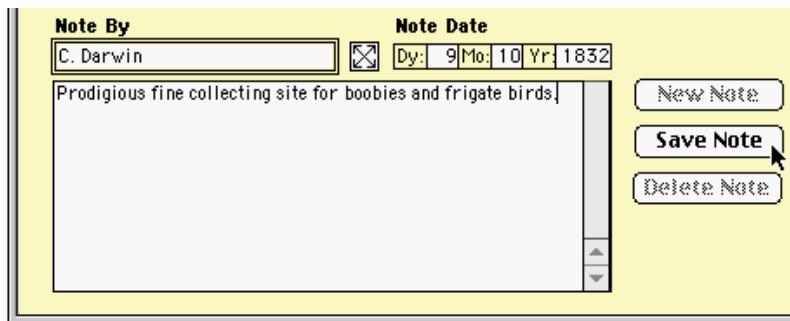
The Note By field is optional. Just “TAB through” the field if you do not want to use it.

3. Enter the Note Date. This field is obligatory, since Notes are sorted by Note Date.

- **To accept today's date,** just “TAB through” the date entry area, or click in the Note Text area below.
- **To enter a different date,** enter a full date. See “[Dates](#)” in Chapter 9 for details on entering dates, date formats (International vs. U.S), full vs. partial dates, and how Biota handles dates in the Data File.

4. Enter the Note Text in the lower-right panel of the Notes screen. (Not required.)

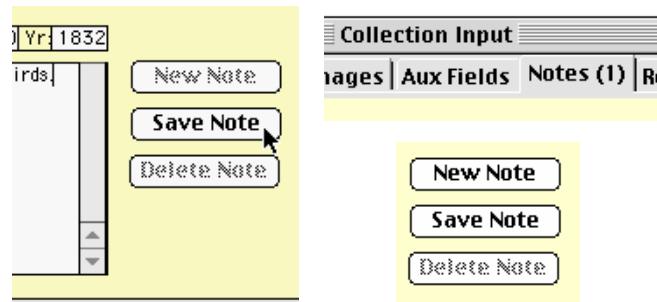
If the length of the Note Text exceeds the size of the display panel, use the scroll bar or the UP and DOWN arrow keys to scroll in the panel.



You can use line breaks (ENTER key in Windows, RETURN key in Mac OS) within the Note Text field to organize the entry.

NOTE: When exporting Notes using the Export Editor (see “[Exporting Notes](#)” in Chapter 27), if you indicate carriage return (Mac OS) or carriage return plus line feed (Windows) as the End of Record delimiter (see “[Exporting by Tables and Fields: Step by Step](#)” in Chapter 27), line breaks *within* Note Text fields are replaced by blanks to keep the Export Editor from interpreting them as End of Record characters. To preserve internal line breaks in exported Notes records, specify a different End of Record delimiter (one not used in Note Text fields), then change this character globally to line breaks with a text editor in the exported records. (The Export Editor automatically replaces your specified End of Record delimiter with blanks *within* text and alphanumeric fields, regardless of which delimiter you specify.)

5. Click the “Save Note” button in the Notes tab. The Note tab label now shows the number of Notes for this Species, Specimen, Collection, or Locality record and the “New Note” button is enabled.
6. To enter another Note, click the “New Note” button in the Notes tab and repeat Steps 2–4, above.



NOTE: If you forget to click the “Save Note” button before going to a different tab, moving to another record using the navigation buttons, Saving the record, or Carrying the record, Biota asks if you would like to save the Note and does so, if you reply affirmatively.

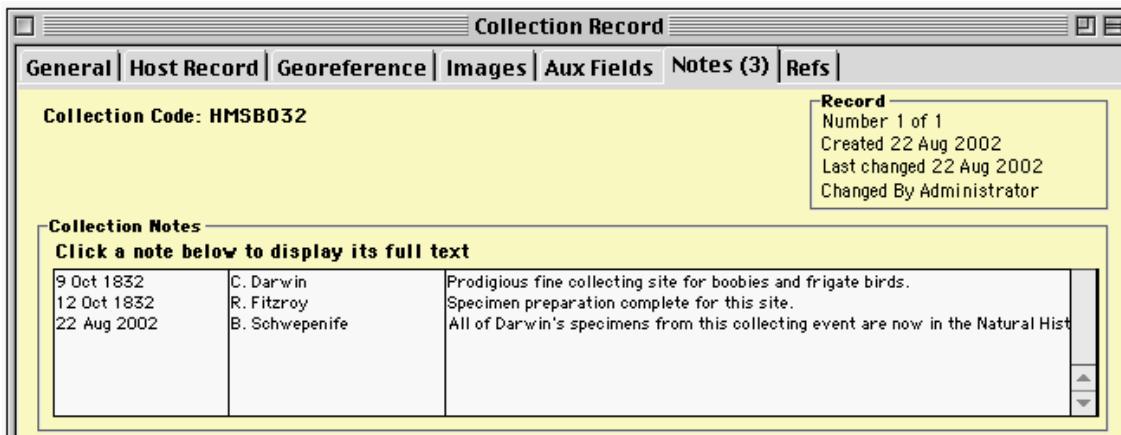
Viewing, Editing, or Deleting a Note

This section uses Collection Notes screens as an example, but all procedures are identical and all screens analogous for Locality, Specimen, Species, and Loans Notes.

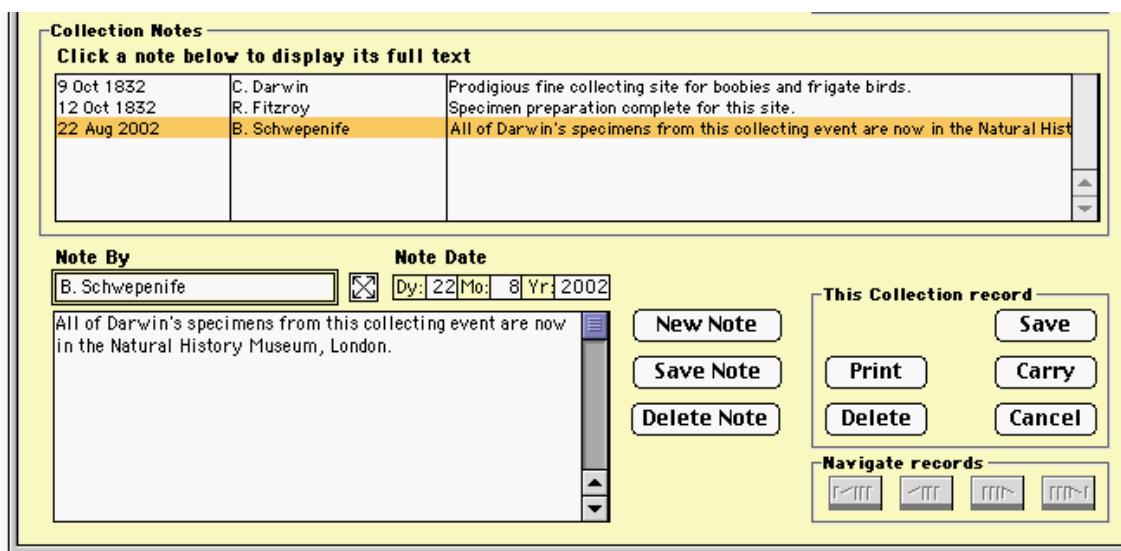
1. Open an existing Collection, Locality, Specimen, Species, or Loans record. The Notes tab shows the number of Notes already created for this record.



- Click the Notes tab. The existing Notes for this record are displayed in the upper panel (the “Collection Notes” panel in the example below), sorted by Note Date.



- To display an individual Note in full, click it in the Note listing panel. The Note By, Note Date, and Note Text fields of the note you clicked appear in the Note display (lower) panel. The “New Note,” “Save Note,” and “Delete Note” buttons are enabled.



If the length of the Note Text exceeds the size of the display panel, use the scroll bar or the UP and DOWN arrow keys to scroll in the panel.

- To edit a Note, select it, make changes, then click the “Save Note” button in the Notes tab.
- To delete a Note, select it, then click the “Delete Note” button in the Notes tab.
- To enter a new Note, click the “New Note” button in the Notes tab, then proceed as in the previous section of this chapter (“[Entering a New Note in the Note Tab \(Species, Specimen, Collection, Locality, and Loans\)](#)”).

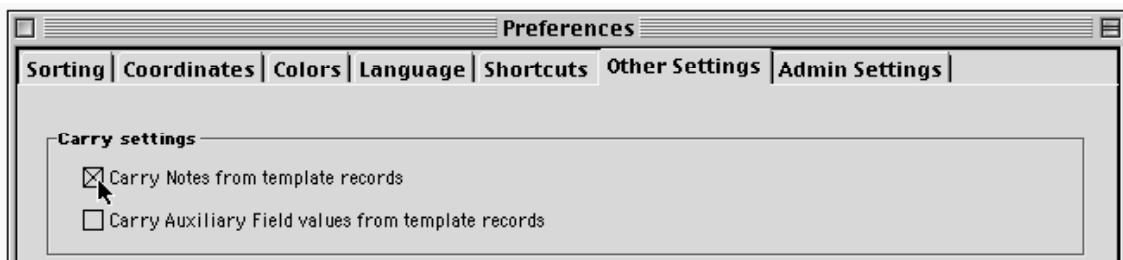
Carrying Notes

The “Carry” button in Biota Input screens allows you to use an existing record (or a record you have just entered) as a template for a new record (see “[Duplicating a Record Displayed in the Input Screen Using the ‘Carry’ Button](#)” in Chapter 10). As an option, you can choose to Carry (copy) all Notes from the existing record to the new record (for the tables that support Notes).

For example, a series of Collection records might share the same note describing meteorological conditions or special equipment used at the time the collections were made.

To enable or disable this option:

1. Choose Preferences from the Special menu. The Preferences screen appears.
2. Click the “Other Settings” tab.
3. Click the “Carry Notes from the template records” checkbox to enable (check) or disable (uncheck) the Carry Notes option. The default setting is disabled (unchecked).



4. Click the “Save” button in the Preferences screen.

PART

3

Finding and Revising Data

Chapter 12 **Finding and Updating Records**

This chapter explains how to use tools from the Find menu and the Special menu to find records already in a Biota Data File—and update them if you wish. Before using these tools, you need to understand the ideas introduced in Chapter 3, “[Key Concepts](#),” especially the distinction between Selections and Record Sets, and the basic procedures outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

Biota offers several different kinds of tools for finding records, ranging from the general to the specialized. This chapter follows the same organization, first presenting the more general tools, then the more specialized ones. Like tools from the hardware store, a specialized software tool applied to the task for which it was designed is almost invariably more efficient and effective than a general-purpose tool applied to the same task, even though the latter might work. Investing a few minutes learning how to use the tools described in this chapter may save you much time in the long run.

Finding and Displaying All Records for a Table

You can find and display all existing records for any of Biota’s Core tables (see “[Core Tables](#)” in Chapter 3) using the “All...” commands from the Find menu.

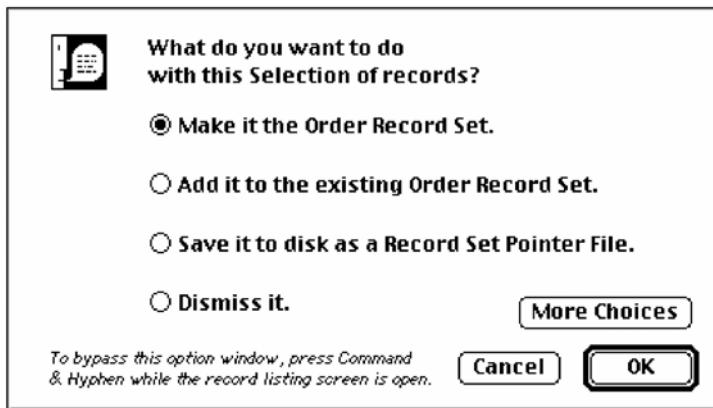
For example, for Specimen records, choose “All Specimens” from the Find menu. For Locality records, choose “All Localities” from the Find menu, and so on for each Core table.

- **If there are no records in the table,** Biota displays a message like the one below for the Kingdom table.



- If there are records in the table, Biota displays them in the standard Record Listing screen for the table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen for the table (for the Order table, in the illustration below). See “[The Record Set Options Screen](#)” in Chapter 3 for an explanation of the options offered.



If you choose to create or modify the active Record Set for a table, you can display the records in the new or changed Record Set using the command from the Display menu for that table.

NOTE: Three special “Find All...” commands have special locations.

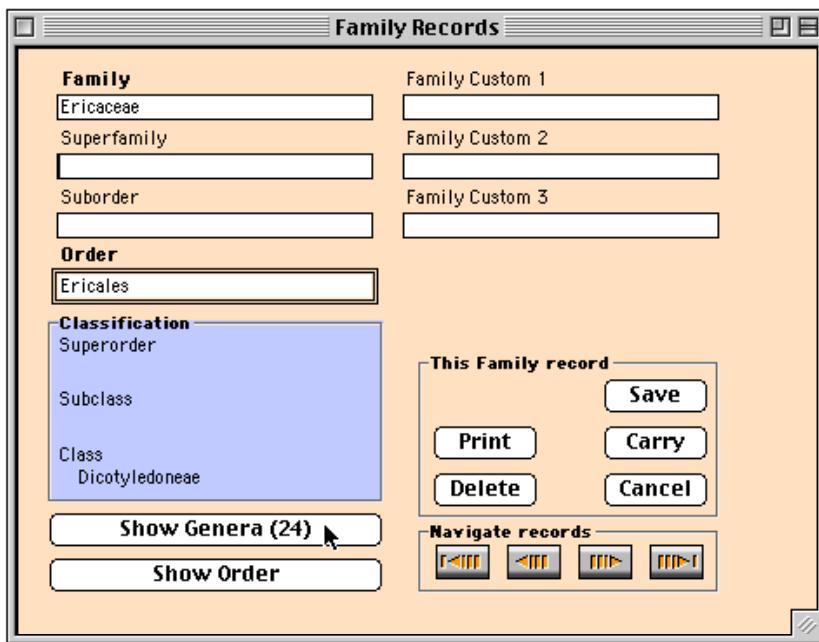
- a. The “All Loans” command is in the Loans menu. See “[Displaying and Editing an Existing Loan](#)” in Chapter 21.
 - b. The “All Determination Histories” command is in the Special menu. See “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22.
 - c. The “All Valid Species” command, in the Find menu, has a special function. See Chapter 23, “[Synonymy System](#).”
-

Finding Records Using the Taxonomic Hierarchy

A natural way to find records for taxa (or for Specimen records) in Biota is to use your knowledge of the higher classification of the taxonomic (or Specimen) records you seek. The Child Record button on the Input screen for each taxonomic rank allows you to display all records for the next lower taxon in the Linnean hierarchy. In the Species Input screen, the Child Record button displays all Specimen records linked to the Species record displayed. (See “[Moving Down the Table Hierarchies From an Input Screen: Child Records Buttons](#)” in Chapter 10.)

For example, suppose you want to find all records for genera of the plant family Ericaceae. Here is how you might do it:

1. From the Find menu, select “All Families.”
2. Find “Ericaceae” (scroll down if necessary) and open the record in the Family Input screen. The Child Record button for the Family table is labeled “Show Genera” and shows that there are 24 Genus records in the Data File for the plant family Ericaceae.



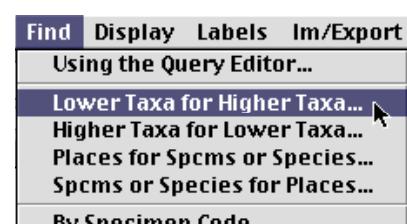
3. Click the “Show Genera” (Child Record) button. Biota displays the 24 records in the Genus Record Listing screen.

You can continue down the hierarchy by opening a Genus record then clicking the “Show Species” button to display the linked Species records in the Species Record Listing screen. You could then repeat the procedure to show the Specimen records linked to a particular Species record.

However, if your search requires finding broader sets of records linked across more than a single level of the taxonomic hierarchy (such as finding *all* the Specimen records for a *Family*), you need to use the “Lower Taxa for Higher Taxa” tool from the Find menu. See [“Finding Records for Lower Taxa Based on Higher Taxa”](#) in the next section of this chapter.

Special Tools for Finding Records in One Table Based on a Set of Records in Another Table

Biota offers four special tools, with a common interface, for the frequent task of finding related records up, down, and across the taxonomic and place hierarchies. As an option, Biota will keep the linking records for all intermediate tables as Record Sets for those tables. These tools support rapid and intuitive query construction and optimized, extremely fast search and display. They can be used sequentially for complex searches. For most users, they are among the most frequently used features of Biota.

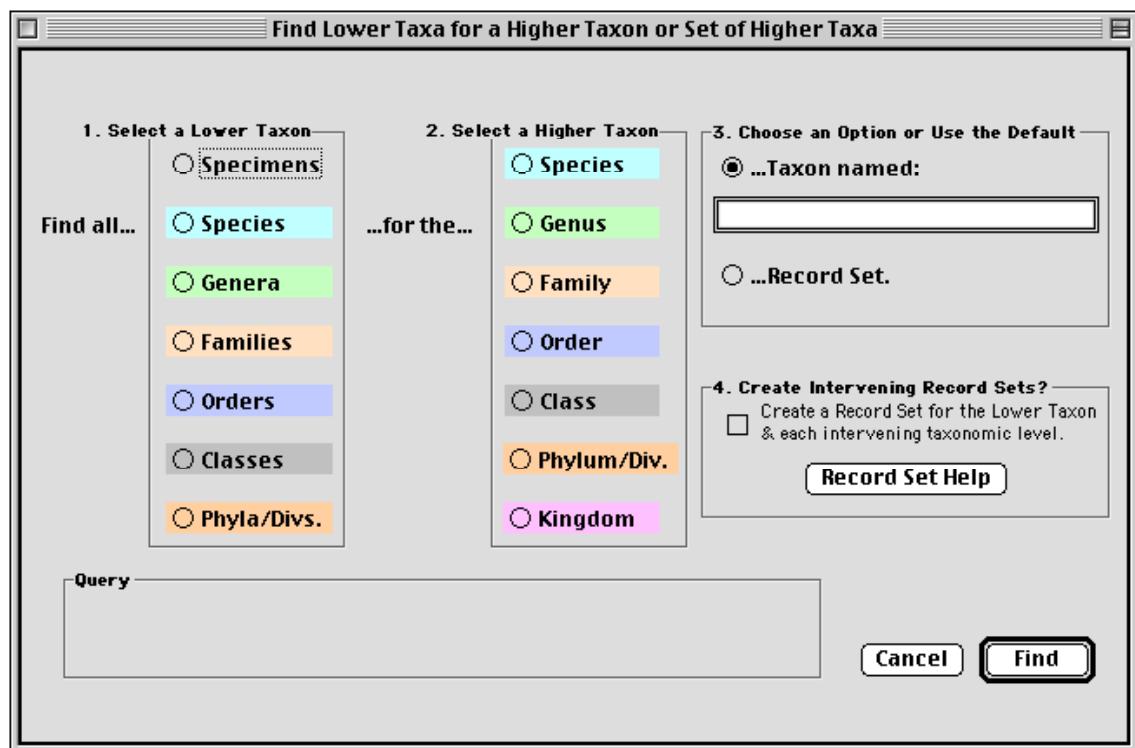


Finding Records for Lower Taxa Based on Higher Taxa

The “Lower Taxa for Higher Taxa” (“top-down”) taxon search tool finds all records for a lower taxonomic rank (the *target table*) that belong to a higher taxon, or a selection of higher taxa at a higher taxonomic rank (the *criterion table*). It does not matter whether the two levels are adjacent in the taxonomic hierarchy or not—for example, you could find all Specimens of a Family, or all Genera of three Orders (nonadjacent levels), or all Specimens for a selection of Species, or all Classes for a Phylum (adjacent levels). For nonadjacent levels, you can tell Biota to keep all related taxa at intermediate levels as Record Sets.

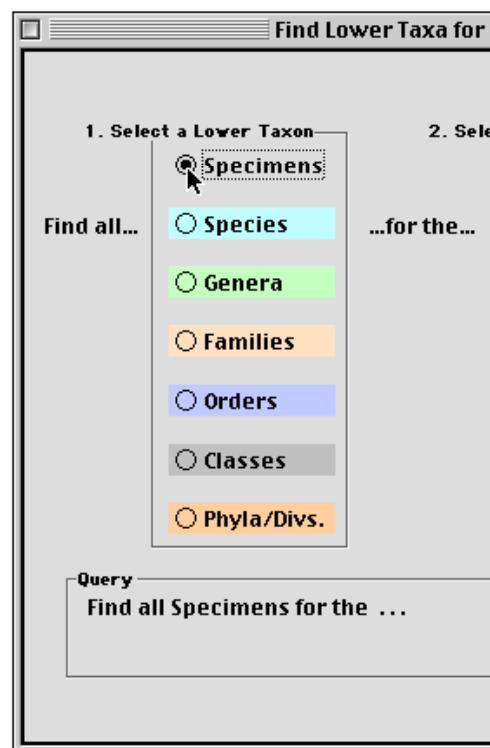
This tool does exactly the opposite task from the “Higher Taxa for Lower Taxa” (“bottom-up”) taxon search tool described in the next section (see “[Finding Records for Higher Taxa Based on Lower Taxa](#)” later in this chapter).

1. From the Find menu, choose “Lower Taxa for Higher Taxa.” The query setup screen appears.



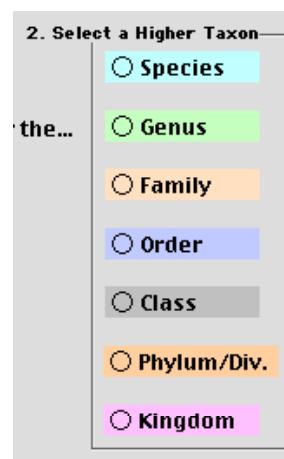
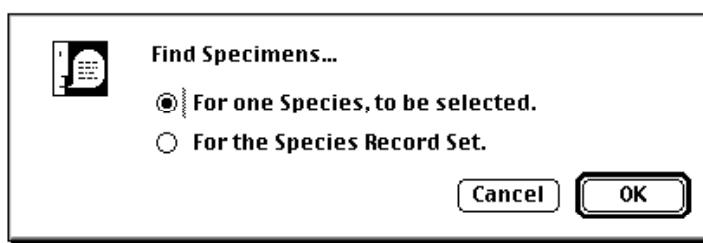
2. From the list of tables in the left panel (the panel labeled “1. Select a Lower Taxon”), click the button for the target table—the table containing the records you seek. In the illustration here, the Specimen table is being selected.

The query panel at the bottom of the screen displays the beginning of the query.



3. From the list of tables in the right panel (the panel labeled “2. Select a Higher Taxon”), click the button for the table to be used in the selection criterion (the criterion table).

- If you choose Species and the Species Record Set is not empty, the option window below appears.



- ◊ If you choose the first (default) option in this window (“For one Species, to be selected”), Biota presents the “Look Up Species” tool so you can look up a Species record according to its Genus. (See the next pair of illustrations.)
 - ◊ If you choose the second option (“For the Species Record Set”), Biota automatically sets the Species Record Set option (see Step 4, below). The Species Record Set may contain many records or only one.
- If you choose Species and the Species Record Set is empty, the “Look Up Species” tool appears. Enter a Genus name or the first few letters of a Genus name in the “Enter Genus, select Species” entry area, then press TAB (wildcard entry method) to display the Species records for that Genus. Click the Species you are looking for to complete the search query.

Here is a completed search query, using the illustration above.

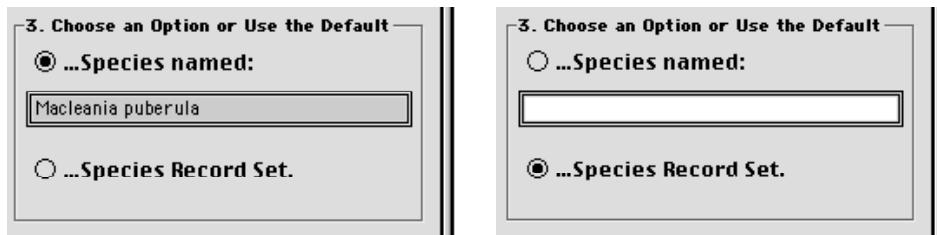
Query	Find all Specimens for the Species Macleania puberula .	Cancel	Find
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- If you choose a criterion table other than Species, the option panel (labeled “3. Choose an Option or Use the Default”) will be set up for the next step. In the example below, the user is asking Biota to find all Specimens for a Family.

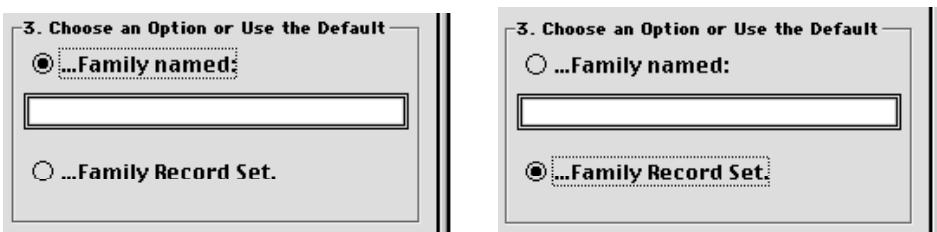
4. Specify whether Biota should use a single record or the current Record Set from the criterion table in constructing the search query. You make this choice in the option panel at the upper right, labeled “3. Choose an Option or Use the Default.”

Find Lower Taxa for a Higher Taxon or Set of Higher Taxa		
<p>1. Select a Lower Taxon</p> <p><input checked="" type="radio"/> Specimens</p> <p><input type="radio"/> Species</p> <p><input type="radio"/> Genera</p> <p><input type="radio"/> Families</p>		
<p>2. Select a Higher Taxon</p> <p><input type="radio"/> Species</p> <p><input type="radio"/> Genus</p> <p><input checked="" type="radio"/> Family</p> <p><input type="radio"/> Order</p>		
<p>3. Choose an Option or Use the Default</p> <p><input checked="" type="radio"/> ...Family named:</p> <p><input type="checkbox"/></p> <p><input type="radio"/> ...Family Record Set.</p>		

- If you choose Species as the criterion table, the option you chose in Step 3 will already be set (one of the two options below).



- If you choose a table other than Species as the criterion table, select the individual record option (below, left) or the Record Set option (below, right). If you choose the Record Set option, the Record Set for the criterion table may contain many records or only one. The Family table was selected as the criterion table in the illustrations below.



- ◊ If you choose the individual record option (above, left), you can use the wildcard entry method to enter the name of the criterion taxon. (Enter the first letter or first few letters of the taxon name and press TAB. See "[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)" in Chapter 7.)
- ◊ If you choose the Record Set option and there are no records in the current Record Set for the criterion table, Biota will post a message like the one below. If you like, you can leave the Lower Taxon for Higher Taxa screen open while you create the appropriate Record Set in another window.



The completed query appears in the search query panel.

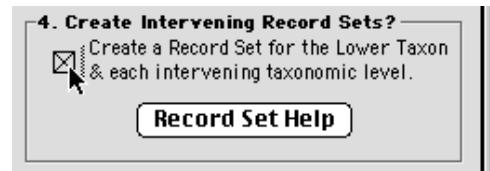


5. **To create Record Sets automatically for the target records and for the linking records in any intervening tables**, click the checkbox.

You make this choice in the option panel at the lower right, labeled “4. Create Intervening Record Sets?”

For example, if you set up the query “Find all Specimens for the Order Hymenoptera” and check this option,

Record Sets for the Family, Genus, and Species tables are automatically created. These Record Sets are composed of the records that link the “Hymenoptera” record (in the Order table) with the Specimen records that Biota finds, based on the query. If the box is checked, a Record Set is also automatically created for the Specimen records found.



It is not necessary to check this option in order to find the target table (Lower Taxon) records you are searching for, nor to create a Record Set for them. If you want to create a Record Set for the target records without checking this option, you may do so by means of the standard Record Set option screen (see “[The Record Set Options Screen](#)” in Chapter 3) when leaving the Record Listing screen for the target table (see Step 6, below).

WARNING: Creating Record Sets for intervening tables during the search replaces any existing current Record Sets for those tables.

6. **To launch the search, click the “Find” button or press the ENTER key (Windows) or RETURN key (Mac OS).**

- **If target table records matching the search query are found**, they are displayed in the standard Record Listing screen for the target table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).“ When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen (see “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered).
- **If no target table records match the search query**, Biota displays the message screen at the right. If you click the “Try Again” button, the search setup screen reappears, with settings as you left them.

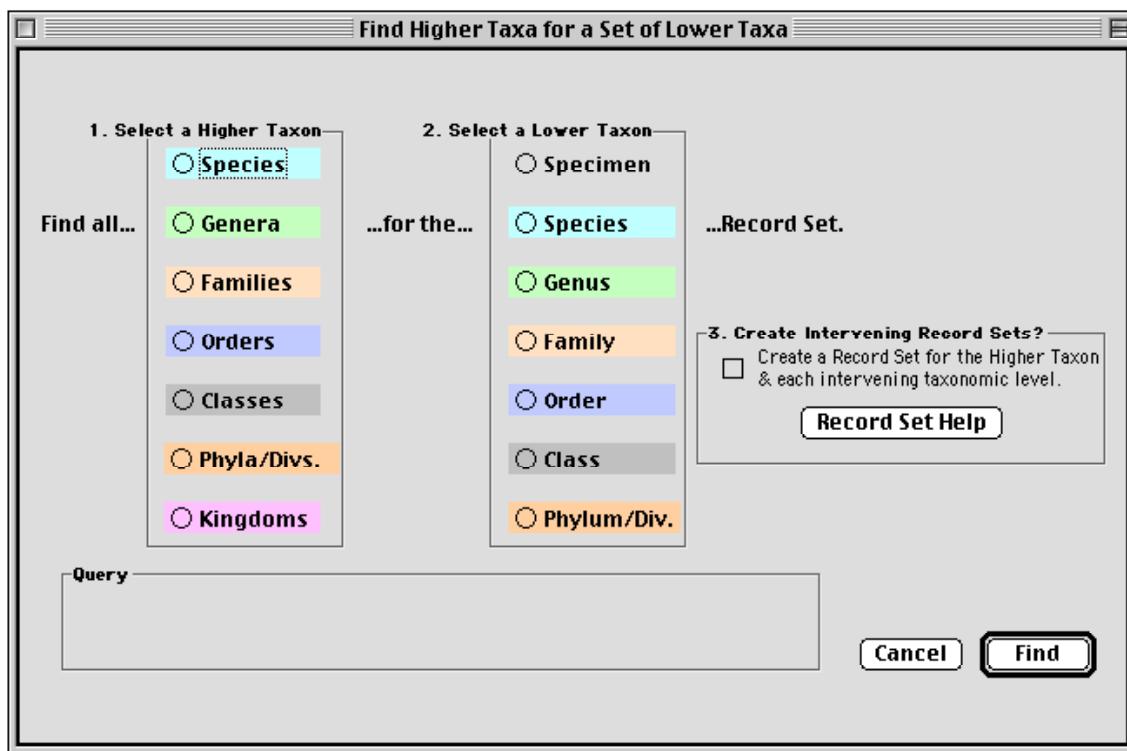


Finding Records for Higher Taxa Based on Lower Taxa

The “Higher Taxa for Lower Taxa” (“bottom-up”) search tool finds all records for a higher taxonomic level (the target table) that belong to the active Record Set for a lower taxonomic level (the criterion table). For example, you could find all Orders for the Specimen Record Set (nonadjacent levels) or all Families for the Genus Record Set (adjacent levels). For nonadjacent levels, you can tell Biota to keep all related taxa at intermediate levels as Record Sets.

This tool does exactly the opposite task from the Lower Taxa for Higher Taxa (“top-down”) search tool described in the previous section (see “[Finding Records for Lower Taxa Based on Higher Taxa](#)” above). In addition to working in the reverse direction along the same set of linked tables, this tool also differs in *requiring* you to designate a Record Set for the criterion table before setting up the search—an optional method in the “Higher Taxa for Lower Taxa” tool. The Record Set for the criterion table may contain many records or only one.

1. From the Find menu, choose “Higher Taxa for Lower Taxa.” The query setup screen below appears.

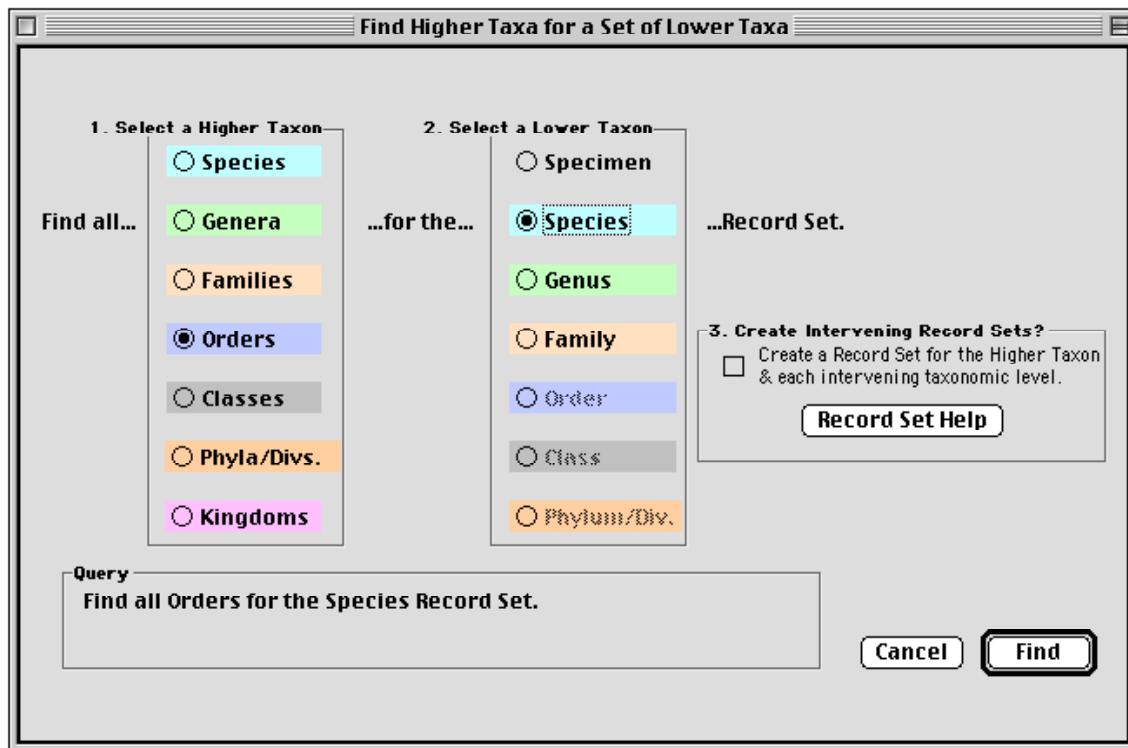


2. From the list of tables in the left panel (the panel labeled “1. Select a Higher Taxon”), click the button for the target table—the table containing the records you seek. In the illustration on the next page, the Order table has been selected.

The query panel displays the beginning of the query.

Query
Find all Orders for the ...

3. From the list of tables in the right panel (the panel labeled “2. Select a Lower Taxon”), click the button for the table to be used in the selection criterion (the criterion table). In the illustration below, the Species table is being selected. The Record Set for the criterion table may contain many records or only one.



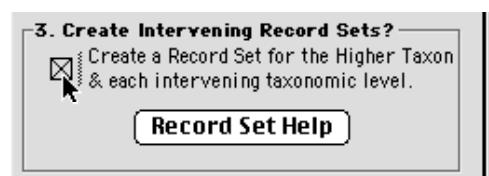
The query panel displays the completed query.

4. If there are no records in the current Record Set for the criterion table, Biota posts a message. If you like, you can leave the Higher Taxon for Lower Taxa screen open while you create the appropriate Record Set in another window.
5. To create Record Sets automatically for the target records and for the linking records in any intervening tables, click the checkbox.

You make this choice in the option panel at the right, labeled “3. Create Intervening Record Sets?”

For example, if you set up the query “Find all Orders for the Species Record Set” and check this option, Record Sets for the Genus and Family tables are automatically created. These Record Sets are composed of the records that link the Species records (the criterion Record Set) with the Order records that Biota finds, based on the query. If the box is checked, a Record Set is also automatically created for the Order records found.

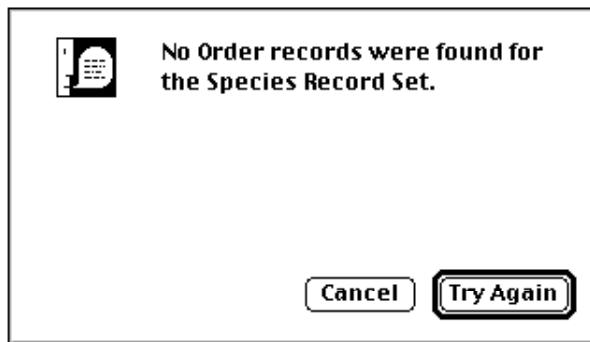
It is not necessary to check this option in order to find the target table (Higher Taxon) records you are searching for, nor to create a Record Set for them. If you want to create a Record Set for the target records without checking this option, you may do so by means of the standard Record Set option screen (see “[The Record](#)



[Set Options Screen](#)” in Chapter 3) when leaving the Record Listing screen for the target table (see Step 6, below).

WARNING: Creating Record Sets for intervening tables during the search replaces any existing current Record Sets for those tables.

6. To launch the search, click the “Find” button or press the ENTER key (Windows) or RETURN key (Mac OS).
 - If target table records matching the search query are found, they are displayed in the standard Record Listing screen for the target table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).” When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen (see “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered).
 - If no target table records match the search query, Biota displays the message screen below. If you click the “Try Again” button, the search setup screen reappears, with settings as you left them.

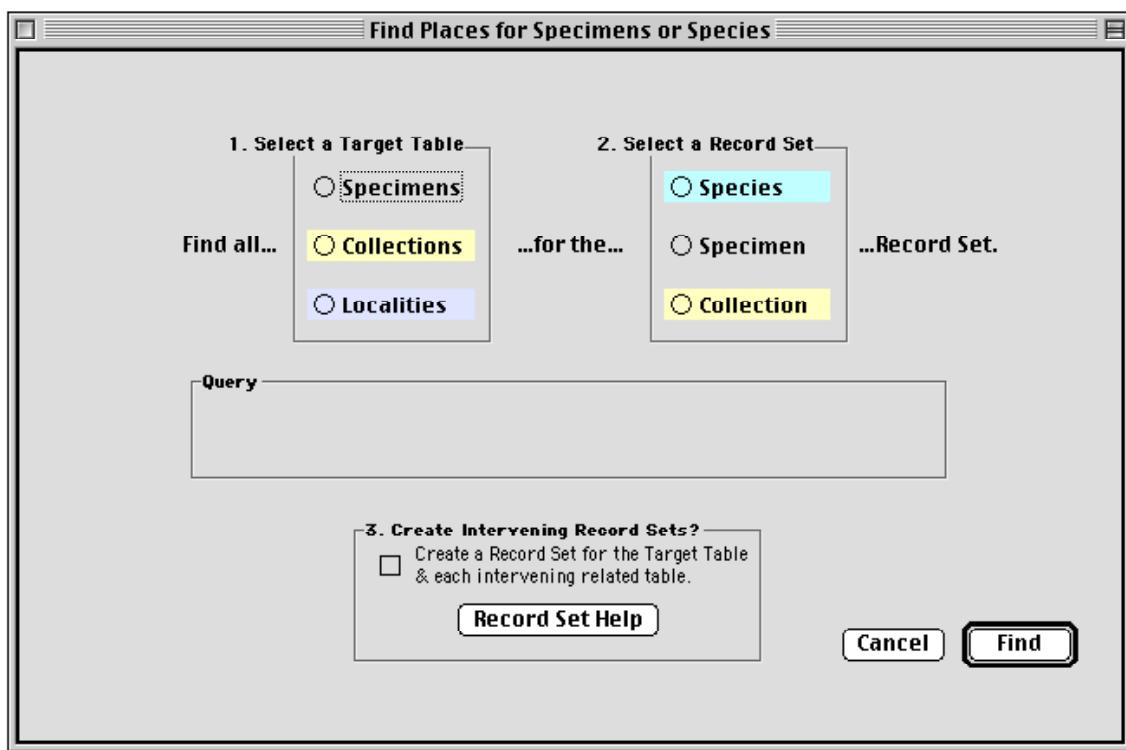


Finding Place Records (Collection or Locality) for Specimens or Species

The “Places for Specimens or Species” search tool finds all Locality or Collection records for the active Specimen or Species Record Set, or all Locality records for the Collection Record Set, according to your query. For example, you could find all Locality records for a group of Species (a cross-hierarchy query), to study their geographic range in the database. You can tell Biota to keep the related Specimen and Collection records (intermediate tables in the search) as Record Sets.

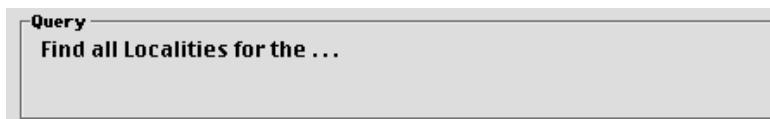
This tool does exactly the opposite task from the Specimens or Species for Places search tool described in the next section (see “[Finding Specimen or Species Records for Places \(Collections or Localities\)](#)” later in this chapter).

1. From the Find menu, choose “Places for Specimens or Species.” The query setup screen below appears.

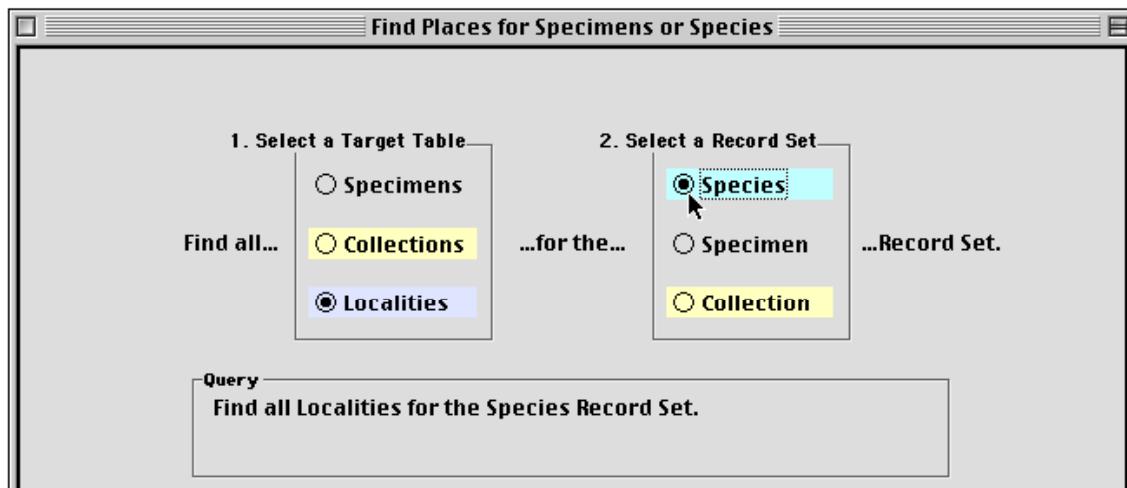


2. From the list of tables in the left panel (the panel labeled “1. Select a Target Table”), click the button for the target table—the table containing the records you seek. In the illustration below, the Localities table has been selected.

The query panel displays the beginning of the query.



3. From the list of tables in the right panel (the panel labeled “2. Select a Record Set”), click the button for the table to be used in the selection criterion (the criterion table). The Record Set for the criterion table may contain many records or only one. In the illustration below, the Species table is being selected.



The query panel displays the completed query.

4. If there are no records in the current Record Set for the criterion table, Biota posts a message like the one below. If you like, you can leave the “Places for Specimens or Species” screen open while you create the appropriate Record Set in another window.



5. To create Record Sets automatically for the target records and for the linking records in any intervening tables, click the checkbox.

You make this choice in the option panel labeled “3. Create Intervening Record Sets?”

For example, if you set up the query “Find all Localities for the Species Record Set” and check this option, Record Sets for the Specimen and Collection tables are automatically created. These Record Sets are composed of the records that link selected Species records (the criterion Record Set) with the Locality records that Biota finds, based on the query. If the box is checked, a Record Set is also automatically created for the Locality records found.



It is not necessary to check this option in order to find the target table records you are searching for, nor to create a Record Set for them. If you want to create a Record Set for the target records without checking this option, you may do so by

means of the standard Record Set option screen (see “[The Record Set Options Screen](#)” in Chapter 3) when leaving the Record Listing screen for the target table (see Step 6, below).

WARNING: Creating Record Sets for intervening tables during the search replaces any existing current Record Sets for those tables.

6. **To launch the search, click the “Find” button or press the ENTER key (Windows) or RETURN key (Mac OS).**
 - **If target table records matching the search query are found,** they are displayed in the standard Record Listing screen for the target table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).” When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen (see “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered).
 - **If no target table records match the search query,** Biota displays the message screen below. If you click the “Try Again” button, the search setup screen reappears, with settings as you left them.

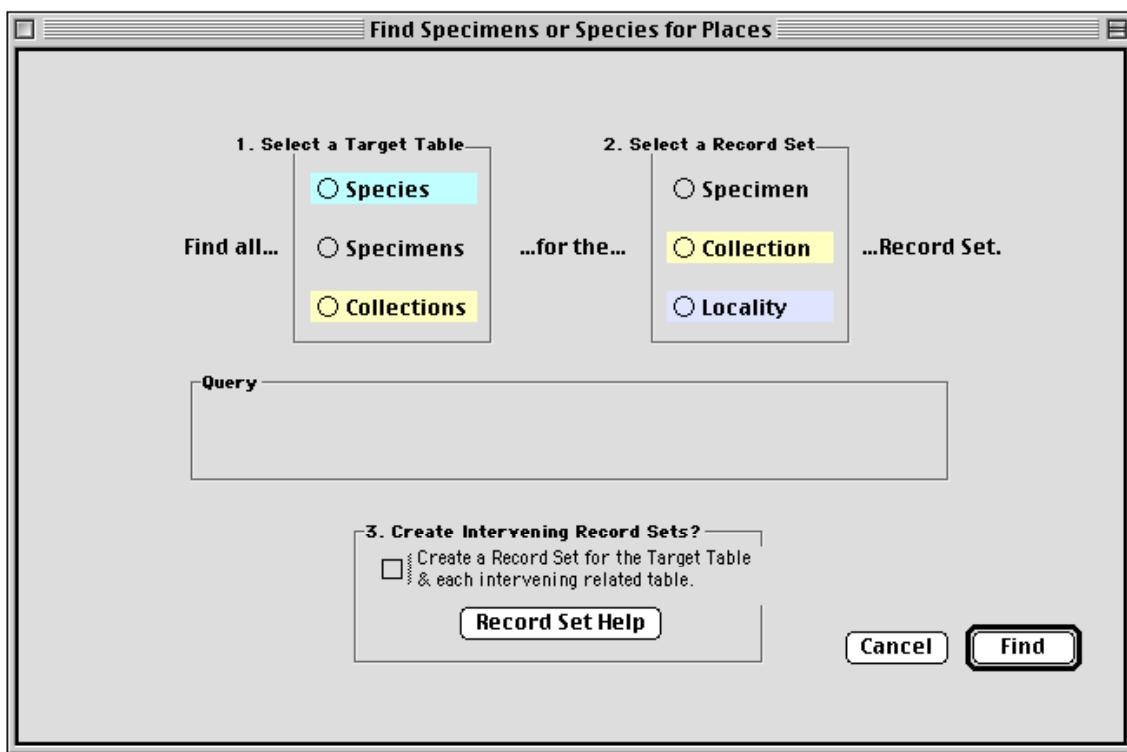


Finding Specimen or Species Records for Places (Collections or Localities)

The “Specimens or Species for Places” search tool finds all Specimen or Species records for the active Collection or Locality Record Set, or all Collection records for the Locality Record Set, according to your query. For example, you could find all Species records for a group of Localities (a cross-hierarchy query) to create a regional fauna or flora list. You can tell Biota to keep the related Collection and Specimen records (intermediate tables in the search) as Record Sets.

This tool does exactly the opposite task from the “Places for Specimens or Species” search tool described in the previous section (see “[Finding Place Records \(Collection or Locality\) for Specimens or Species](#)” earlier in this chapter).

- From the Find menu, choose “Specimens or Species for Places.” The query setup screen below appears.

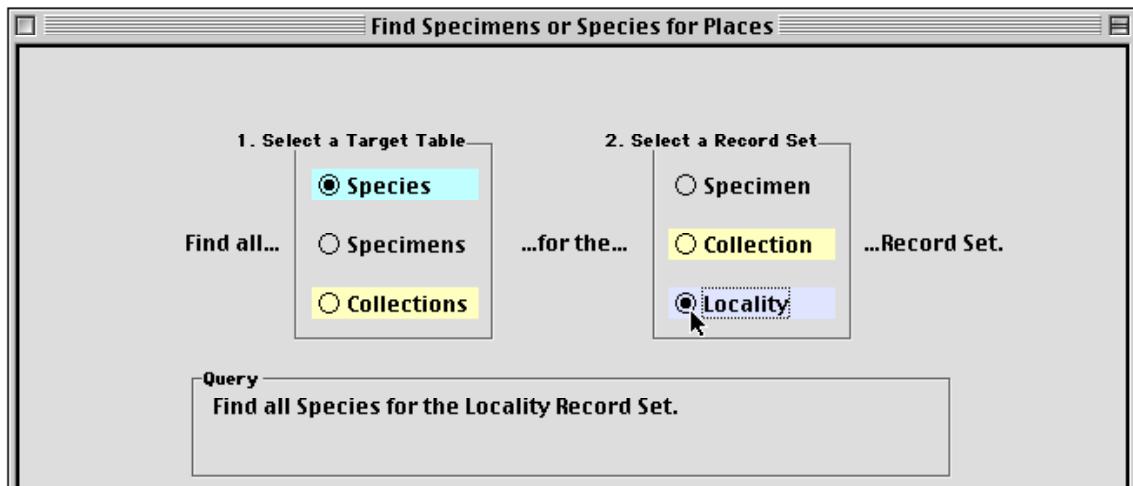


- From the list of tables in the left panel (the panel labeled “1. Select a Target Table”), click the button for the target table—the table containing the records you seek. In the illustration below, the Species table has been selected.



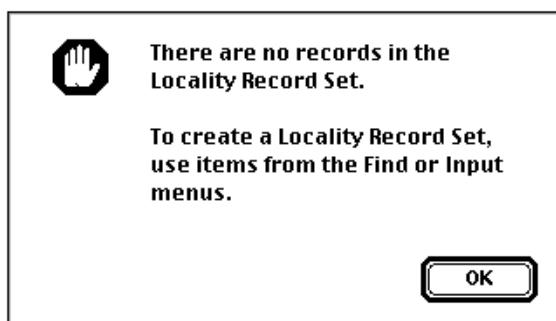
The query panel displays the beginning of the query.

- From the list of tables in the right panel (the panel labeled “2. Select a Record Set”), click the button for the table to be used in the selection criterion (the criterion table). The Record Set for the criterion table may contain many records or only one. In the illustration below, the Locality table is being selected.



The query panel displays the completed query.

4. If there are no records in the current Record Set for the criterion table, Biota posts a message like the one below. If you like, you can leave the Specimens or Species for Places screen open while you create the appropriate Record Set in another window.

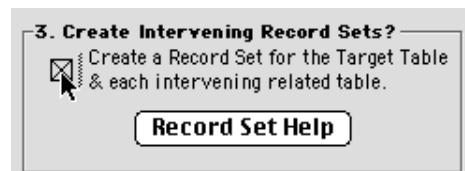


5. To create Record Sets automatically for the target records and for the linking records in any intervening tables, click the checkbox.

You make this choice in the option panel at the right, labeled “3. Create Intervening Record Sets?”

For example, if you set up the query “Find all Species for the Locality Record Set” and check this option, Record Sets for the Collection and Specimen tables are automatically created. These Record Sets are composed of the records that link the Locality records (the criterion Record Set) with the Species records that Biota finds, based on the query. If the box is checked, a Record Set is also automatically created for the Species records found.

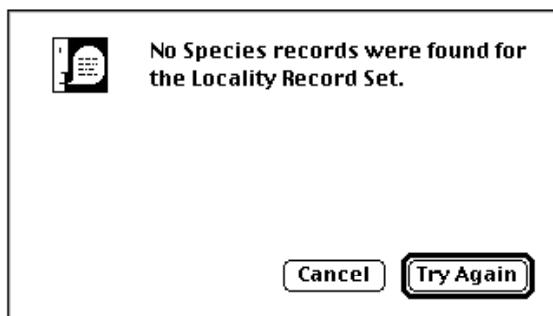
It is not necessary to check this option in order to find the target table (Higher Taxon) records you are searching for, nor to create a Record Set for them. If you want to create a Record Set for the target records without checking this option, you may do so by means of the standard Record Set option screen (see “[The Record](#)



[Set Options Screen](#)” in Chapter 3) when leaving the Record Listing screen for the target table (see Step 6, below).

WARNING: Creating Record Sets for intervening tables during the search replaces any existing current Record Sets for those tables.

6. To launch the search, click the “Find” button or press the ENTER key (Windows) or RETURN key (Mac OS).
 - If target table records matching the search query are found, they are displayed in the standard Record Listing screen for the target table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).” When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen (see “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered).
 - If no target table records match the search query, Biota displays the message screen below. If you click the “Try Again” button, the search setup screen reappears, with settings as you left them.



Sequential, Cross-Hierarchy Searches

If you want to find Collections or Localities for taxa above the level of Species, or discover which higher taxa are represented in Collections or Localities, you can use the appropriate pair of search tools sequentially, choosing among the tools introduced in the preceding four sections of this chapter.

- [Finding Records for Lower Taxa Based on Higher Taxa](#)
- [Finding Records for Higher Taxa Based on Lower Taxa](#)
- [Finding Place Records \(Collection or Locality\) for Specimens or Species](#)
- [Finding Specimen or Species Records for Places \(Collections or Localities\)](#)

For example, to find all the Localities for an Order:

1. Find all Species for the Order using the “Lower Taxa for Higher Taxa tool” ([Finding Records for Lower Taxa Based on Higher Taxa](#)).
2. Declare the group of Species records found to be the current Species Record Set. (See “[The Record Set Options Screen](#)” in Chapter 3.)

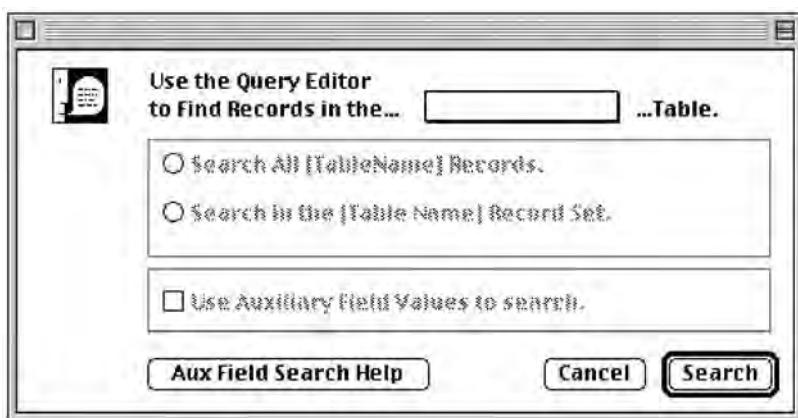
- Find all Localities for the Species Record Set using the Places for Specimens or Species tool ([Finding Place Records \(Collection or Locality\) for Specimens or Species](#)). The Locality records found will encompass all Localities in which any Specimen of the original criterion Order has been found, as recorded in the Data File.

The Query Editor, a General-Purpose Tool for Finding Records Based on Content

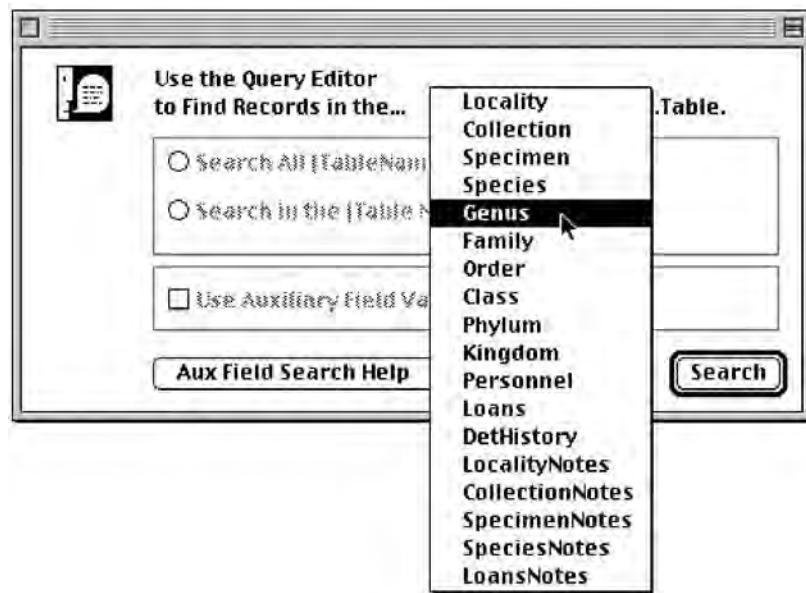
When none of the specialized tools from the Find menu fits the record-finding task you have in mind, the Query Editor may be the answer. The Query Editor is often the tool of choice when you need to find records based on their content, although displaying all records for a table (see “[Finding and Displaying All Records for a Table](#)” earlier in this chapter), then using the Sort Editor (see the four sections beginning at “[Sorting Records in Record Listing Screens](#)” in Chapter 10) is often just as efficient. The Query Editor is restricted to finding Core table records, but the query can be based on fields and values in virtually any Biota table.

Using the Query Editor: Step by Step

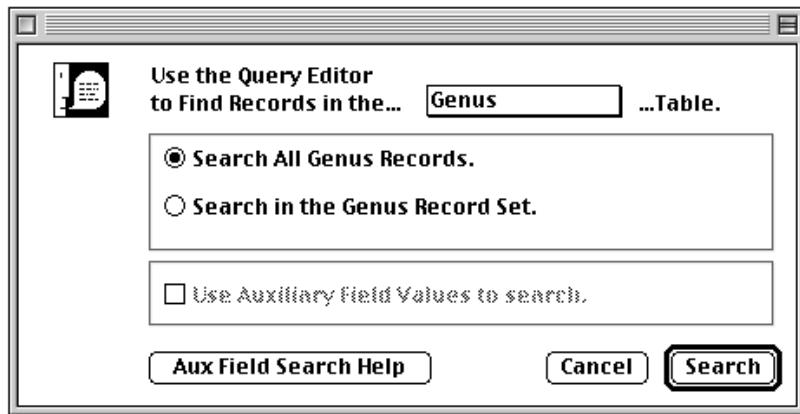
- From the Find menu, choose “Using the Query Editor.” A table selection window appears.



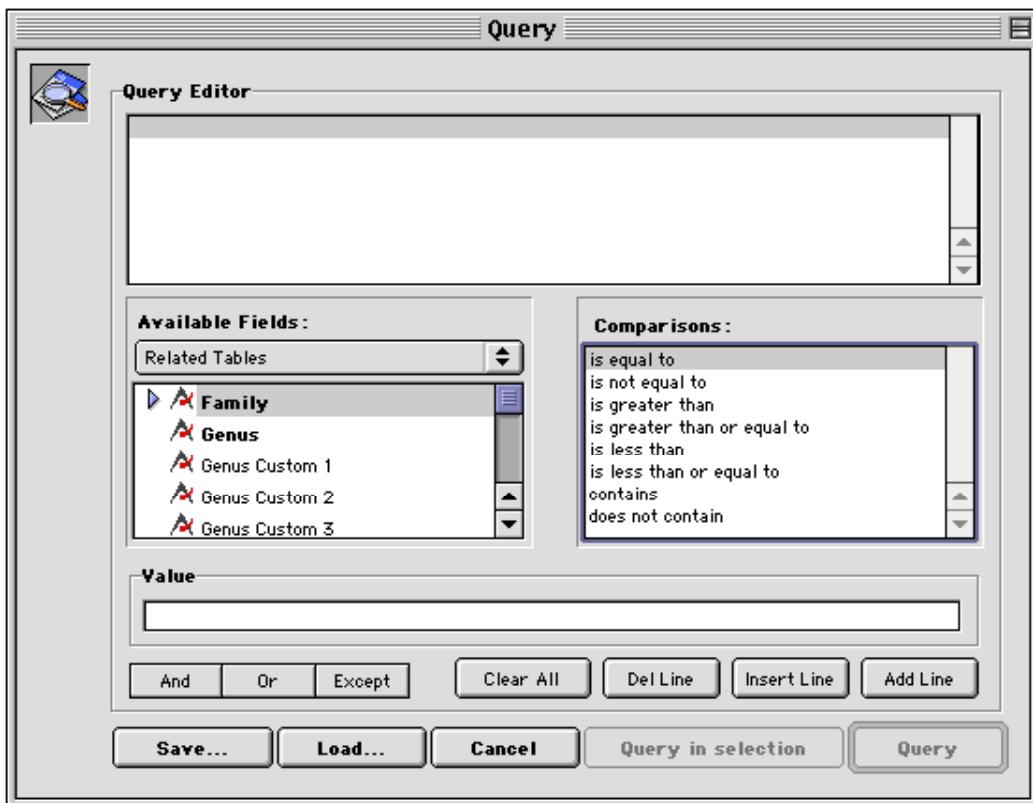
- Click and hold the popup list to select the table containing the records you seek—called the *target table*. In the illustration below, the Genus table is being selected as the target table for the search.



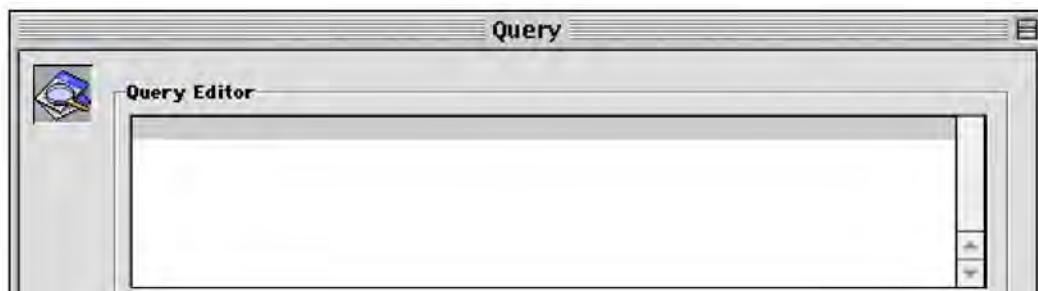
When you have chosen a table, the search option buttons are activated.



3. Choose a search option in the window (above).
 - **Either:** Search all records in the selected table.
 - **Or:** Search only in the active Record Set for the table.
- If there are no records in the active Record Set for the table, the lower button is disabled (dimmed). If there are no records in the table, Biota informs you with a message, neither button is activated, and the search is canceled.
4. Click the “Search” button or press the ENTER key (Windows) or RETURN key (Mac OS) to launch the Query Editor. The Query Editor window appears.

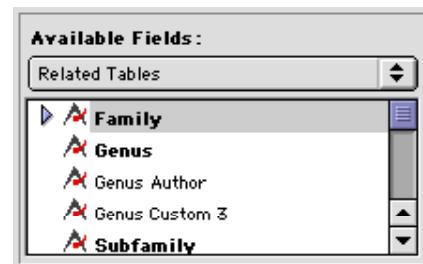


- The **Query panel** of the Query Editor (initially blank) will display the search query, once you have set it up. This is the upper panel in the window.



- The “**Available Fields**” panel (the scrollable panel on the center left) is used to display and select fields (and tables), which are listed alphabetically.

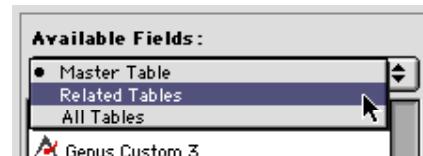
Field names in **boldfaced** type are indexed fields. Searches for values in indexed fields proceed faster than searches for values in non-indexed fields—but you can search on any field. (Indexes take up space in data files and processor time to maintain, so not all fields in Biota are indexed.)



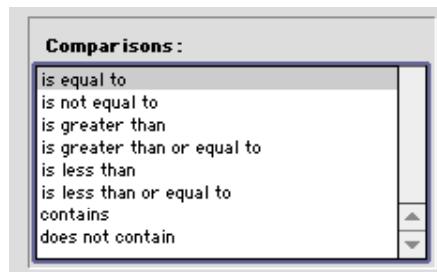
When fields are displayed in the “Available Fields panel,” the icon to the left of each field name indicates the field type, as follows:

- ◊ **Alphanumeric field**
- ◊ **Text field**
- ◊ **Integer field**
- ◊ **Real number (decimal) field**
- ◊ **Date field**
- ◊ **Boolean field**

- The **popup menu** just below the panel title “Available Fields” controls the display of fields. The popup menu retains its setting between uses of the Query Editor.



- **The Comparisons panel** (the scrollable panel on the center right) is used to display and select comparison operators for building queries.
- **The Value entry area** (running across the window above the buttons) is the entry area for field values used in search queries.



- **The logical operator buttons** (And, Or, and Except) are used to create and compound queries.
 - **The line manipulation buttons** (Clear All, Del Line, Insert Line, and Add Line) are used to create and edit lines (criteria) for compound queries.
 - **The “Save” and “Load” buttons** allow you to save queries (which are sometimes complex to set up) to disk file, then reload them at a later date.
 - **The “Cancel” and “Query” buttons** are used to dismiss the Query Editor and launch a search, respectively.
 - **The “Query in selection” button** has no function in Biota. (The Query Editor is a predefined 4D tool.) If you want to search in a particular selection of records, declare them the current Record Set for the table (See "[The Record Set Options Screen](#)" in Chapter 3) and choose the second option in Step 3, above.
5. **If you have defined any Core Field Aliases** (see Chapter 18, "[Renaming Fields](#)"), the aliases are displayed in the Query Editor instead of the Internal Field Names.
- In the example here, the fields Genus Custom 1 and Genus Custom 2 (Internal Field Names) have been given the Aliases Genus Author and Tribe Author, respectively.
6. **Set the popup menu to either “Related Tables” or “Master Table.”** All fields of the target (= “master”) table will be shown in either case.
7. **Click a field name from the “Available Fields” panel to select it.** When the Query Editor first opens, this scrollable panel shows the names of all fields for the table you selected in Step 2. (You may have to scroll to see them all.) In the

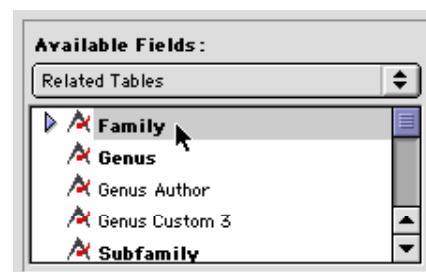
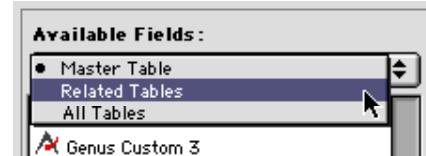
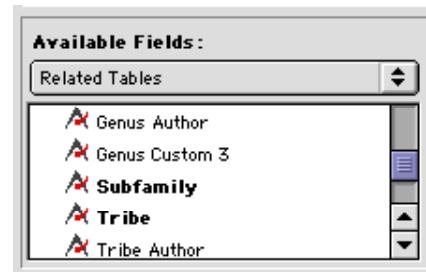
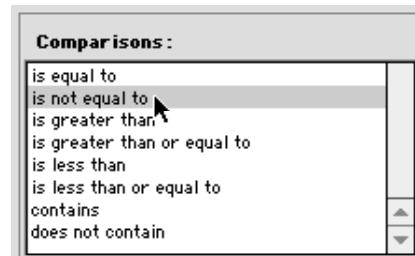


illustration above, the Family linking field in the Genus table is being selected for the query. The field name you select appears in the query panel (see the illustration in Step 8).

8. Click an operator from the Comparisons panel to add it to the query. In the illustration below, the operator “is not equal to” is being selected.

The operator you selected appears in the query panel (see the second illustration in Step 9).

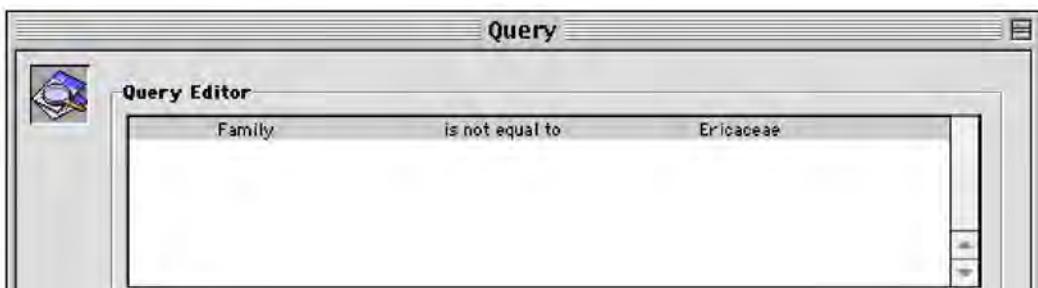


NOTE: The quantitative operators (*is greater than*, *is greater than or equal to*, and *is less than*) can be used not only on numeric fields, but also on values in alphabetic fields. When used on alphanumeric values, these operators evaluate the ASCII code of the characters, left to right. Thus 01 is less than 10, but 1 is evaluated as “greater than” 10. The digits 0–9 are “less than” the letters A–Z. In short, the order of alphanumeric values is the same as their alphanumeric sort order.

9. Enter a field value in the Value entry area to complete the query line.



The field value appears simultaneously in the query panel. In the illustration above, the family name Ericaceae is the field value entered, completing the query line “Family is not equal to Ericaceae.”

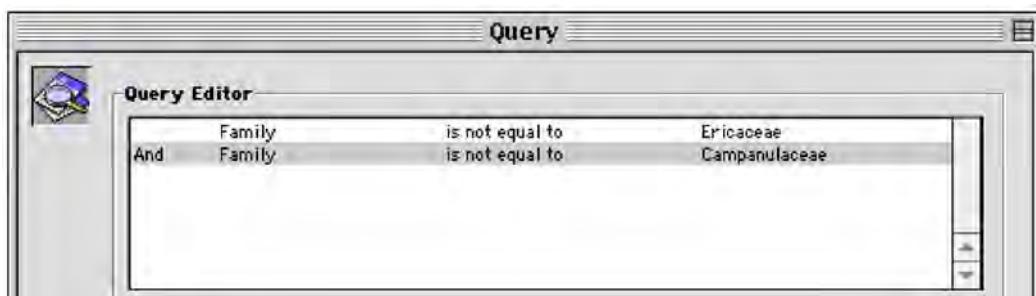


NOTE: Field values are not case-sensitive: Ericaceae, ericaceae, and ERICACEAE would all have the same meaning in the query illustrated above.

10. To create a compound query, take these steps:

- Click the “Add Line” button** to start a new query line. (Or click the “Insert Line” button to insert a new line above the highlighted query line.)
- Click a button in the logical operators panel.** The “And” button is being clicked in the illustration at the right
- Follow steps 7–9, above**, to construct an additional query line.
- Repeat as many times as necessary** to complete the query.

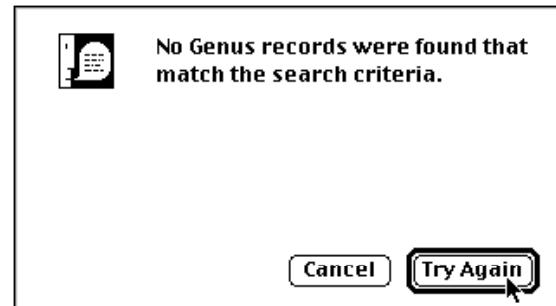
In the completed example below, the compound query seeks all Genus records for which the [Genus] Family field is *neither* Ericaceae *nor* Campanulaceae.



Note: Compound searches are performed in the order the lines appear in the search query, top to bottom, regardless of the conjunction used (i.e., there is no fixed precedence among the three conjunctions).

11. To launch the search, click the “Query” button in the Query Editor.

- If target table records matching the search query are found, they are displayed in the standard Record Listing screen for the target table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).” When you click the “Done” button in the Record Listing screen, Biota displays the standard Record Set options screen (see “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered).
- If no records are found that match the criteria in the search query, Biota displays the message screen below. If you click the “Try Again” button, the Query Editor reappears, set to search for records in the same target table as before.



Using Fields from Parent Tables in the Query Editor

Before consulting this section, please review the previous section, “[Using the Query Editor: Step by Step](#)” and the section “[Linking Fields: Parent and Child Records](#)” in Chapter 3.

When you open the Query Editor, you specify the table containing the records you seek—the *target table* for the search (Step 2 in the previous section). In the previous section, the search queries illustrated all relied solely on fields of the target table itself. You can also use fields from linked tables in search queries you build with the Query Editor. This section explains how to use fields from *parent tables* to build query criteria. To learn how to use fields from *child tables* to construct query criteria, consult the section “[Using Fields from Child Tables in the Query Editor](#)” later in this chapter.

1. **Launch the Query Editor** following steps 1 through 4 in the previous section, “[Using the Query Editor: Step by Step](#).”

In the illustration here, the Collection table was selected as the target table for the search.

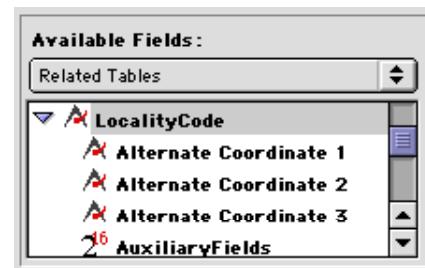
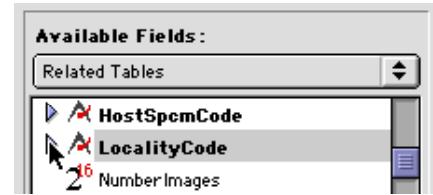
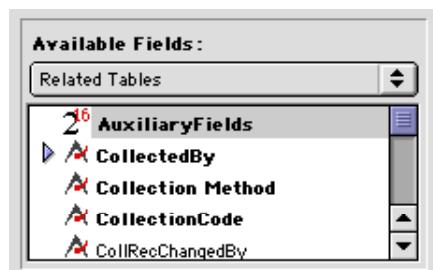
2. **From the popup menu above the list of fields, select “Related Tables.”** To include a field from a parent table in a query criterion, set the popup (or leave it set) to “Related Tables.”
3. **Display the fields for a parent table** by clicking on the expansion triangle to the left of the name of the parent-table linking field in the target table.

For example, if you want to search for Collection records from Ecuador, you will need to set up a query based on the Country field of the Locality table. You can do this because Locality is a parent table to the Collection table (each Locality record may be linked to many Collection records). Because the [Collection] LocalityCode field is the linking field, click on the expansion triangle next to that field.

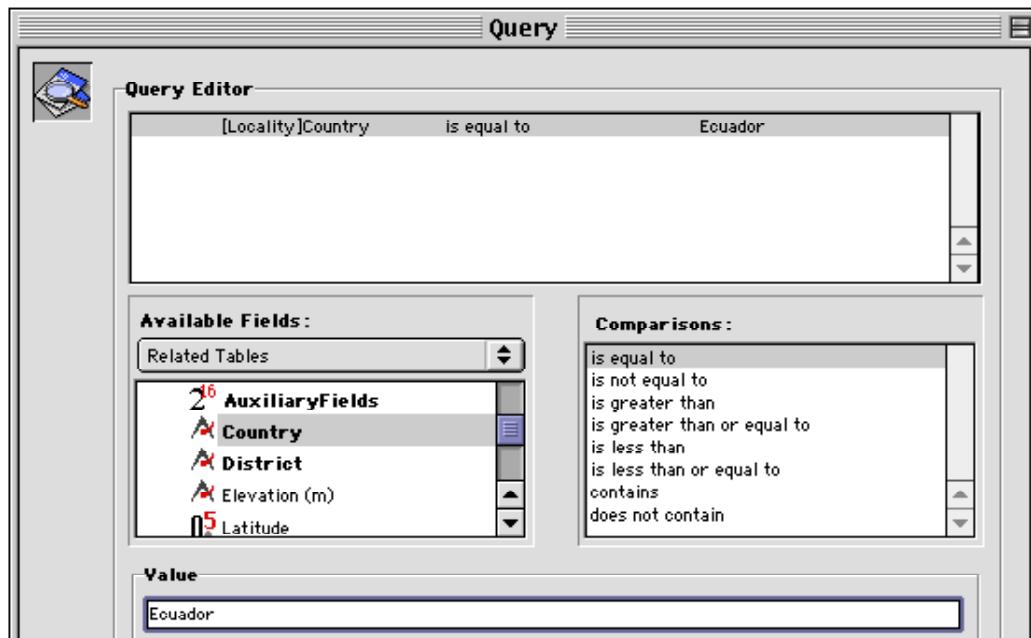
All fields of the parent table (Locality) are displayed, indented below the linking field name (LocalityCode).

NOTE: There is an alternate way to display fields from a parent table: Select “All Tables” from the popup menu above the list of fields, then click the parent table name to display its fields.

4. **Select a field from the parent table to use in the query criterion, and enter a field value to search for.** Once the fields for the parent table appear in the field list, you can include these fields in search criteria, using the same techniques described in the previous section, “[Using the Query Editor: Step by Step](#).”



Below, the Country field of the Locality table has been used to set up a query to find Collection records linked to Localities in Ecuador. (Note that the table name, “[Locality],” appears in the query window to make clear that a field from a linked table has been used.)



Note: In the case of parent-child (many-to-one) links, you can reference fields from a related table *at any level up a hierarchy*. For example, you could find all Genus records linked to a specified Kingdom or to a specified value in any other field from a higher taxon table. Or, you could find all Specimen records linked to Locality records from a certain Country.

5. When the query is ready, complete the search as described in Step 10 of the previous section “[Using the Query Editor: Step by Step.](#)”

Using Fields from Child Tables in the Query Editor

Before consulting this section, please review the sections “[Using the Query Editor: Step by Step](#)” and “[Using Fields from Parent Tables in the Query Editor](#),” earlier in this chapter, and the section “[Linking Fields: Parent and Child Records](#)” in Chapter 3.

When you open the Query Editor, you specify the table containing the records you seek—the *target table* for the search. The search queries illustrated in the section “[Using the Query Editor: Step by Step](#),” earlier in this chapter, all relied solely on fields of the target table itself. You can also use fields from linked tables in search queries you build with the Query Editor. The section “[Using Fields from Parent Tables in the Query Editor](#),” earlier in this chapter, explains how to use fields from *parent tables* to build query criteria. This section explains how to use fields from *child tables* to construct query criteria.

Here is the rule for using child tables in a query: If a query criterion refers to a field in a child table, each record in the target table that is linked to *at least one* child record meeting the search criterion will be found by the query.

For example, with Genus as the target table, you could use the “Number Images” field from the Species table (which specifies the number of Image Archive records linked to each Species record) to set up the search query “Number Images is greater than 0.” This search would find all Genus records that are linked to at least one Species record that has at least one linked Image Archive record.

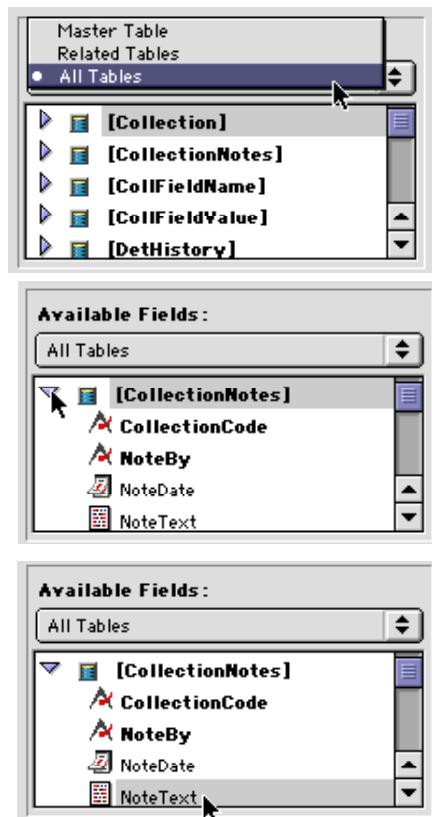
1. **Launch the Query Editor** following steps 1 through 4 in the section “[Using the Query Editor: Step by Step](#)” earlier in this chapter.

In the illustration here, the Collection table was selected as the target table for the search.

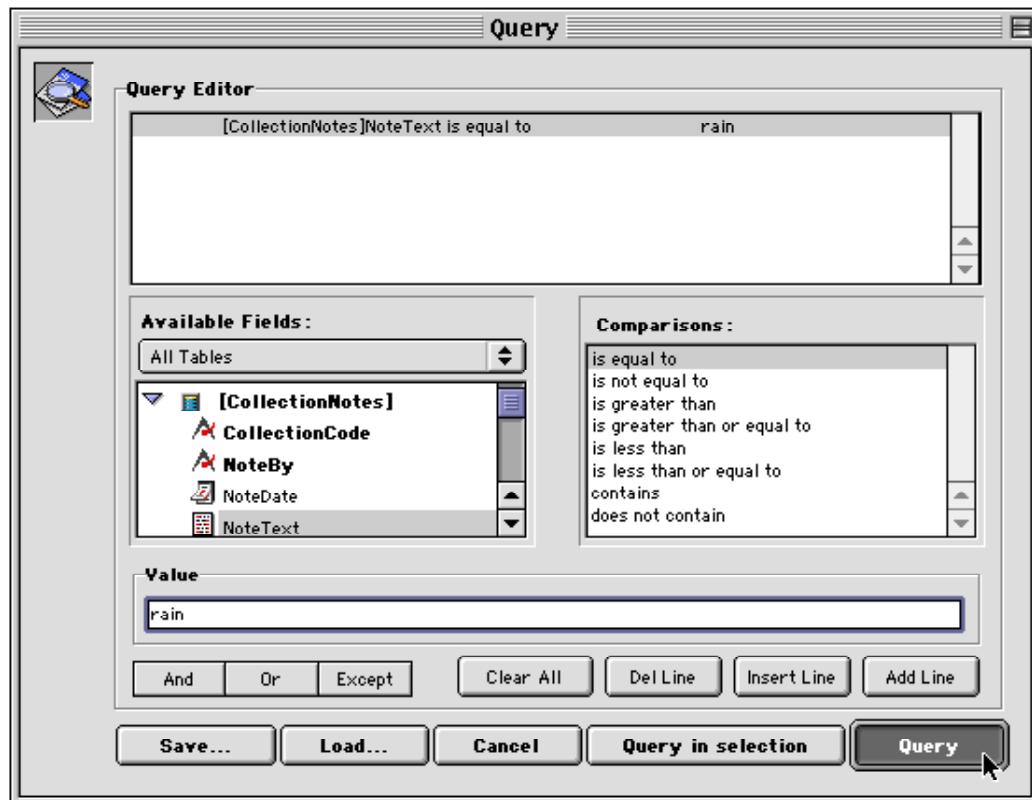
2. **From the popup menu above the list of fields, select “All Tables.”** To include a field from a child table in a query criterion, you *must* set the popup (or leave it set) to “All Tables.”
3. **Display the fields for a child table linked to the target table by clicking on the expansion triangle to the left of the name of the child table.**

For example, if you want to search for Collection records that have Collection Notes containing the word “rain,” you can set up a query based on the “Note Text” field of the Collection Notes table. You can do this because Collection Notes is a child table to the Collection table (each Collection record may be linked to many Collection Notes).

4. **Select a field from the child table to use in the query criterion, and enter a field value to search for.** Once the fields for the child table appear in the field list, you can include these fields in the search criteria, using the same techniques described in the section “[Using the Query Editor: Step by Step](#),” earlier in this chapter. The “Note Text” field of the Collection Notes table is being selected here.



Below, the full query criterion appears for finding Collection records that have Collection Notes containing the word “rain.” (Note that the table name, “[Collection Notes],” appears in the query window to make clear that a field from a linked table has been used.)



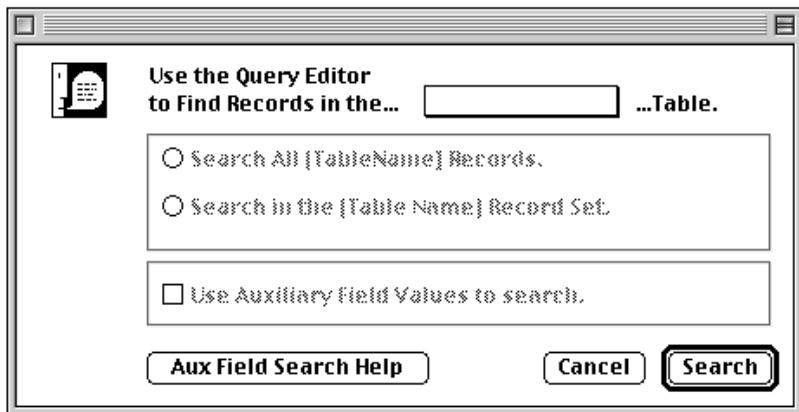
NOTE: In searching for records based on values in a child table, you can use fields *only from a directly linked child table*. For example, you could not use a field of the Specimen table in a search criterion for Genus records, because the Species table is interposed. (In contrast, *parent* tables linked through intermediate tables may be used in queries.)

5. When the query is ready, complete the search as in described in Step 10 of the previous section, “[Using the Query Editor: Step by Step.](#)”

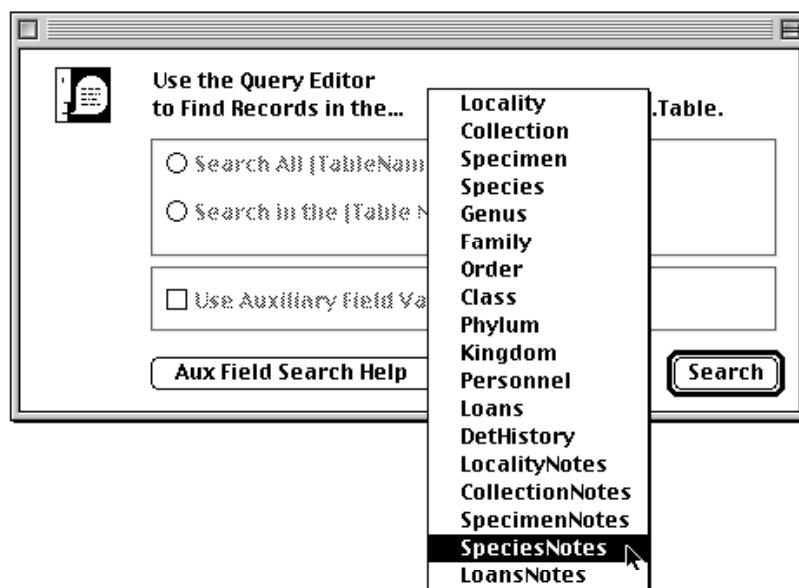
Using the Query Editor to Find Records Based on Notes

You can use the Query Editor to find records in the Locality, Collection, Specimen, Species, or Loans table based on text in linked Notes records. You can search in the “Note Date,” “Note By” (note author), or “Note Text” fields.

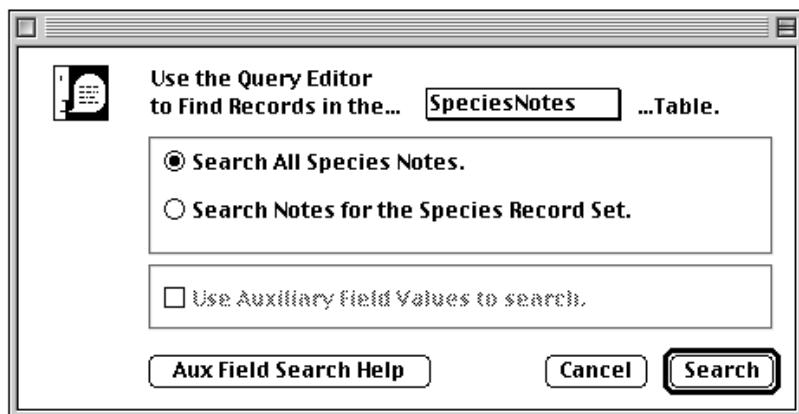
1. From the Find menu, choose “By Using Query Editor.” A table selection window appears.



2. Click and hold the popup list to select the Notes table you want to search. In the illustration below, the Species Notes table is being selected.



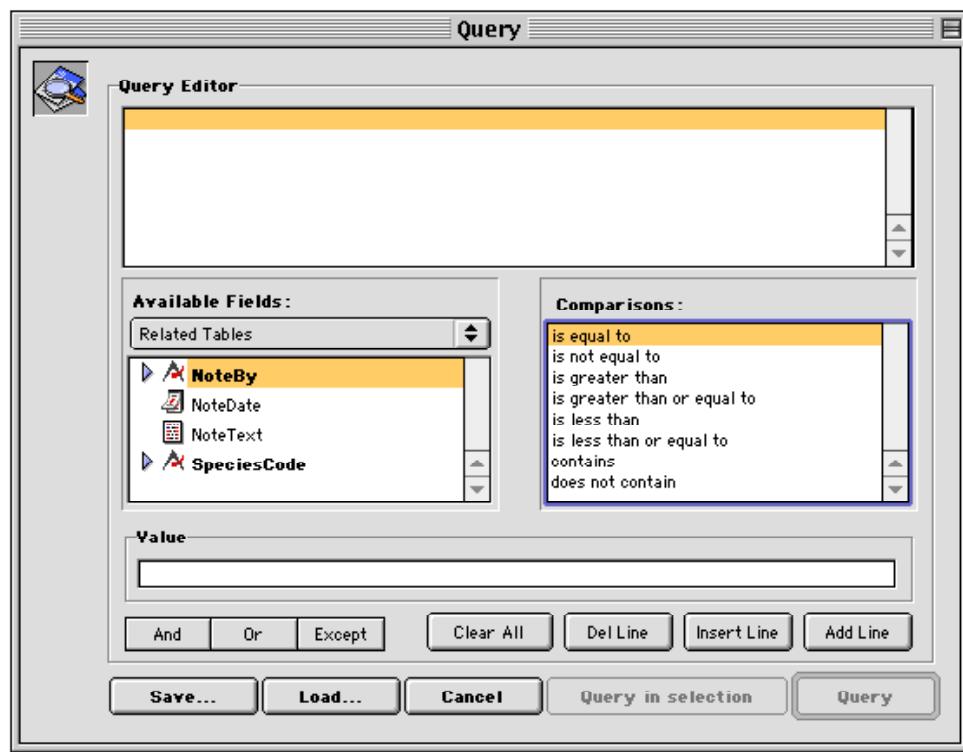
The appropriate search options in the window are activated.



3. Choose a search option in the window (above).
 - **Either:** Search all records in the selected Notes table.
 - **Or:** Search only those Notes linked to records in the active Record Set for the *parent* table.

If there are no records in the active Record Set for the *parent* table (the Species table, in this example), the lower button is not activated.

4. Click the “Search” button in the options window to launch the Query Editor. The Query Editor window appears, displaying the fields of the Notes table (Species Notes, in this example). Set up a query based on values in the Note Date, Note By, and/or Note Text fields.



NOTE: If you are not familiar with the Query Editor, please consult the section “[Using the Query Editor: Step by Step](#)” earlier in this chapter.

5. Click the “OK” button to launch the search. Biota finds and displays all the *parent* table records (Species records, in this example) for which the criteria you set are true in the linked Species Notes records.

NOTES:

- a. You can also include criteria from the parent table or any table linked to it, with the same restrictions as for any other query. See “[Using Fields from Parent Tables in the Query Editor](#)” earlier in this chapter.
- b. For any complex and time-consuming search, it is a good idea to create a Record Set Pointer File to record the results for future reference or use. These files are very small and very efficient. See “[Record Set Pointer Files](#)” in Chapter 3

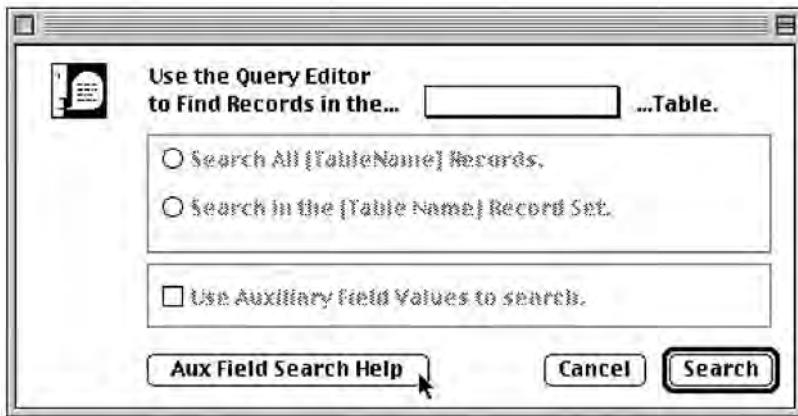
Using the Query Editor with Auxiliary Field Values

You can use the Query Editor to search for Specimen, Species, Collection, or Locality records based on values in Auxiliary Fields for those records.

WARNING: If you are not familiar with Auxiliary Fields in Biota, or you are not sure how they work, be sure to consult Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#),” before using the Query Editor with Auxiliary Field Values. If you are unfamiliar with the Query Editor, please review the sections “[Using the Query Editor: Step by Step](#)” earlier in this chapter.

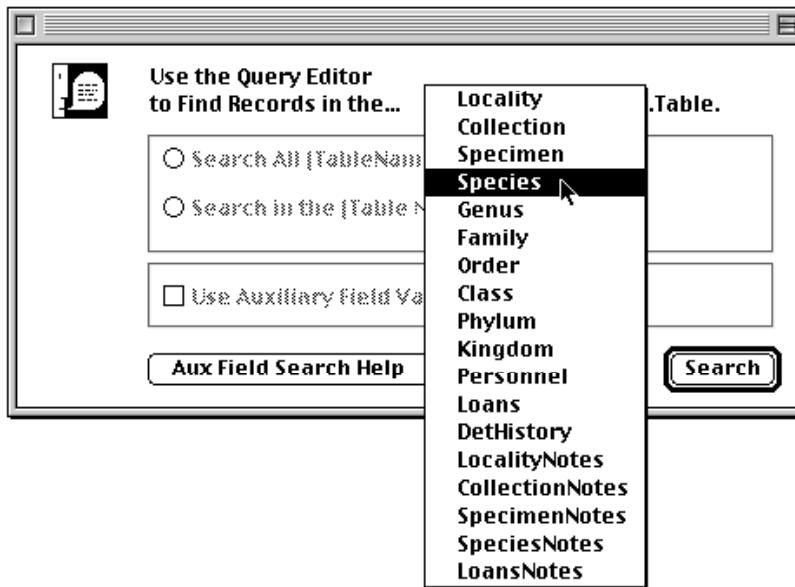
Here are the steps to take:

1. **From the Find menu, choose “Using Query Editor.”** The table selection window appears.

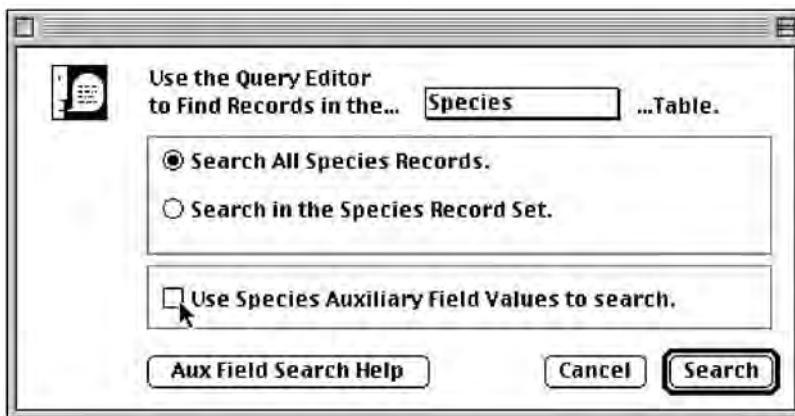


NOTE: Notice the “Aux Field Search Help” button, which displays a succinct version of these instructions, should you need help.

2. Click and hold the popup list to select the table containing the records you seek—called the *target table*. In the illustration below, the Species table is being selected as the target table for the search.



- If you choose a table that does not support Auxiliary Fields (e.g., Genus), the “Use Auxiliary Field Values checkbox” remains disabled (dimmed).
- If you choose one of the four tables that support Auxiliary Fields (Specimen, Species, Collection, or Locality), the “Use Auxiliary Field Values” checkbox is activated.



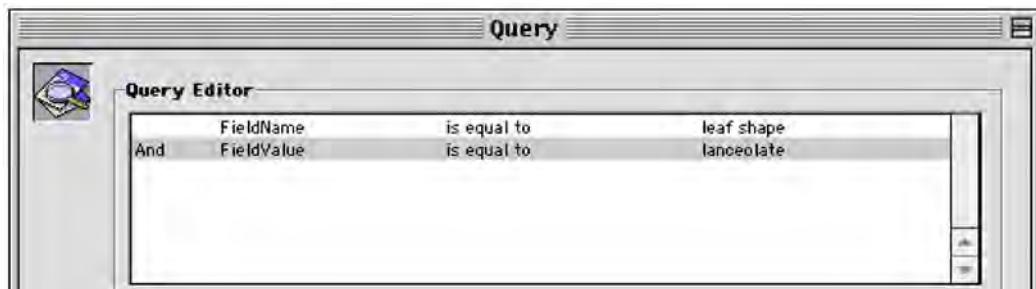
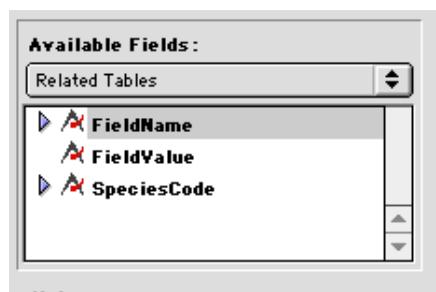
3. Choose a search option in the window (above).
- Either: Search all records in the selected table.
 - Or: Search only in the active Record Set for the table.

If there are no records in the active Record Set for the table, the lower button is disabled (dimmed). If there are no records in the table, Biota informs you with a message, neither button is activated, and the search is canceled.

4. **Check (enable) the Use Auxiliary Field Values checkbox.** If you do not want to use Auxiliary Field Values in the search, leave the checkbox unchecked and proceed according to the instructions in the section “[Using the Query Editor: Step by Step](#)” earlier in this chapter.



5. **Click the “Search” button or press the ENTER key (Windows) or RETURN key (Mac OS) to launch the Query Editor.** The Query Editor window appears, with the “Available Fields” panel displaying not the fields of the target table (Species, in this example), but rather the three fields of the corresponding Auxiliary Field Value table (the Species Field Value table, in this example).
6. **Set up a query based on both the “Field Name” and the “Field Value” fields.** For example, to find all Species records that have the value “lanceolate” in a Species Auxiliary Field you have named “Leaf Shape,” you would set up the query: “FieldName is equal to Leaf Shape And FieldValue is equal to lanceolate,” as shown below.



7. **To launch the search, click the “Query” button in the Query Editor.** Biota finds and displays all the parent table records (Species records, in this example) for which the criteria you set are true in the linked Auxiliary Field Value table.

WARNING: In a search based on Auxiliary Field Values, you must use *only* Auxiliary Field Names and Auxiliary Field Values in the search criteria. You cannot use fields from the parent table itself (the Species table, in the example) nor from any other table in such a search. Moreover, you can search for only one Auxiliary Field based criterion at a time. For more complex searches, see the next section of this chapter, “[Using the Query Editor with Auxiliary Field Values in Combination with Other Criteria](#).”

Using the Query Editor with Auxiliary Field Values in Combination with Other Criteria

If you need to perform a search based on Auxiliary Field Values as well as values in other fields, you must use a two- or three-step process.

WARNING: This section assumes you are thoroughly familiar with the previous section of this chapter, “[Using the Query Editor with Auxiliary Field Values](#),” with Auxiliary Fields (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#),” and with the Query Editor (see “[Using the Query Editor: Step by Step](#)” earlier in this chapter).

- **Case 1: Finding records for a target table based on values in Core fields as well as Auxiliary Fields of the target table.**

Suppose you have defined an Auxiliary Field named “Weather” for the Collection table, to record conditions at the time of each collecting event. Possible values for Weather might include “Fair,” “Overcast,” “Rain,” and so on. Now suppose you wish to find all Collection records for which the “Collected By” field of the Collection table shows that the collection was made by C. Darwin, the “Country” field of the linked Locality record shows that the collection was made in Ecuador, and the linked “Coll Field Value” (Collection Auxiliary Field Value) record for “Weather” indicates an “Overcast” day.

For this example, you would use the following strategy:

1. **Use the Query Editor to find all records in the target table that meet the criteria based on Auxiliary Field Values.** In this example, you would select the Collection table in the field selection window (see step 2 in the previous section, “[Using the Query Editor with Auxiliary Field Values](#)”), select “Search All Collection Records,” and check the “Use Collection Auxiliary Fields” checkbox in the window. When the Query Editor appears, set up the query, “FieldName is equal to Weather And FieldValue is equal to Overcast,” and launch the search.
2. **When the records Biota finds are displayed, declare them to be the current Record Set for the target table.** In the example, you would declare the Collection records for overcast days to be the current Collection Record Set, using the Record Set Options screen that appears when you click the “Done” button in the Collection Record Listing screen (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **Use the Query Editor to search within the Record Set according to the remaining criteria.** In the example, you would again select the Collection table in the field selection window (step 2 in the previous section, “[Using the Query Editor with Auxiliary Field Values](#)”), but then choose the “Search in the Collection Record Set” option. This time, do *not* check the “Use Collection Auxiliary Fields” checkbox in the window. When the Query Editor appears, set up the query, “CollectedBy is equal to C. Darwin And [Locality]Country is equal to Ecuador,” and launch the search. (See “[Using Fields from Parent Tables in the Query Editor](#),” earlier in this chapter, if you need help using fields from the Locality table in this example.)

- **Case 2: Finding records for a target table based on values in Core fields as well as Auxiliary Fields of a parent table.**

What if you need to find records in one table based on Auxiliary Field Values linked to a different (parent) table? Building on the previous example, what if you need to find all *Specimen* records for specimens collected on overcast days by Darwin in Ecuador?

In this case, you must add a new step to the strategy outlined above.

1. **Use the Query Editor to find all records in the parent table that meet the criteria based on Auxiliary Field Values and Core field values.** In this example, the Collection table is the parent table of the target table (*Specimen*). Proceed exactly as in the previous example, finding all *Collection* records for overcast days made by Darwin in Ecuador.
 2. **When the records Biota finds are displayed, declare them to be the current Record Set for the target table.** In the example, you would declare the *Collection* records for overcast days to be the current Collection Record Set, using the Record Set Options screen that appears when you click the “Done” button in the Collection Record Listing screen (see “[The Record Set Options Screen](#)” in Chapter 3).
 3. **Find all records in the target table that are linked to the Record Set in the parent table,** using the tools of the Find menu for finding records in one table based on a Record Set for another table (see “[Special Tools for Finding Records in One Table Based on a Set of Records in Another Table](#)” earlier in this chapter). In this example, you would use the “Specimen or Species for Places” tool (Find menu) to find all Specimen records linked to the Collection record set. These Specimen records are the ones you are looking for.
- **More complex cases.** You can use Biota’s capability for manipulating Record Sets (see “[The Record Set Options Screen](#)” in Chapter 3) to carry out more complex searches involving Auxiliary Field Values from two different tables or two different Auxiliary Field Value criteria for the same target table.

Building again on the previous example, suppose you had also defined a *Specimen* Auxiliary Field named “Condition” to record the current condition of mounted specimens. Now suppose you need to find all Specimen records for specimens collected on overcast days by Darwin in Ecuador, for which the Condition is “Good.”

To do so, you would first carry out a search just as described in the previous section, finding all Specimen records for specimens collected on overcast days by Darwin in Ecuador. Then declare these Specimen records to be the current Specimen Record Set. Next, carry out a search, using the Query Editor, for all Specimen records for which the “Condition” Auxiliary Field Value is “Good.” Click the “Done” button in the Specimen Record Listing screen. When the Record Code Options screen appears, click the “More Choices” button on it, then click the button labeled “Make shared records the new Record Set” to find the intersection of the set of records for specimens in good condition and the Record Set of specimens collected on overcast days by Darwin in Ecuador. The resulting set of records meets all criteria.

NOTE: For any complex and time-consuming search, it is a good idea to create a Record Set Pointer File to record the result for future reference or use. These files are very small and very efficient. See “[Record Set Pointer Files](#)” in Chapter 3.

Finding Records by Record Codes

Because Record Codes uniquely identify each record in the Specimen, Collection, Locality, and Species tables (see Chapter 8, “[Record Codes](#)”), finding a record in one of these tables by its Record Code is sometimes the fastest way to retrieve, display, and—if necessary—edit an existing record. If you use barcodes (see Appendix K, “[Barcodes](#)”) for Specimen Codes or other Record Codes, these tools are especially fast to use.

Four commands from the Find menu (“By Specimen Code,” “By Collection Code,” “By Locality Code,” and “By Species Code”), all with the same interface, take care of this straightforward task. A fifth “Find” command with a different interface, “By Specimen Code Series,” is covered in Chapter 13, “[Creating, Finding, and Updating Specimen Series](#).”

- From the Find menu, choose “By Specimen Code,” “By Collection Code,” “By Locality Code,” and “By Species Code.”** The Record Code query screen appears (illustrated below for the Specimen table).
- In the entry area of the request window, enter the full Record Code** (Specimen Code, Collection Code, Locality Code, or Species Code) for the record you want to find, manually or with a barcode reader.

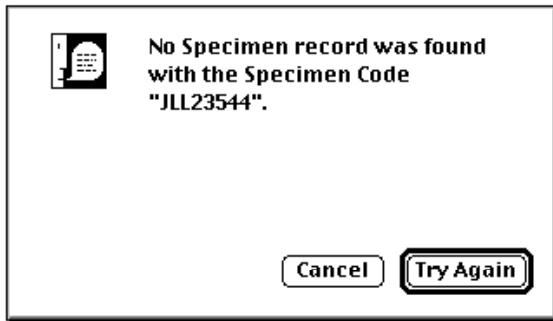


NOTE: You cannot use the wildcard entry method with these tools.

- Click the “OK” button in the request window to launch the search.**
- If the record is found,** it is displayed in the standard Input screen for the target table, where you can work with it using the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

When you click the “Cancel” button in the target table Input screen, above, Biota displays the standard Record Set options screen for the target table. See “[The Record Set Options Screen](#)” in Chapter 3 for explanation of the options offered.

- If the record is not found, Biota displays a message like the one below (illustrated for the Specimen table). If you click the “Try Again” button, the Record Code request screen for the same target table reappears.



Finding Host and Guest Specimens and Collections

Four commands in the Find menu (“Host Specimens & Collections,” “Guest Specimens & Collections,” “Host Specimens for Guest Specimens,” and “Guest Specimens for Host Specimens”) find and display Specimen and Collection records linked through the Host Specimen Code field in the Collection table to the Specimen Code field in the Specimen table.

These commands are discussed in Chapter 24, “[Host-Guest Relations](#).”

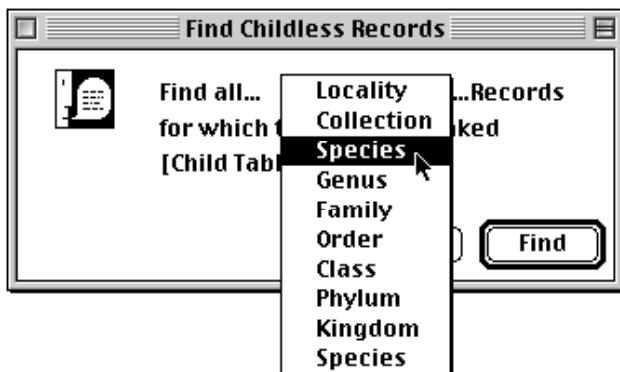
Finding Childless and Orphan Records

The section “[Linking Fields: Parent and Child Records](#)” in Chapter 3 introduces the concepts of *child* and *parent* records. For example, as a consequence of the many-to-one relation between the Species and Genus tables, a Species record (if linked) is a child record of a particular Genus record; the Genus record is the parent record of the Species record (and perhaps the parent of other Species records as well).

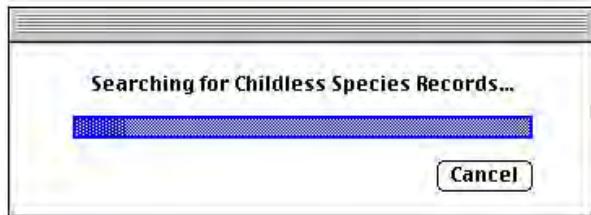
The metaphor is carried further in the concepts of *orphan* records (those that are not linked to any record in the parent table) and *childless* records (those not linked to any record in the child table, for a particular database relation). For example, a Genus record not linked to any Family record is an orphan record. A Genus record not linked to any Species record is a childless record. Orphan records, especially, and childless records, to a lesser extent, tend to be “invisible” in relational searches. (In relational database terminology, orphan records compromise the *referential integrity* of the database.) This section explains how to use Biota’s search tools for finding and displaying orphan and childless records.

Finding Childless Records

1. From the Find menu, select “Find Childless Records.” A table selection window appears.
2. Using the mouse, select a parent table from the popup list. The Species table is being selected in the illustration below.



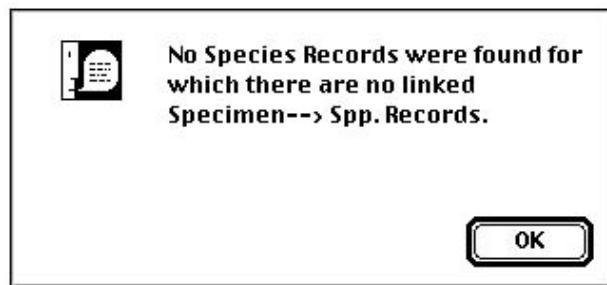
3. When the table has been selected, click the “Find” button in the table selection window to launch the search. The progress indicator appears during the search, which may be lengthy if there are many records in the tables.



You can click the “Cancel” button in the progress indicator at any time to halt the search.

Note: You can carry on other Biota tasks during the search, as long as you do not edit records, delete records, or add new records to either of the two tables involved in the search.

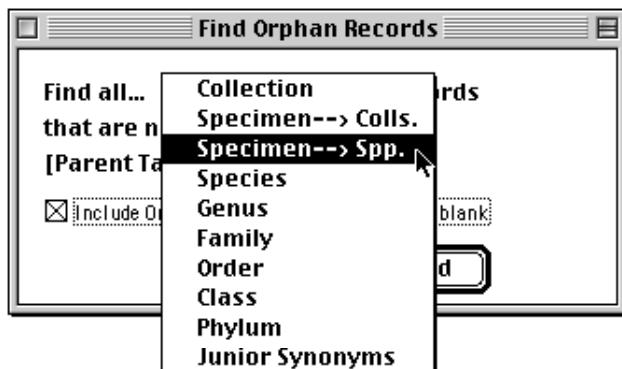
- If no childless records are found, Biota displays a message like the one below.



- If one or more childless records are found, Biota displays the records in the standard Record Listing screen for the parent table, where you can work with them using all the techniques outlined in Chapter 10, "[Working With Records in Record Listing and Input Screens](#)."

Finding Orphan Records

1. From the Find menu, select Find Orphan Records. A table selection window appears.
2. Using the mouse, select a child table from the popup list. The Specimen table, with the Species table as parent, is being selected in the illustration below.



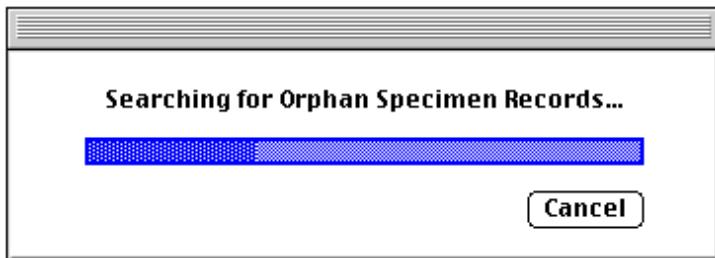
Notice that the popup includes two options for the Specimen table, since it is a child of both the Species and the Collection tables. A Specimen record can be an orphan of either table or of both.

Note: For information on finding Orphan Junior Synonyms, see "[Finding Orphan Junior Synonym Records](#)" in Chapter 23.

3. To limit the search to child records that have an entry in the linking field, uncheck the checkbox in the table selection window. (By default all Orphan records are included in the search, even those with no entry in the linking field.) If you uncheck the checkbox, the search will gather only those child records for which the (nonblank) entry in the relating field matches no Key value (see the section “[Key Fields](#)” in Chapter 3) in the parent table.



4. Click the “Find” button in the table selection window to launch the search. The progress indicator appears during the search, which may be lengthy if there are many records in the tables.



You can click the “Cancel” button in the progress indicator at any time to halt the search.

NOTE: You can carry on other Biota tasks during the search, as long as you do not edit records, delete records, or add new records to either of the two tables involved in the search.

- If no orphan records are found, Biota displays a message like the one below.



- If one or more orphan records are found, Biota displays the records in the standard Record Listing screen for the child table, where you can work with them using all the techniques outlined in Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”

Automatically Updating Child Records by Changing a Parent Record

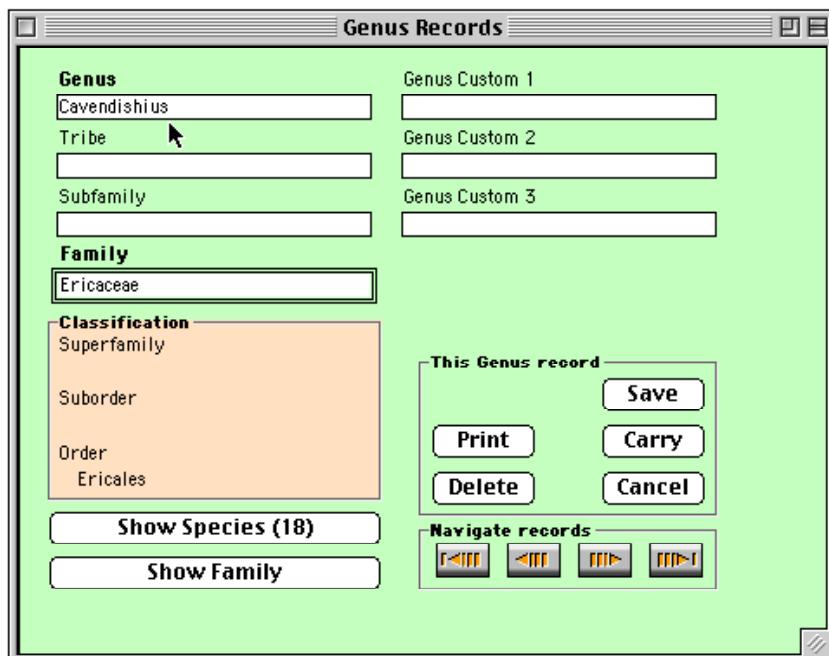
Sometimes, you need to change the Key field in a record (for background see “[Key Fields](#)” in Chapter 3). For example, you may discover that a Genus name is misspelled in your database, or perhaps the name of a Genus is changed for nomenclatural reasons and you want to update the record. If the Genus record to be changed has any linked Species records, however, the new version of the generic name must also replace the old version in the [Species] Genus linking field. Otherwise, the Species records will be orphaned (they will no longer be linked to any Genus record).

Biota takes care of updating child records for you. If you confirm the change, Biota updates the relating field in all child records when you change the value in the Key field of the parent record. This feature applies to all relations between Core tables. In contrast, updates of relating values in child tables are made automatically, without confirmation, when the child table is a Peripheral table (for example, Images, Notes, Determination History, and Auxiliary Field Value tables). (See “[Peripheral Tables](#)” in Chapter 3.)

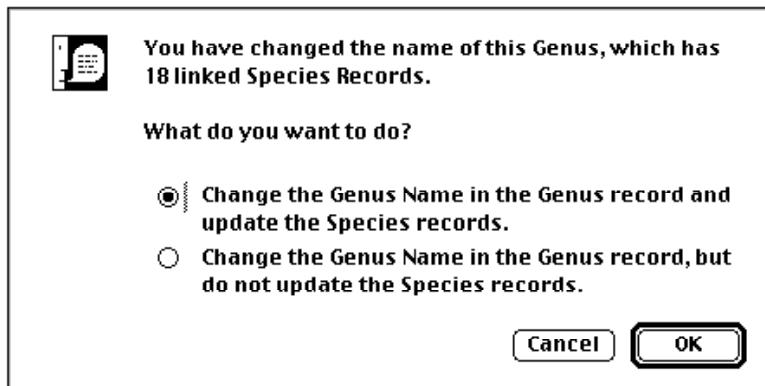
Updating All Child Records by Changing a Parent Record

To illustrate, suppose you need to correct the misspelled genus name “*Cavendishius*” to *Cavendishia*.

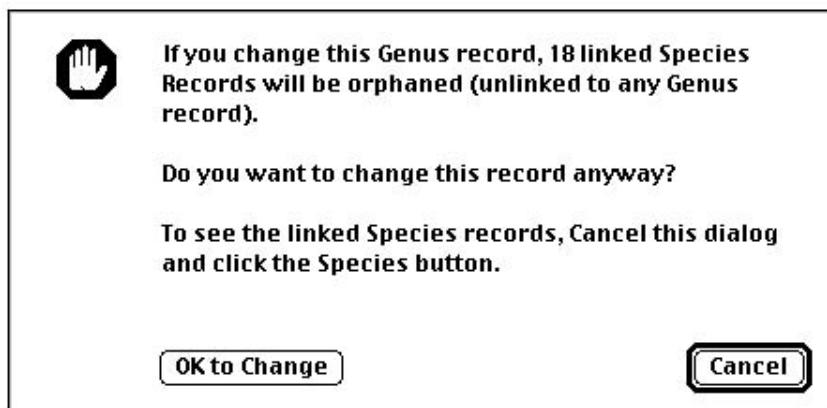
1. Find the parent record to be changed and display it in the Input screen for the parent table.



2. **Edit the Key field, then click the “Save” button** in the Input screen to register the changes. If the record is linked to child records, Biota offers two options, explained in the screen below.



- If you choose to update the child records** (the default option), all relating fields in linked child records are updated to match the change in the parent record Key field.
- If you choose to change the Key field in the parent record without updating the relating field in the child records** (the second option), Biota offers you another chance to change your mind.



As suggested in the warning above, if you want to take a look at the child records that will be orphaned before severing their link with the parent record, click the “Cancel” button in the warning screen above. Then use the Child Records button (see “[Displaying Records with a Child Records Button](#)” in Chapter 10)—the “Show Species” button in the Genus Input screen illustrated in Step 1—to display the child records in a separate window.

NOTE: If the Determination History system has been enabled (see Chapter 22, “[Determination Histories](#)”), and you change a Genus name in the Genus table, Biota also posts a message warning that the Genus change will create a new Determination History record. This message appears only for the Genus table.



“Splitting” a Taxon: Linking a Subset of the Child Records to a New Parent Record

If you need to “split” a taxon, leaving some child records linked to an existing parent record (an old name) while reassigning other child records to a new parent record, you can speed the process and avoid errors by using the following procedure:

1. **Display all child records for the *old* parent record**, using the Child Records button (see “[Displaying Records with a Child Records Button](#)” in Chapter 10).
2. **Create a Sub-Selection of the child records to be assigned to the *new* parent record** (see the section “[Creating a Sub-Selection of Records](#)” in Chapter 10).
3. **Declare the Sub-Selection a Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
4. **Change the linking field in the child table Record Set to the new parent record name** using the Find and Replace tool (see “[Updating Records Using the Find and Replace Tool](#)” later in this chapter).
5. **Create the new parent record**.
6. **Click the Child Record button in the new parent record** to check the new links.

Updating Records Using the Find and Replace Tool

The Find and Replace tool (in the Special menu) is a powerful—and therefore dangerous—utility for correcting errors or updating records in any table in the Biota structure. Not only Core tables but Peripheral tables can be accessed with this tool. The search can be restricted to the records of a current Record Set (for tables that have them) or limited to a selection of records you find using the Query Editor (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” earlier in this chapter), or the search can encompass all records in a table.

Because of the potential for massive changes in your Data File, this tool can be used only by a user with Administration access privileges, if you have enabled Biota’s user password system (see Chapter 26, “[Security: Passwords and Access Privileges](#)”). If you have not enabled the user password system, anyone can use this tool. In any case, be sure you understand how it works and *be sure to make a backup copy of your Data File before you use the tool, just in case* (see Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#)”).

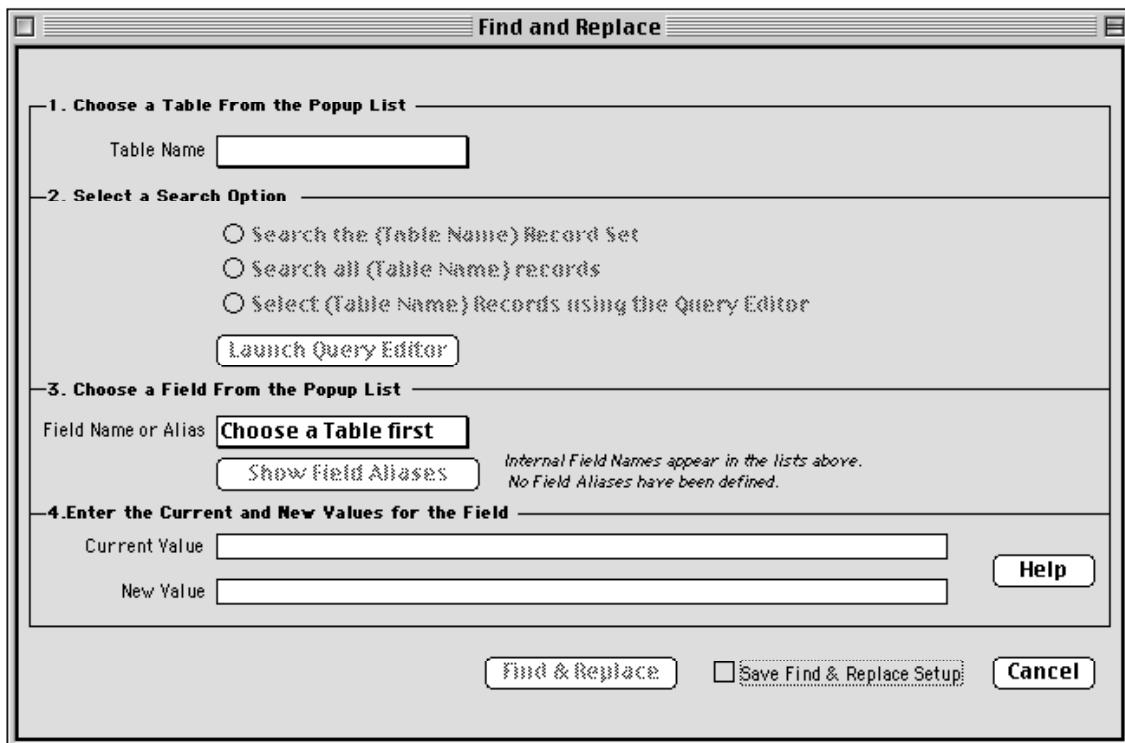
WARNING: Changes made with this tool cannot be undone, except by using the tool in reverse to change records back to their previous values.

The Find and Replace tool searches for and replaces field values in one field at a time. Like the Replace command in a text processing application, the Biota tool looks for a “current value” that you specify. When Biota finds the current value in a record, it replaces it with the “new value” that you specify.

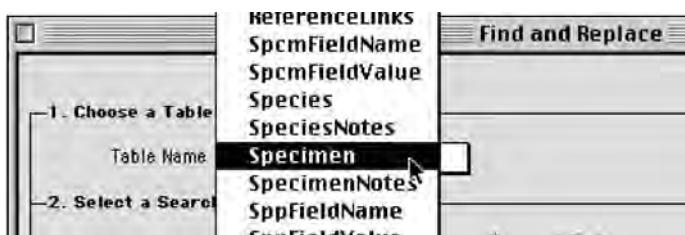
Using the Find and Replace Tool: Step by Step

In the example below, suppose that a botanist has replaced the fluid in which 23 plant specimens are stored, and he or she needs to update the Specimen records to reflect the change. The entry “FAA” (for formalin and acetic acid) will be replaced by the entry “90% Ethanol” in the “Medium” field of the Specimen table, in all records in which “FAA” currently appears in the active Specimen Record Set.

1. **Create a Record Set for the records to be searched, if necessary.**
 - **If you want to restrict the search to certain records** in a Core table or the Determination History table, create a Record Set for the records to be changed (see “[Core Tables](#)” in Chapter 3; see “[Displaying, Editing, or Deleting Determination History Records](#)” in Chapter 22).
 - **If you want the search to encompass all records in a table, or the table does not support Record Sets** (among Peripheral tables, only the Determination History table supports Record Sets), proceed to Step 2.
 - **If you want to use the Query Editor** to find the records to be searched by the Search and Replace tool, proceed to Step 2.
2. **From the Special menu, choose Find & Replace.** The screen below appears.

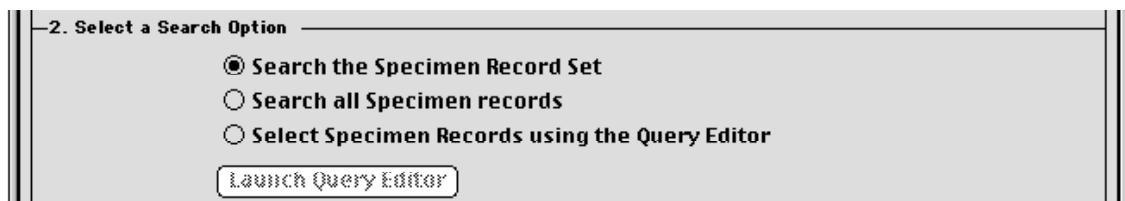


3. Choose a table from the popup list in the top panel. Table names are listed alphabetically.



The text of the search option button in the second panel is updated to reflect the choice of table. The field list in the third panel is created for the table you choose.

4. Select a search option from the second panel.



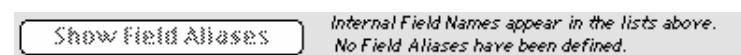
- The **Record Set option is enabled** only if the table you chose in Step 3 is a table that supports Record Sets and the current Record Set for the table is not empty. Otherwise, Biota posts a message highlighting the other two options in this panel.
- The “all records” option is always enabled and is the default when the Record Set option is unavailable (dimmed).
- The **Query Editor option is always enabled**. If you select it, the “Launch Query Editor” button is enabled. If you click the button, the Query Editor is displayed for selecting records for the Find and Replace operation. (The Find and Replace tool will nonetheless replace values only in records in which the Current Value matches, not in *all* records found by the Query Editor.) See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#),” earlier in this chapter, if you need help using the Query Editor.

5. Choose a field from the popup list in the third panel. Field names are listed alphabetically.

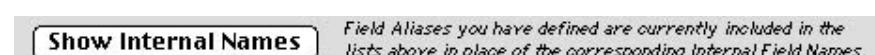


6. **Using the “Field Name/Alias” Button.** The button below the field name popup list controls whether Biota lists strictly Internal Field Names (as given in Appendix A) or substitutes a Field Alias for the corresponding Internal Field Name for each field you have given an Alias. (See Chapter 18, “[Renaming Fields](#).”)

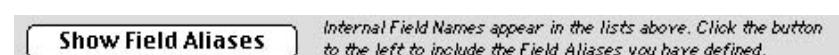
- **If no Aliases have been defined,** the button is disabled. The caption to the right of the button reads “Internal Field Names appear in the lists above. No Field Aliases have been defined.”



- **If any Aliases have been defined,** when you first open the Find and Replace screen, the button is enabled and reads “Show Internal Names.” The caption to the right of the button reads “Field Aliases you have defined are currently included in the lists above in place of the corresponding Internal Field Names.”



- **If you click the “Show Internal Names” button,** the button text changes to “Show Field Aliases” and the caption reads “Internal Field Names appear in the lists above. Click the button to the left to include the Field Aliases you have defined.”



7. **Enter the Current Value to be replaced and press the TAB key.** In the illustration below, “FAA” has been entered as the Current Value to be found.

Biota now searches in the field you selected in Step 5, within the selection of records indicated in Step 4, for records with the Current Value. In the example, Biota looks for “FAA” in the Medium field of the Specimen records in the current Specimen Record Set.

4. Enter the Current and New Values for the Field

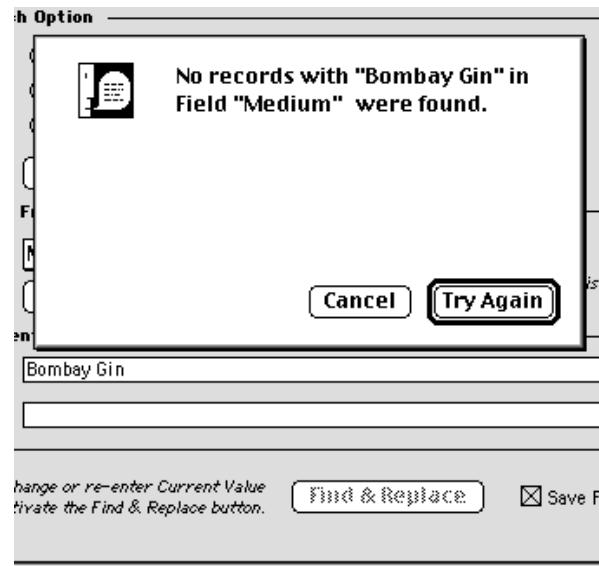
Current Value

New Value

Help

- If no records are found that meet these criteria, a message like the one at the right appears, and the “Find & Replace” button remains disabled.

If you click the “Try Again” button in the message window, the Current Value entry area is cleared for a new value. If you click the “Cancel” button, the Find and Replace screen is dismissed.



- If records are found that meet the criteria, the “Find & Replace” button is enabled and the cursor moves to the New Value entry area.

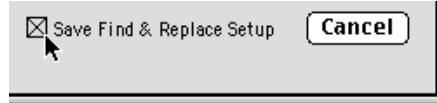
NOTE: For Alphanumeric or Text fields (only), you can use the wildcard character, @, in the Current Value entry area. For example, entering *B@* finds all records (among those you have designated) that have a value beginning with the letter *b* (either lower or uppercase) for the field indicated in Step 5. Entering *Ba@* finds values that begin with *Ba*, and so on. If you enter only the wildcard character @, all values for the field are found.

The wildcard character, @, cannot be used to search in Numeric (Integer or Real Number), Date fields, or Boolean fields. See Appendix A, “[Biota Tables, Fields, and Relational Links](#),” if you are uncertain of the field type for a field you want to search. If you want to replace all values in a Numeric, Date, or Boolean field (or for that matter, in an Alphanumeric or Text field), you can use the Import Editor to update them (see the next section, “[Updating Records Using the Import Editor](#)”).

- Enter the New Value to be substituted for the Current Value and press the TAB key. In the illustration here, “90% Ethanol” has been entered as the New Value to be substituted for “FAA.”

Note: If you leave the New Value field blank, the Current Value is replaced with a blank entry in each record found.

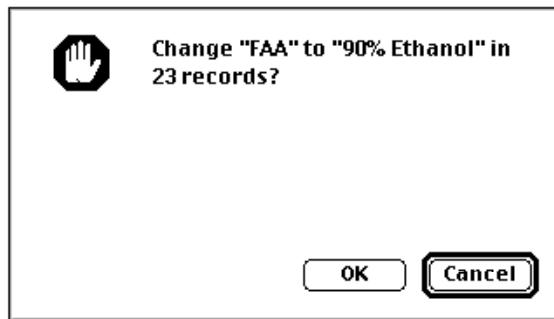
9. If you want to save the Find and Replace setup, click the checkbox.



10. Click the “Find & Replace” button to launch the search and replacement process. Biota asks you to confirm the proposed changes.

Notice that the default button is “Cancel,” for safety’s sake.

The changed records are displayed in the standard Record Listing screen for their table.

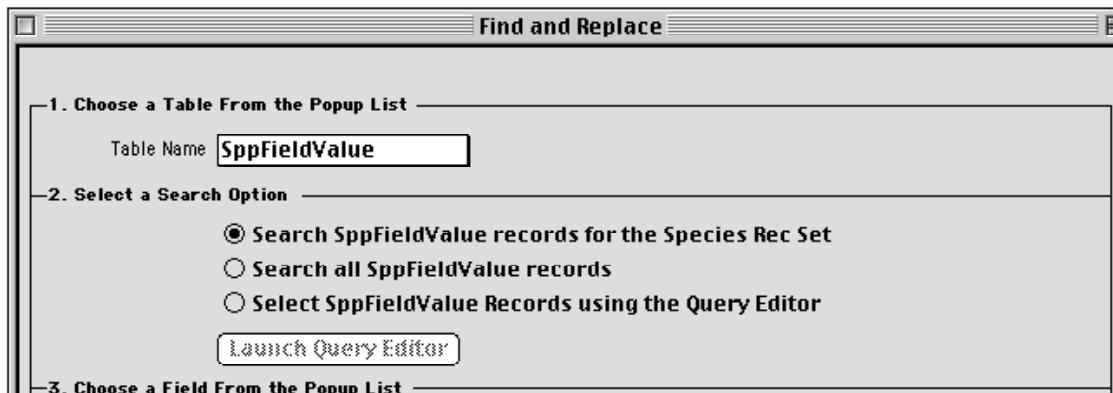


Using the Find and Replace Tool for Auxiliary Fields and Notes Tables

The example in the previous section, “[Using the Find and Replace Tool: Step by Step](#)” focused on replacing values in a field from a Core table. You can also use the Find and Replace tool to change field values in Peripheral tables. Because Biota does not support Record Sets for Peripheral tables (with the exception of the Determination History table), you must define the scope of certain key Peripheral tables in terms of the Parent table Record Set.

These tables are the Notes tables (Species Notes, Specimen Notes, Collection Notes, Locality Notes, or Loans Notes tables) and the Auxiliary Field Value tables (Species Field Value, Specimen Field Value, Collection Field Value, or Locality Field Value tables).

If you need to “Find and Replace” values in a Notes table or an Auxiliary Field Value table, and the parent table currently has a Record Set designated, the Find and Replace tool automatically offers the option of searching and replacing values in the child records (Notes or Auxiliary Field Value records) that are linked to the parent table Record Set.



Suppose, for example, that you have created Species Auxiliary Fields named “Leaf Shape” and “Bract Shape.” You could instruct the Search and Replace tool to replace the value “Pointed” with the value “Acuminate” each time it occurs in a Species Field Value record linked to any record in the current Species Record Set. Each occurrence of “Pointed” in a Species Field Value record linked to any record in the active Species Record Set will be changed to “Acuminate,” whether the value occurs in the “Leaf Shape” or the “Bract Shape” Auxiliary Field.

Updating Records Using the Import Editor

By selecting the “Update existing records” option in the Import Editor (the “Import by Tables and Fields” tool in the Special menu), you can use the Import Editor to update fields in existing records in a Biota data file (see Chapter 28, “[Importing Data](#)”).



The Import Editor can update data in any Biota table using input from free-format, delimited text (ASCII) files, such as the column-by-row text files you can create with a spreadsheet application or export as text flatfiles from database management applications.

There is no search for “current values” when you use the Import Editor to update records. When you use the Import Editor to update a record in a Core table, Biota matches the Key field in the text file with the Key field in the existing Biota record, then replaces field values in the existing record with the corresponding values from the text file record, *regardless* of field values.

The complete process is described in detail in Chapter 28, “[Importing Data by Tables and Fields](#),” which you should consult before attempting to update records with the Import Editor.

Chapter 13

Creating, Finding, and Updating Specimen Series

Biota's origin as a data management system for a biodiversity inventory involving large numbers of new specimens (see the “[Preface](#)”) is nowhere more apparent than in the tools of the Series menu. The “industrial strength” Series tools are designed to carry out several kinds of repetitive operations on groups of Specimen records, with an absolute minimum of human effort.

The Series menu offers four special tools for efficient entry, updating, and retrieval of groups of Specimen records. Although all four tools can be used efficiently with manual Specimen Code entry, they are optimized for use of Specimen barcodes (see “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” in Chapter 8 and Appendix K, “[Barcodes](#)”).

Series	Find	Display	Labels
Input Specimen Series			
Input & Identify Spcm Series			

Find	Specimen Series
Find Specimen Series	Find & Identify Spcm Series

- **Input Specimen Series** creates groups of *new* Specimen records—with consecutive Specimen Codes—that share the same Collection data.
- **Input and Identify Specimen Series** creates groups of *new* Specimen records—with consecutive Specimen Codes—that share the same Collection data, the same identification data (Species Code and determination information), or both collection and identification data.
- **Find Specimen Series** (also in the Find menu as “By Specimen Code Series”) finds groups of *existing* Specimen records. The Specimen Codes for these records can be consecutive or in random order.
- **Find and Identify Specimen Series** finds groups of *existing* Specimen records and adds identification data (Species Code and determination information) and/or updates other Specimen fields (Stage/Sex, Storage, Type Status) in these records. The Specimen Codes for these records can be consecutive or in random order.

NOTE: In spite of the verb “Identify” in the name of this tool, implying the addition or updating a Species Code link, the “Find and Identify Specimen Series” tool serves as a general-purpose updating tool for virtually any field or fields in groups of Specimen records.

Using the “Input Specimen Series” and “Input and Identify Specimen Series” Tools

In the field collection of specimens, it is common for a group of specimens to be collected in the same “collecting event”—from the same site, quadrat, trap, trawl, extraction, host, or modular organism—on the same day by the same collector(s). In the Biota data model (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”), the Specimen records for such a group of specimens share the same Collection Code, uniquely identifying a single Collection record that shows the details of the collecting event.

In some situations, a group of new specimens not only share the same Collection Code, but also have been identified as representatives of the same species (or infraspecific entity)—and thus require the same Species Code in their Specimen records.

It is certainly possible to create individual Specimen records for each specimen in a group in either of these situations using the ordinary Specimen Input screen (see “[Specimen Input](#)” in Chapter 11), accelerated by using the “Carry” button (see “[Duplicating a Record Displayed in the Input Screen Using the ‘Carry’ button](#)” in Chapter 10), but Biota offers a much more efficient way to do the job.

With the “Input Specimen Series” tool, you set up the Input screen, shown below, by entering the first and last of a series of consecutive Specimen Codes for a group of records, plus the Collection, preparation, and related data that the Specimen records share. Biota then creates all the records automatically when you are ready.

The “Input and Identify Specimen Series” tool, shown on the next page, is identical to the Input Specimen Series tool above, except for the addition of the Species Code and Determination input areas, familiar from the standard Specimen Input screen.

NOTE: Using the “Input and Identify Specimen Series” tool without entering a Species Code or determination information is exactly equivalent to using the “Input Specimen Series” tool for the same information. The latter is simply a subset of the former.

Input and Identify Specimen Series

Primary Fields		Other Fields
Specimen Code Series First Specimen Code <input type="text"/> Last Specimen Code <input type="text"/> Last Code used <input type="text"/> <input type="checkbox"/> Prefix		
Species Code <input type="text"/> Assign Look Up Species Show Species Record		
Genus	Species	Family
Collection Code <input type="text"/> Assign Look Up Collection Show Collection Record		
Coll. By	Date	Locality
Prepared By <input type="text"/> <input type="checkbox"/> Date Prepared <input type="text"/> Mo: 0 Dy: 0 Yr: 00 Today Last Determined by <input type="text"/> <input type="checkbox"/> Date Last Determined <input type="text"/> Mo: 0 Dy: 0 Yr: 00 Today		
Stage/Sex <input type="text"/> DBH <input type="text"/> Storage <input type="text"/>		Records Created on Aug 30, 2002 Next Specimen Sequence Number 1726
Record Series <input type="button" value="Save"/> <input type="button" value="Carry"/> <input type="button" value="Cancel"/>		

Specimen Series Input: Step by Step

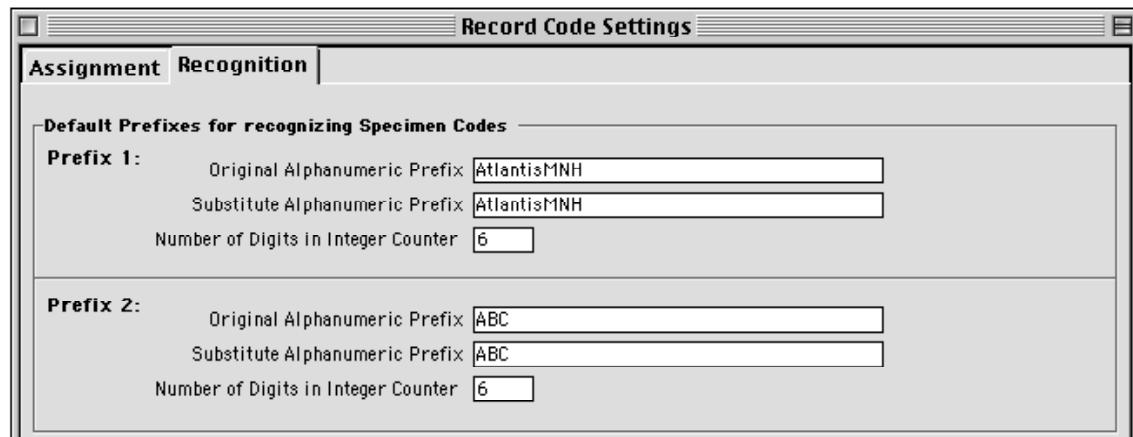
Before using these tools, you should read “[Specimen Input](#),” in Chapter 11, and Chapter 8, “[Record Codes](#),” especially “[Using Alphanumeric Specimen Codes With the Series Tools](#).”

1. From the Special menu, select “Record Code Prefixes” to confirm that the Specimen Code settings are correct (see “[Setting Up for Automatic Record Code Prefix Recognition](#)” in Chapter 8).
 - In the Assignment tab, check that the Specimen settings are correct. These settings control the number of digits that the “Series Input” tools generate for new Specimen Codes. The settings also specify the “Alphanumeric Prefix” for these codes, if you use the “Default Prefix” approach (see “[Assigning New Record Codes Using an ‘Assign’ Button: Step by Step](#)” in Chapter 8).

Record Code Settings

Assignment		Recognition
Default Prefixes and Integer Counters for assigning new Record Codes		
Alphanumeric Prefix <input type="text"/> Next value of Integer Counter <input type="text"/> Number of digits <input type="text"/> Specimen Codes <input type="text"/> 000000 <input type="checkbox"/> User-Defined Counter <input type="checkbox"/> Assign Code without asking		

- In the Recognition tab, check that the “Alphanumeric Prefix” (both “Original” and “Substitute,” which are normally identical) and the “Number of Digits in Integer Counter” settings match the values for your barcodes. (Note that two different barcode prefixes and counter settings can be recognized.)



The same settings specify the prefixes and number of digits the “Find Specimen Series” tools expect for recognizing existing Specimen Codes. See the next section, [“Finding \(or Finding and Identifying\) Specimen Series: First Steps.”](#)

NOTE: The settings in the “Record Code Settings” screen for tables other than Specimen are irrelevant to the operation of the Series tools.

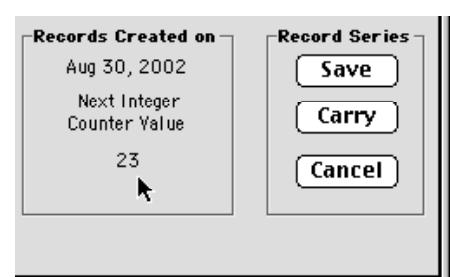
2. Click the “Save” Button in the “Record Code Prefixes” screen to record any changes and dismiss the screen.
3. From the Series menu, choose Input Specimen Series or Input and Identify Specimen Series. The Input screen appears (screens for both commands are illustrated in the previous section, [“Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series’ Tools”](#)).



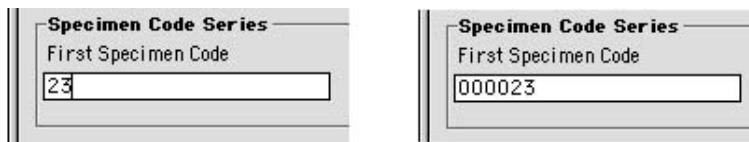
4. In the Specimen Code Series panel:

- Either: In the “First Specimen Code” entry area, manually enter the Integer Counter for the numerically lowest Specimen Code in the series for which you want to create Specimen records, then press the TAB key.

To begin the Specimen Series with the next Integer Counter available (as specified in the Record Code Settings screen, Special menu), use the “Next Integer Counter Value” displayed in the “Records Created on” panel at the lower right of the Series input screen.

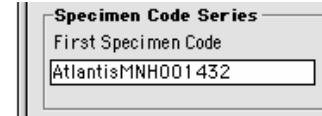


NOTE: If the counter has any leading zeros, omit them (left illustration, below). Biota prefixes leading zeros (right illustration, below), if necessary, to complete the number of digits you specified in the Record Code Prefixes screen. (If you enter leading zeros in the “First Specimen Code” or “Last Specimen Code” entry areas, Biota posts an error message.)



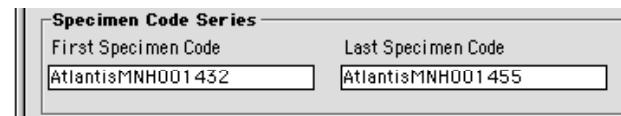
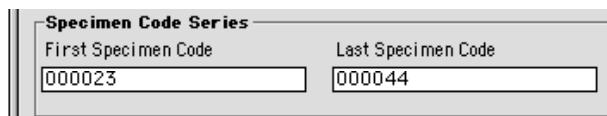
Do not enter any alphabetic characters in these entry areas. If you do, Biota posts an error message.

- **Or: Read in the barcode for the “First Specimen Code” in the series for which you want to create Specimen records. Then press the TAB key if your barcode reader is not set to enter an end-of-line character automatically.**

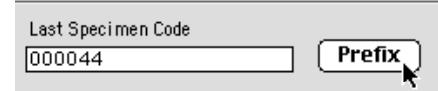


If the alphanumeric prefix correctly matches the barcode prefix setting in the “Recognition” tab of the “Record Code Prefixes” screen, Biota accepts the barcode. Otherwise, you will see the alphabetic character error message mentioned in the Note above.

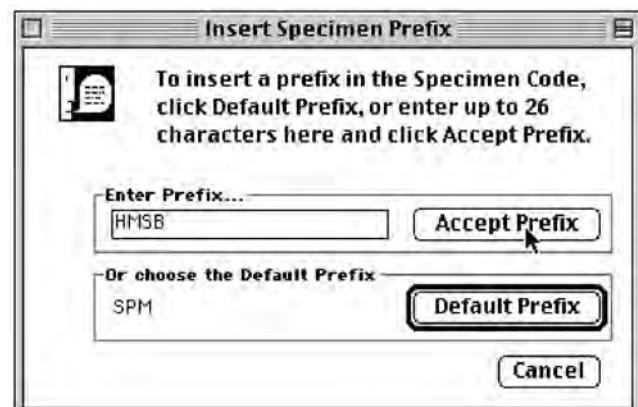
5. In the “Specimen Code Series” panel, repeat step 3 for the “Last Specimen Code” entry area. If there is only one specimen in the series, you can skip this step. (Integer Counter entry is illustrated on the left, barcode entry on the right, below.)



6. If you entered an Integer Counter manually, and wish to insert a Specimen Code Prefix to complete the Specimen Codes, click the “Prefix” button. (If you entered a barcode, the “Prefix” button has no effect.)



The Insert Specimen Prefix window appears.



7. In the Prefix window:

- **Either:** Enter an ad hoc prefix in the **Enter Prefix area** (in the illustration above, the prefix **HMSB** has been entered) and click the “Accept Prefix” button.
- **Or:** Click the “Default Prefix” button to enter the prefix displayed next to the button (**SPM** in the illustration; see Step 1 to change the default prefix). Biota completes the “First Specimen Code” and “Last Specimen Code” entries by inserting the prefix.

Specimen Code Series	
First Specimen Code	Last Specimen Code
HMSB000023	HMSB000044

NOTE: If you prefer, you can use the “Prefix” button to set a prefix first, then enter the Integer Counters for the First and Last Specimen Codes. In this case, the codes are completed as you enter them.

8. Enter links to Parent tables:

- **“Input Specimen Series” tool.** Complete the Collection Code link, following instructions at Step 3 in the section [“Specimen Input”](#) in Chapter 11.
- **“Input and Identify Specimen Series” tool.** Complete the Species Code and Collection Code links, following instructions in [Steps 2 and 3 of the section “Specimen Input”](#) in Chapter 11.

9. Enter data for “Stage/Sex,” “Medium,” “Storage,” “Deposited,” “Specimen Custom 1,” “Specimen Custom 2,” and “Type Status,” following the instructions for the standard Specimen Input screen (see [“Specimen Input”](#) in Chapter 11). Notice that some of these fields in the “Input Series” tools are on a second tab, “Other Fields.”

All records in the range of codes you specified in the “Specimen Code Series” panel will include the entries you make on either tab.

You can set any of the following options for each of these seven Specimen fields:

- **Aliases.** Each field can be renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, [“Renaming Fields”](#)).
- **Field Value Defaults.** You can ask Biota to enter a particular value in each new record automatically using the “Field Value Defaults” tool from the Special menu (see [“Setting Default Entries: Field Value Defaults”](#) in Chapter 17).
- **Entry Choice Lists.** You can enable an Entry Choice List (pick list) for each field using the “Entry Choice Lists” tool in the Special menu (see [“Using Entry Choice Lists”](#) in Chapter 17).

Input and Identify Spec	
Primary Fields	Other Fields
Deposited	<input type="text"/>
Specimen Custom 1	<input type="text"/>
Specimen Custom 2	<input type="text"/>
Type Status	<input type="text"/>
Abundance	<input type="text"/> 1

NOTE: The “Deposited” field in the Specimen table is used by the Specimen Loans system in Biota. If you intend to use the Loans system do not use this field for another purpose. See Chapter 21, “[Specimen Loan System](#)” for details.

10. Click the Save or “Carry” button to create the series of Specimen records.
 - If you use the “Carry” button, all entries except for the “First Specimen Code” and “Last Specimen Code” are carried forward. You can edit entries in any field, if necessary, for the next series.
 - If the records were created successfully, the “Last Code Used” display area (below) now shows the former “Last Specimen Code” entry, to guide your input for the next series. The Sequence Number display (step 4) is updated.
 - If you have requested the creation of more than 20 records, a confirmation screen appears.
 - If the password system has been enabled (see Chapter 26, “[Security: Passwords and Access Privileges](#)”) and you have requested the creation of more records than the limit set in the “Admin Settings” tab of the Preferences screen (Special menu; illustrated here), a message appears explaining that you cannot complete the action. (A user with administration access privileges can change the limit. See “[The ‘Admin Settings’ Tab](#)” in Appendix B.)
11. Create additional series of records if you wish, following steps 4 through 9.
12. To examine the records created, click the “Cancel” Button in the Series Input screen. The series you have created appear in a special version of the Specimen Record Listing screen. In place of the standard “Add Specimen” button, an “Add New Series” button is present.
13. To create another series of Specimen records, click the “Add New Series” button (above). An option screen appears.
 

You can choose to carry forward all entries except the First and Last Specimen Code entries (exactly the equivalent of having clicked the “Carry” button after the last series you created), or start fresh.
14. Select an option and click OK. The Specimen Series Input screen you were using before reappears.

15. When you are finished creating series, click the “Done” Button in the Record Listing screen to present the standard Record Set option screen (see “[The Record Set Options Screen](#)” in Chapter 3).

Using the “Find Specimen Series” and “Find and Identify Specimen Series” Tools

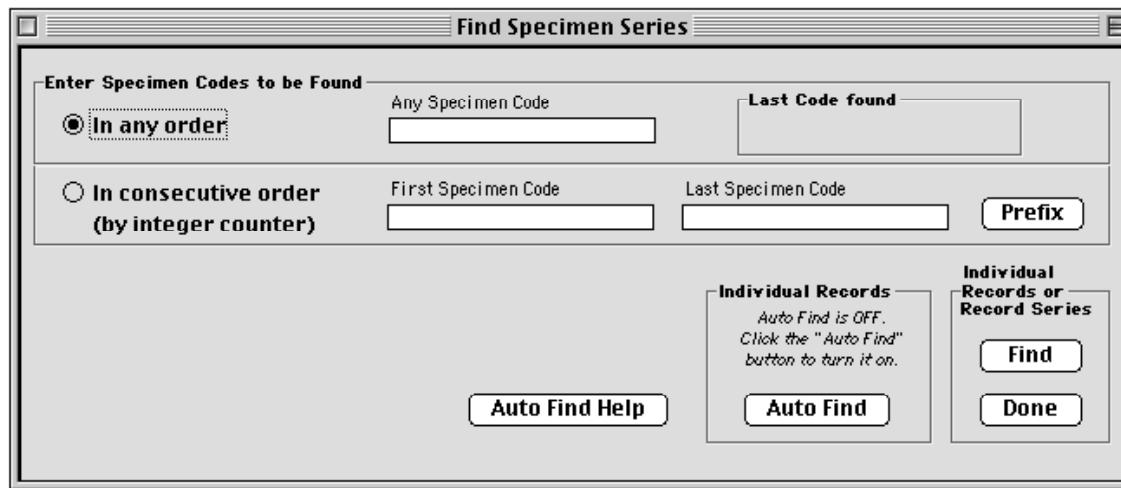
The tools of the Find menu offer many ways to find existing records, based on their content or their linkage to other records, and several ways to update records if necessary, once found (Chapter 12, “[Finding and Updating Records](#)”). The “Find Specimen Series” and “Find and Identify Specimen Series” tools have the specialized purposes of finding Specimen records based strictly on Specimen Code and updating the records found, if you wish.

Specimen Codes may be entered in any order. Neither tool requires that Specimen Codes be sequential, although they may be.

These two tools share a common interface for entering individual Specimen Codes or Specimen Code series.

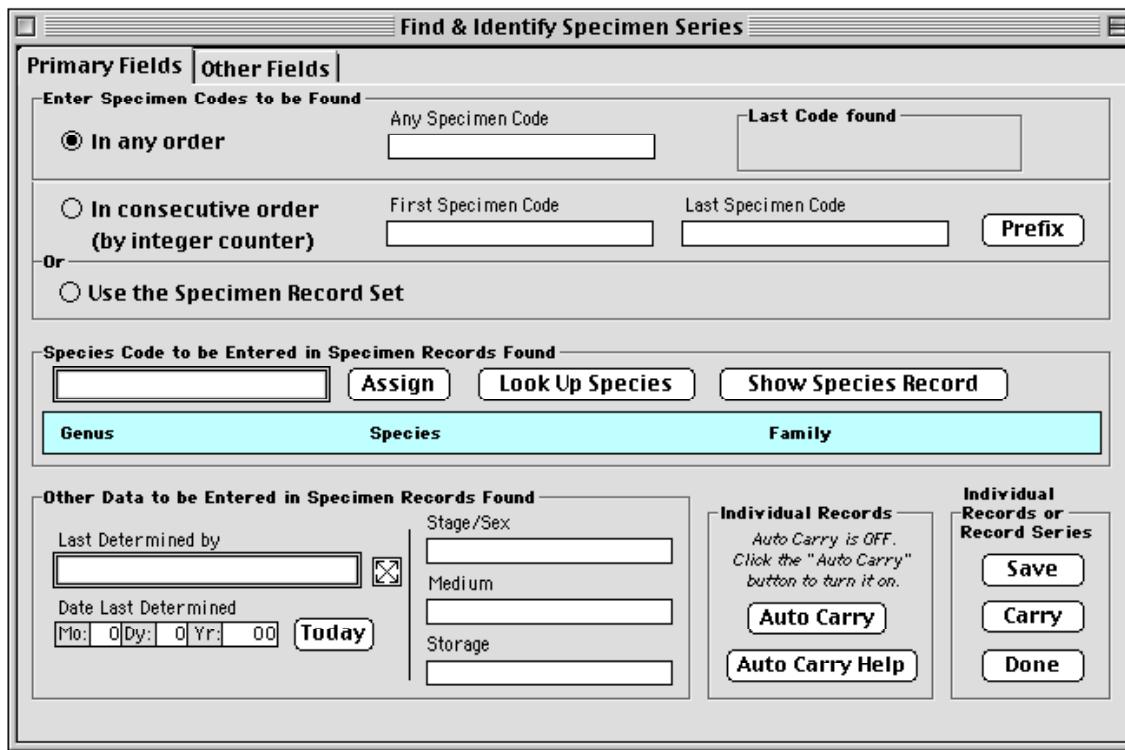
The “Find Specimen Series” tool (below) simply finds a group of Specimen records, based on Specimen Code. One common use for the tool is to gather Specimen records into a Record Set to record those specimens as a Specimen Loan or to record their return from an existing Specimen loan. (The “New Loan” screen has additional tools for gathering Specimen records to record a new loan.) See Chapter 21, “[Specimen Loan System](#)”.

Series	Find	Display	Labels
Input Specimen Series			
Input & Identify Spcm Series			
Find Specimen Series			
	Find & Identify Spcm Series		



In addition to finding Specimen records based on Specimen Code, the “Find and Identify Specimen Series tool” (next page) automatically updates the Species Code and other fields you specify, in all records found.

NOTE: In spite of the verb “Identify” in the name of this tool, implying the addition or updating a Species Code link, the “Find and Identify Specimen Series” tool serves as a general-purpose updating tool for virtually any field or fields in groups of Specimen records.



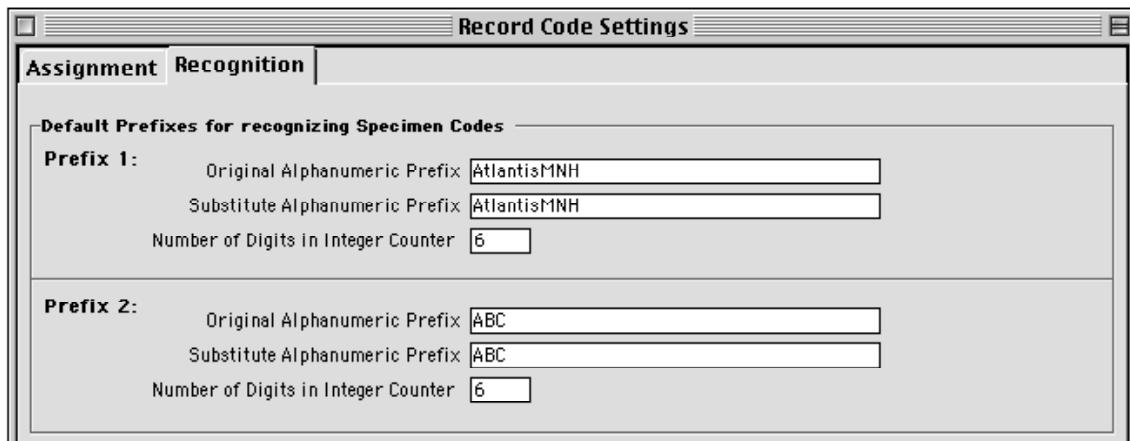
This tool is ideal for efficiently updating information in groups of existing Specimen records, whether or not their Specimen Codes are numerically sequential. Some common uses include:

- **Recording or changing the determination data** (Species Code, Last Determined By, Date of Determination) in the records for a group of specimens that have been determined to represent the same species (whether named or not).
- **Recording or changing “Stage/Sex,” “Storage,” or “Type Status” data** for a group of records. For example, the “Storage” field could be updated for a group of duplicate specimens or vouchers that have been moved to an auxiliary storage location. The “Type Status” field could be updated when a type series is designated. All three of these fields can be renamed for other uses. (See Chapter 18, “[Renaming Fields.](#)”)

Finding (or Finding and Identifying) Specimen Series: First Steps

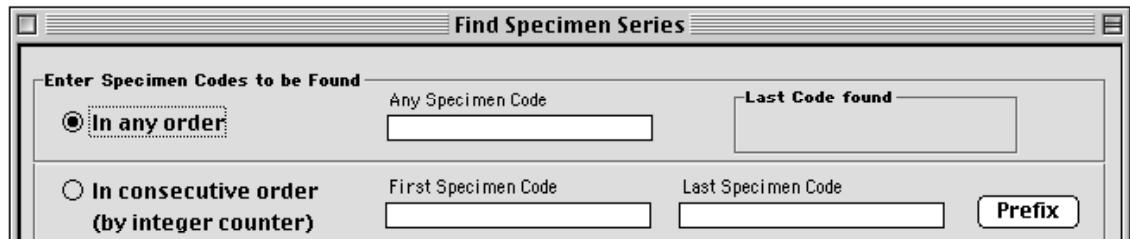
Before using these tools, you should read “[Specimen Input](#),” in Chapter 11, and Chapter 8, “[Record Codes](#),” especially “[Using Alphanumeric Specimen Codes With the Series Tools](#).”

1. **From the Special menu, select “Record Code Prefixes,” and click the “Recognition” tab** to confirm that the Specimen Code recognition settings are correct (illustrated on the next page). These settings specify the prefixes and number of digits the “Find Specimen Series” tools expect for recognizing existing Specimen Codes. check that the “Alphanumeric Prefix” (both “Original” and “Substitute,” which are normally identical) and the “Number of Digits in Integer Counter” settings match the values for your barcodes. (Note that two different barcode prefixes and counter settings can be recognized.)



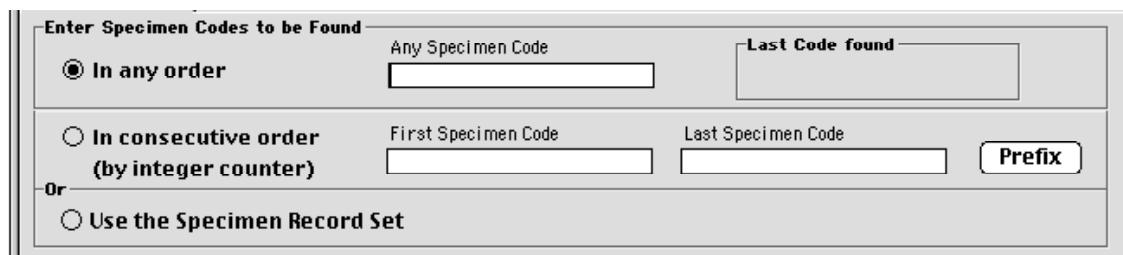
Note: The settings in the “Assignment” tab and the settings for Species Codes in the “Recognition” tab are irrelevant to the operation of the “Find Specimen Series” tools.

2. Click the “Save” Button in the “Record Code Prefixes” screen to record any changes and dismiss the screen.
 3. From the Series menu, choose “Find Specimen Series” or “Find and Identify Specimen Series.” The Input screen appears (full screens for both commands are illustrated in the previous section, [“Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools”](#)).
- In “Find Specimen Series”: Choose a search option in the upper panel, labeled “Enter Specimen Codes to be Found.”



- ◊ **Option 1: “In any order.”** With this option selected, you enter complete Specimen Codes, in any order. Continue with steps in the next section of this chapter, [“If You Choose ‘In Any Order.’”](#)
- ◊ **Option 2: “In consecutive order.”** If you select this option, you enter the Integer Counter portion of the “First Specimen Code” and “Last Specimen Code” of a consecutive series, then add a Prefix if necessary. Continue with the section [“If You Choose ‘In Consecutive Order.’”](#) later in this chapter.

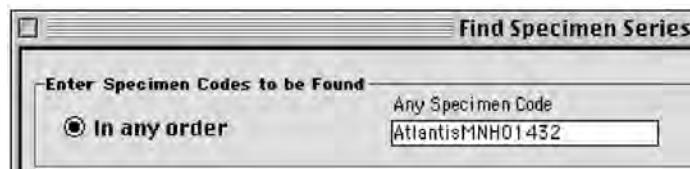
- In “Find and Identify Specimen Series”: Choose a search option in the upper panel, labeled “Enter Specimen Codes to be Found,” or select the third option, “Use the Specimen Record Set.”



- ◊ **Option 1: “In any order.”** With this option selected, you enter complete Specimen Codes, in any order. Continue with steps in the next section of this chapter, “[If You Choose ‘In Any Order.’](#)”
- ◊ **Option 2: “In consecutive order.”** If you select this option, you enter the Integer Counter portion of the “First Specimen Code” and “Last Specimen Code” of a consecutive series, then add a Prefix if necessary. Continue with the section “[If You Choose ‘In Consecutive Order.’](#)” later in this chapter.
- ◊ **Option 3: “Use the Specimen Record Set.”** To use this option, you must first have found the records to be updated and declared them the active Specimen Record Set. Continue with the section “[If You Choose ‘Use the Specimen Record Set’](#)”, later in this chapter.

If You Choose “In Any Order”

1. Enter a complete Specimen Code for an existing Specimen record, manually or using a barcode reader, in the “Any Specimen Code” entry area, illustrated here.
2. Press TAB. Biota searches immediately for the record.



NOTE: You need not press TAB if you are using a barcode reader that has been set to enter an end-of-line character (RETURN [Macintosh] or ENTER [Windows]) automatically after each read.

- **If the record is found,** the Specimen Code remains entered in the input area.
 - **If the record cannot be found,** an error message appears and the Specimen Code entry area is cleared.
3. If you are using the “Find and Identify Specimen Series” tool, complete as many of the remaining entries in the screen as you wish, following the instructions for the standard Specimen Input screen in the section “[Specimen Input](#)” in Chapter 11, with the following guidelines:

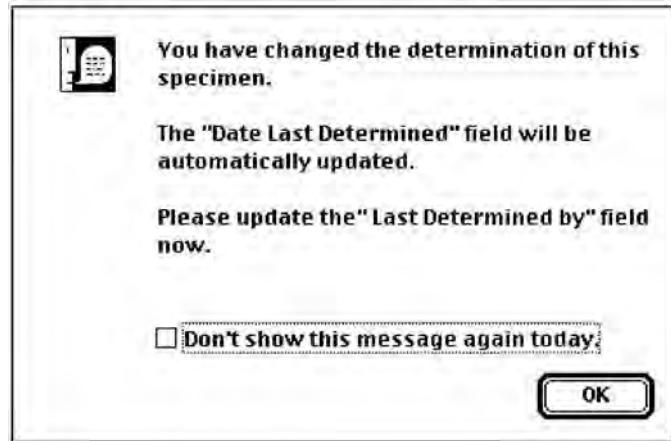
- Enter the Species Code link in the panel labeled “Species Code to be Entered in Specimen Records Found,” following instructions in [Step 2](#) of the section [“Specimen Input”](#) in Chapter 11.

Species Code to be Entered in Specimen Records Found

Assign Look Up Species Show Species Record

Genus Species Family

Once the link to a Species record is made, Biota posts the message on the right. If you enter a value for Species Code, then “Last Determined By” and “Date Last Determined” are required entries, to make sure that changes in determination can be tracked.



- Enter data for “Last Determined By,” “Date Last Determined” (if not already entered automatically), “Stage/Sex,” “Medium,” “Storage,” “Deposited,” “Specimen Custom 1,” “Specimen Custom 2,” and “Type Status,” following the instructions for the standard Specimen Input screen (see [“Specimen Input”](#) in Chapter 11). Notice that some of these fields in the “Find and Identify Specimen Series” tool are on a second tab, “Other Fields.”

Last Determined by

Date Last Determined

Mo: 0 Dy: 0 Yr: 00 Today

Stage/Sex

Medium

Storage

Find & Identify Specimen Series

Primary Fields Other Fields

Deposited

Specimen Custom 1

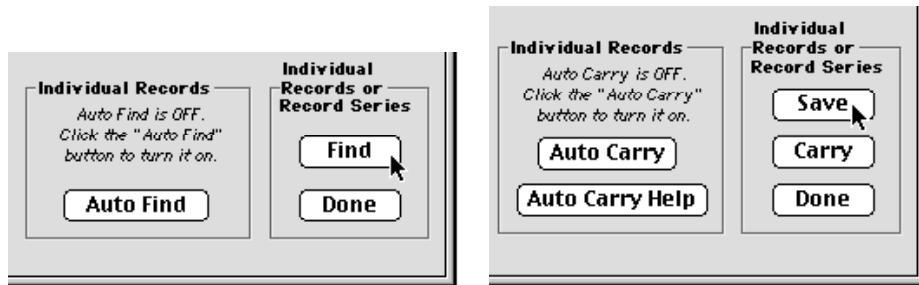
Specimen Custom 2

Type Status

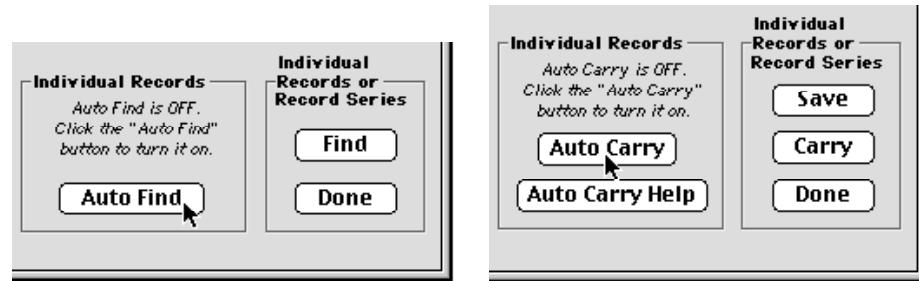
Abundance

NOTE: Any or all of the fields “Stage/Sex,” “Medium,” “Storage,” “Deposited,” “Specimen Custom 1,” “Specimen Custom 2,” and “Type Status” may have been renamed using the “Core Field Aliases” tool from the Special menu (see Chapter 18, “[Renaming Fields](#)”).

- **Existing values that will be replaced:** The Specimen record with the Specimen Code you just entered—and any additional records whose Specimen Codes you enter after using the “Carry” button—*will be updated with the entries you make in the “Find and Identify Specimen Series” screen for these fields, regardless of the existing values in the fields.*
 - **Existing values that will not be replaced:** Existing values in any field that you leave blank in the “Find and Identify Specimen Series screen” *will not be altered* in the Specimen records found. (In the case of the numerical field “Abundance,” located in the “Other Fields” tab, a zero in the “Find and Identify Specimen Series screen” indicates no change in existing records.)
4. To find the first Specimen record and clear the Specimen Code entry area for the next record, you have three options.
- **Option 1: Click the “Find” button** (“Find Specimen Series,” below left) **or the “Save” button** (“Find and Identify Specimen Series,” below right) if you want to make another manual entry.



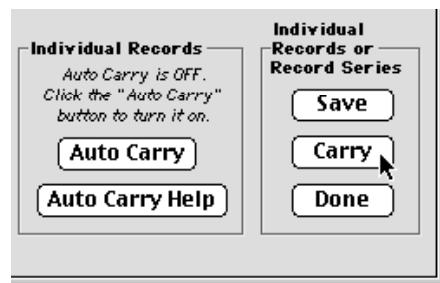
- **Option 2: Click the “Auto Find” button** (“Find Specimen Series,” below left) **or the “Auto Carry” button** (“Find and Identify Specimen Series,” below right), if you want to set up for automatic Specimen Code entries.



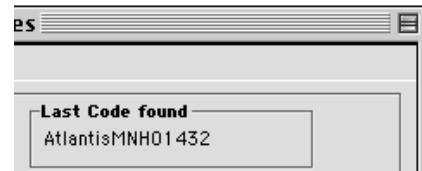
These are toggle buttons. Click once to turn on “Auto Save” or “Auto Carry,” click the button again to turn it off.

- **Option 3: Click the “Carry” button** (“Find and Identify Specimen Series” only).

If you click “Auto Carry” or “Carry” in the “Find and Identify Specimen Series” screen, any entries you made in the update fields are carried over to the next record to be updated.



Regardless of which approach you use to find the first record, the “**Last Specimen Code**” entry from the previous series is displayed in the “Last Code Found” panel (upper right corner of the screen), for both the “Find and Identify Specimen Series” and the “Find and Identify Specimen Series” screens.



5. If you clicked the “Auto Find” or “Auto Carry” button to toggle it on, you can now proceed to enter additional Specimen Codes without having to click any buttons on the screen.

Each time you enter a new Specimen Code and press TAB (or the barcode reader reads a Specimen barcode and enters an end-of-line character), the Specimen record is found automatically. If you are using the “Find and Identify Specimen Series” screen, the record is not only found automatically, but also updated automatically.

With a barcode reader set to append the end-of-line character, the entire process requires neither keyboard nor mouse once the Auto Find or Auto “Carry” button is toggled on. You can use both hands, uninterrupted, to handle specimens.

6. Follow the steps in the section entitled “[Finding \(or Finding and Identifying\) Specimen Series: Final Steps](#),” later in this chapter.

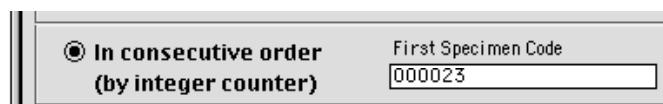
If You Choose “In Consecutive Order”

1. In the “In consecutive order” panel:

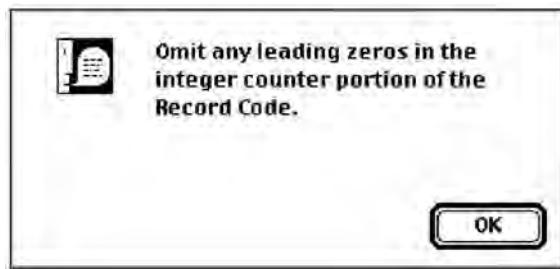
- *Either: In the “First Specimen Code” entry area, manually enter the Integer Counter for the numerically lowest Specimen Code in the series you want to find (or find and update). If the counter has any leading zeros, omit them. Press the TAB key.*



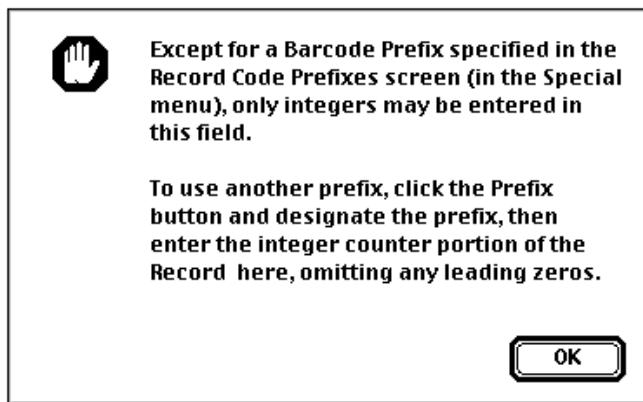
Biota prefixes leading zeros, if necessary, to complete the number of digits you specified in the “Recognition” tab of the “Record Code Prefixes” screen (see Step 1 of the section “[Finding \(or Finding and Identifying\) Specimen Series: First Steps](#)” earlier in this chapter.)



- ◊ If you enter leading zeros, Biota posts this error message:



- ◊ If you entered an alphabetic character, Biota posts this error message:



- Or: Read in the barcode for the “First Specimen Code” in the series for the numerically lowest Specimen Code in the series you want to find (or find and update). *If the counter has any leading zeros, omit them.* Then press TAB if your barcode reader is not set to enter an end-of-line character automatically.

<input checked="" type="radio"/> In consecutive order (by integer counter)	First Specimen Code AtlantisNMH001432
---	--

If the alphanumeric prefix correctly matches the barcode prefix setting in the “Recognition” tab of the “Record Code Prefixes” screen, Biota accepts the barcode. Otherwise, you will see the alphabetic character error message illustrated in the previous paragraph.

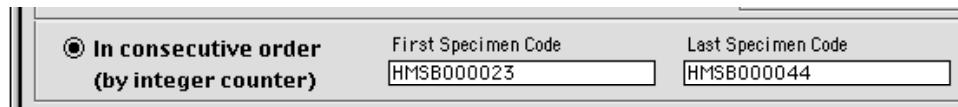
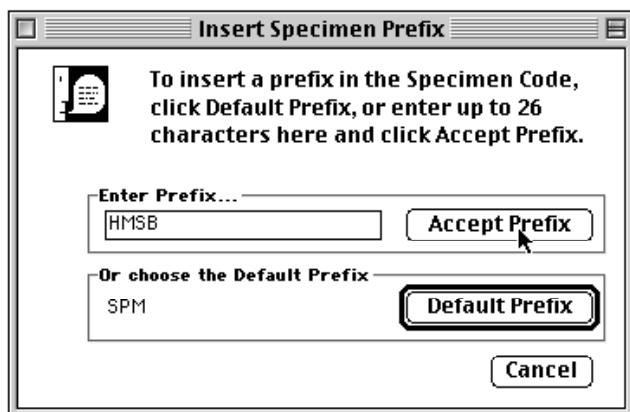
2. Repeat Step 1 for the “Last Specimen Code” entry area in the “In consecutive order” panel. If there is only one specimen in the series, you can skip this step.
3. If you entered an Integer Counter manually, and wish to insert a Specimen Code Prefix to complete the Specimen Codes, click the “Prefix” button. (If you entered a barcode, the “Prefix” button has no effect.)

Last Specimen Code 000044	Prefix
------------------------------	--------

The Insert Specimen Prefix window appears.

4. In the Prefix window:

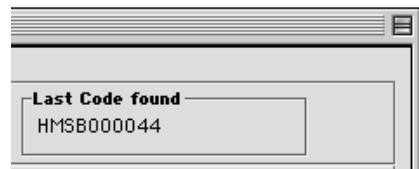
- **Either:** Enter an ad hoc prefix in the **Enter Prefix area** (in the illustration on the right, the prefix *HMSB* has been entered) and click the “Accept Prefix” button.
- **Or:** Click the “Default Prefix” button to enter the prefix displayed next to the button (*SPM* in the illustration on the right; see Step 1 of the section “[Finding \(or Finding and Identifying\) Specimen Series: First Steps](#),” earlier in this chapter, to change the default prefix). Biota completes the “First Specimen Code” and “Last Specimen Code” entries by inserting the prefix.



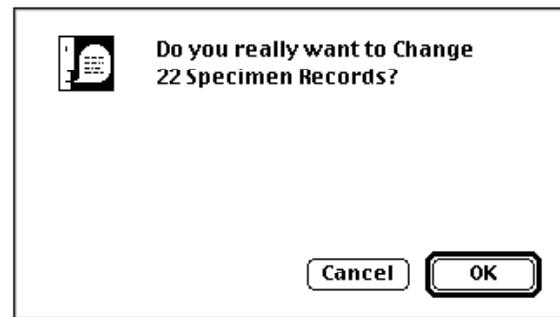
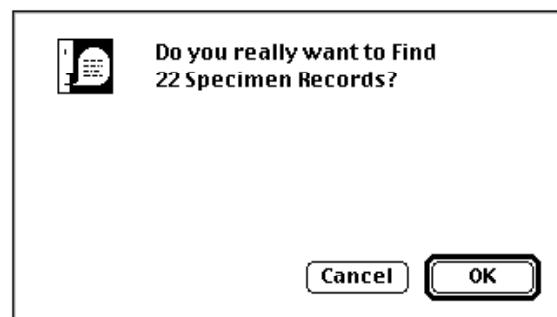
NOTE: If you prefer, you can use the “Prefix” button to set a prefix first, then enter the Integer Counters for the First and Last Specimen Codes. In this case, the Codes will be completed as you enter them.

- 5. If you are using the Find and Identify Specimen Series tool,** complete as many of the rest of the entries in the screen as you wish, following the instructions in [Step 3 of the previous section of the chapter, “If You Choose ‘In Any Order.’”](#)
- 6. Click the “Find” button (“Find and Identify Specimen Series” tool) or click the “Save” or “Carry” button (“Find and Identify Specimen Series” tool) to accept the first series of consecutive Specimen Codes.**

The “Last Specimen Code” entry is displayed in the “Last Code Found” panel (upper-right corner of the screen), and Specimen Code entry areas are cleared for the next series.



- **If you asked Biota to find (left, below) or find and update (right, below) more than 20 records,** a confirmation screen appears.



- If the password system has been enabled (see Chapter 26, “[Security: Passwords and Access Privileges](#)”) and you have requested the updating of more records than the limit set in the Preferences screen (see Appendix B, “[Setting Preferences](#)”), a message appears explaining that you cannot complete the action. (A user with Administration privileges can change the limit.)

NOTE: The “Auto Find” or “Auto Carry” toggle button is disabled when you choose the “Consecutive order” option (or the “Use the Specimen Record Set” option in the “Find and Identify Specimen Series” tool), since these buttons are used only for single Specimen Code entry.

7. Follow the steps in the section entitled “[Finding \(or Finding and Identifying\) Specimen Series: Final Steps](#),” later in this chapter.

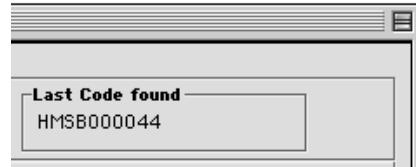
If You Choose “Use the Specimen Record Set”

This third option for identifying a group of specimen records in the “Find and Identify Specimen Series” screen allows you to use any tool in the Find menu to bring together the group of records to be updated.

1. Create a Specimen Record Set composed of the Specimen records you want to update, using any of the tools of the Find menu.
2. Choose the option “Use the Specimen Record Set” in the “Find and Identify Specimen Series” screen.
3. Complete as many of the rest of the entries in the screen as you wish, following the instructions in [Step 3 of the section “If You Choose ‘In Any Order,’”](#) earlier in this chapter.
4. Click the “Save” or “Carry” button to find the records that compose the active Specimen Record Set and make the changes you have set up.

The “Last Specimen Code” entry is displayed in the “Last Code Found” panel (upper-right corner of the screen), and Specimen Code entry areas are cleared for the next series.

- If you have asked Biota to find and update more than 20 records, a confirmation screen appears.



- If the password system has been enabled (see Chapter 26, “[Security: Passwords and Access Privileges](#)”) and you have requested the updating of more records than the limit set in the Preferences screen (see Appendix B, “[Setting Preferences](#)”), a message appears explaining that you cannot complete the action. (A user with Administration privileges can change the limit.)

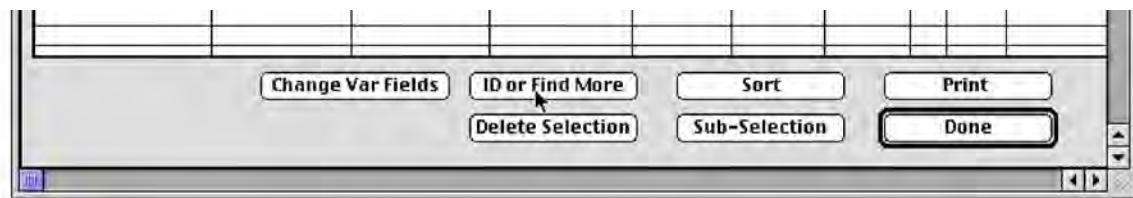
NOTE: The “Auto Carry” toggle button is disabled when you choose the “Use the Specimen Record Set” option in the “Find and Identify Specimen Series” tool, since this button is used only for single Specimen Code entry.

5. Follow the steps in the section entitled “Finding (or Finding and Identifying) Specimen Series: Final Steps,” next in this chapter.

Finding (or Finding and Identifying) Specimen Series: Final Steps

This section specifies the final steps for using the “Find Specimen Series” and “Find and Identify Specimen Series” tools. These steps are the same for the “In any order,” “In consecutive order,” and (for the “Find and Identify Specimen Series” tool) the “Use Specimen Record Set” options described in the previous three sections.

1. Create additional series of records if you wish, following the steps in the appropriate preceding section. (See “[If You Choose ‘In Any Order’](#),” “[If You Choose ‘In Consecutive Order’](#),” or “[If You Choose ‘Use the Specimen Record Set’](#),” earlier in this chapter.)
2. To examine the records found (or found and updated), click the “Cancel” button in either the “Find Specimen Series” or “Find and Identify Specimen Series” Input screen. The records appear in a special version of the Specimen Record Listing screen. In place of the standard “Add Specimen” button, an “ID or Find More” button is offered.

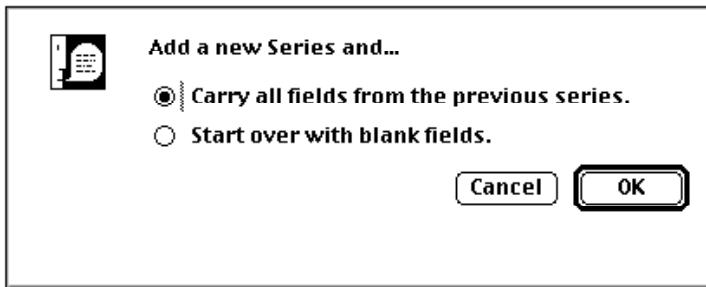


3. To find (or find and update) another series of Specimen records, click the “ID or Find More” button (above).

If you are using the “Find and Identify Specimen Series” tool, an option screen appears.

You can choose to carry forward all entries except the “First Specimen Code” and “Last Specimen Code” entries (exactly the equivalent of having clicked the “Carry” button after the last series you created), or start fresh. (There is nothing to “carry” with the “Find Specimen Series tool,” so this option screen does not appear.)

4. If the option screen (below) appears, select an option and click OK. The Specimen Series screen you were using before reappears.



5. When you are finished using the Series tool, click the “Done” Button in the Record Listing screen to present the standard Record Set option screen (see “[The Record Set Options Screen](#)” in Chapter 3).

PART

4

Printing Reports and Labels

Chapter 14 **Printing Reports**

Biota offers printed reports for individual records as well as groups of records.

- **For an individual record** from any Core table, Biota offers a standard, pre-formatted report form. (To print an Image record linked to the Species, Specimen, Collection, or Locality table, use the "Print" button in the "This Image record" panel of the Images tab for the parent record.)
- **For the records displayed in a Record Listing Screen** (whether or not they have been declared a Record Set), you can use the "Print" button on the Record Listing Screen or the Print command from the File menu to print a list of the records displayed. You can choose a preformatted Biota report or use the Quick Report Editor, instead, to design your own printed report forms. You can save and reload the formats you create in the Quick Report Editor. (See "[Designing and Printing Reports with the Quick Report Editor](#)" later in this chapter).

WARNING: All Biota preformatted reports use the Geneva font (Mac OS) or the Arial font (Windows). If you do not have the appropriate font installed (in the printer's memory as well as on your computer, for some printers), the layout of reports will probably not be correct, depending on what font is substituted for Geneva or Arial. Because these fonts are automatically installed with their respective operating systems, this problem is unlikely to arise.

Printing and Previewing Procedures for Reports and Labels

For all printed reports and labels, Biota presents the same series of screens and options when you are ready to preview and print. This section outlines the steps to take once you have chosen the report or label options you want. See the section that applies to the report (this chapter) or labels (see Chapter 15, "[Printing Labels](#)") you are printing, before using the steps below.

1. **Launch the printing process** by clicking a “Print” button (Reports), selecting the Print command from the File menu (Record Listing Reports), or clicking the “OK” button (Label Option screen), after setting up any options for the report or labels.

The “Print Setup” (Windows) or “Page Setup” (Mac OS) window for your active printer appears. (Because these windows vary greatly among printers and between operating systems, none is illustrated here.)

2. **Check or adjust any settings** in the “Print Setup” (Windows) or “Page Setup” (Mac OS) window, **then click the “OK” button**. The “Print” window for your active printer appears. (Because “Print” windows vary greatly among printers and between operating systems, none is illustrated here.)

3. **Choose a Preview option.** Look for a “Print preview” (Windows) or “Preview on screen” (Mac OS) checkbox in the lower-left corner of the Print window. If you don’t see the checkbox, look for a popup menu of print options and select “4D x.x.x” (where “x.x.x” is the version number of 4th Dimension used to compile the current version of Biota), then locate the checkbox.



- **If you leave the Preview checkbox unchecked**, reports or labels or go directly to your printer.
- **If you click the Preview checkbox**, you can check the labels or report onscreen and then Print or Cancel.

4. **Click the “OK” button (Windows) or “Print” button (Mac OS) in the Print window.** If you checked the Preview box, the first page of the report or the first page of labels appear in a Preview window with a column of icon buttons at the left, illustrated here. Using these buttons you can check the labels or report onscreen and then Print or Cancel.

- **The “X” icon** dismisses the screen, or stops a print job already underway.
- **The printer icon** sends the report or labels to the printer.
- **The page-with-arrow icons** move the view forward or backward one page in the print job.
- **The magnifying glass icon** zooms the page image and changes the cursor to a “hand” icon that can be used to move the page image within the window.



NOTE: If you do not have a printer attached to your computer, the computer may lock up if you click the OK or “Print” button in Print screen. If you are working without a printer, you can avoid this behavior if you remember to click the “Stop/Hand” icon button when you are through with the preview.

Printing an Individual Record

To print a copy of an individual record from a Core table, follow these steps.

1. **Display the record you want to print** in the Input screen for its table. Use the techniques described in Chapter 10, “[Working With Records in Record Listing and Input Screens](#)” to find and display the record.
2. **Click the “Print” button in the Input screen** to print the standard report for the table.
The “Print Setup” (Windows) or “Page Setup” (Mac OS) window for your active printer appears.
3. **To preview the printed record**, see “[Printing and Previewing Procedures for Reports and Labels](#)” earlier in this chapter.



Printing a Report Based on a Selection of Records

Printing a Report Based on the Active Record Set for a Table

To print a report listing all the records in the active Record Set (see “[Record Sets](#)” in Chapter 3) for a Core table or for the Determination History table:

1. **Display the Record Set** in the standard Record Listing Screen for the table.
 - **For Core tables:** From the Display menu, choose the command for the table.
 - **For the Determination History table:** From the Special menu, choose “Display Determination Histories.” If you have enabled the password system, only the Administrator can use this command.
2. **Follow the directions** in the section “[Printing a Standard or Custom Report Based on the Records in a Record Listing Screen](#)” later in this chapter.

Printing a Report Based on a Record Set Pointer File

To print a report listing all the records in a Record Set pointer file (see “[Record Set Pointer Files](#)” in Chapter 3):

1. **Load the Record Set Pointer File** from disk to display the records in the Record Listing Screen for the table.
2. **Follow the directions in the next section, “[Printing a Standard or Custom Report Based on the Records in a Record Listing Screen](#).”**

Printing a Standard or Custom Report Based on the Records in a Record Listing Screen

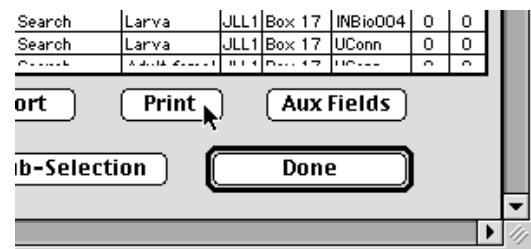
For each Core table and the Determination History table, Biota offers a preformatted report that you can print, listing all records in the current Selection, including fields from related tables where appropriate. Each table has its own, specially designed report. Rather than attempt to display them in this book, the best way to evaluate these report formats is to print some records from your own Data File or from the Biota Demo Data File (see Chapter 6, “[A Brief Tutorial With the Demo Database](#)”), or preview reports on the screen (see “[Printing and Previewing Procedures for Reports and Labels](#)” earlier in this chapter).

If the preformatted report for a table does not suit your needs, you can print the records using a custom report layout that you design yourself using the Quick Report Editor (see “[Designing and Printing Reports With the Quick Report Editor](#)” later in this chapter).

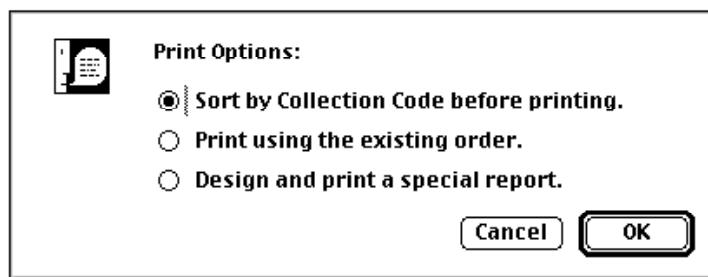
Here are the steps to follow for printing a standard report:

- Display the records to be printed in the Record Listing Screen.** See the preceding two sections of this chapter (“[Printing a Report Based on the Active Record Set for a Table](#)” and “[Printing a Report Based on a Record Set Pointer File](#)”) and consult Chapter 10, “[Working With Records in Record Listing and Input Screens](#)” and Chapter 12, “[Finding and Updating Records](#)” for help, if you need any.
- Click the “Print” button at the base of the Record Listing Screen.**

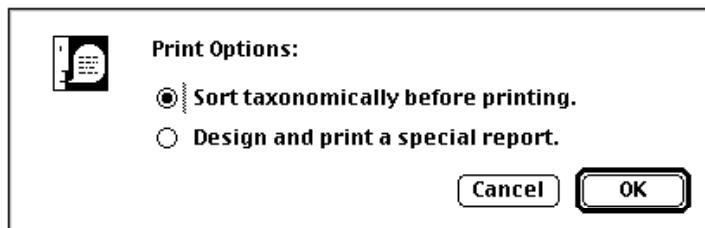
Alternatively, you can select “Print” from the File menu while the records are displayed in the Record Listing Screen.



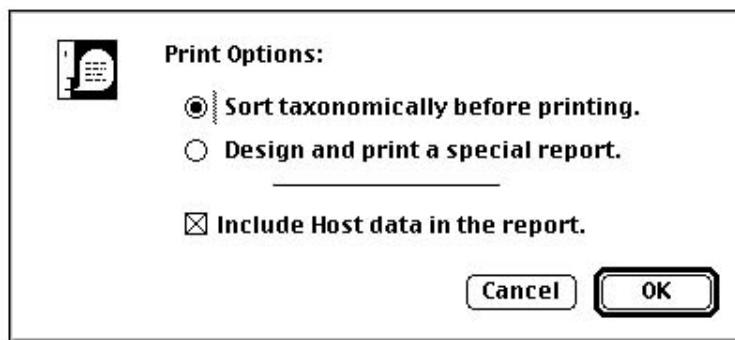
- Choose a print option.** A print option window appears offering two or three choices, depending on the table for which you are printing records. (The Determination History table has no options.) Three different option windows are illustrated below.



- Sort by Record Code before printing.** Use this option to print a report with the records sorted by Record Code (Species Code, Specimen Code, Collection Code—illustrated above, or Locality Code). The Loans report can be sorted by Loan Code.
- Print using the existing order.** If you have used the “Sort” button (the “Order by” Editor) to create a special order for the records that you want maintained in the report, choose this option.
- Design and print a special report.** If you choose this option, Biota presents the 4th Dimension “Quick Report Editor,” which you can use to design, save, and/or load custom report formats that you create yourself. The report will be based on the Selection of records in the output layout when you clicked the “Print” button or selected Print from the File menu. See “[Designing and Printing Reports With the Quick Report Editor](#)” later in this chapter.



- **Sort taxonomically before printing.** For records from taxonomic tables (Species, Genus, Family, etc., and Specimen as well), this option prints the records for the table in alphabetical order within taxonomic levels (ranks) in a hierarchical report organized by rank (as in the table in the section, “[The Relational Model](#)” in Chapter 2).



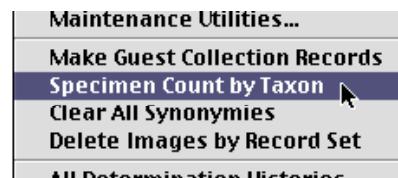
- **Include Host data in the report.** For the Specimen table, an additional option is offered. If the “Include Host data in the report” checkbox is checked, the report will include, for each Specimen record, the Specimen Code of the Host for that specimen (see Chapter 24, “[Host-Guest Relations](#)”).

NOTE: This option is automatically checked if any Specimen records in the current selection have host data. Otherwise, it appears unchecked. In either case, you can override the setting manually. The host data checkbox is disabled when the “Design and print a special report” option is clicked.

4. Click the “OK” button in the print option screen.
 - If you chose the standard Biota report, see “[Printing and Previewing Procedures for Reports and Labels](#)” earlier in this chapter.
 - If you chose “Design and Print a Special Report,” see “[Designing and Printing Reports with the Quick Report Editor](#)” later in this chapter.

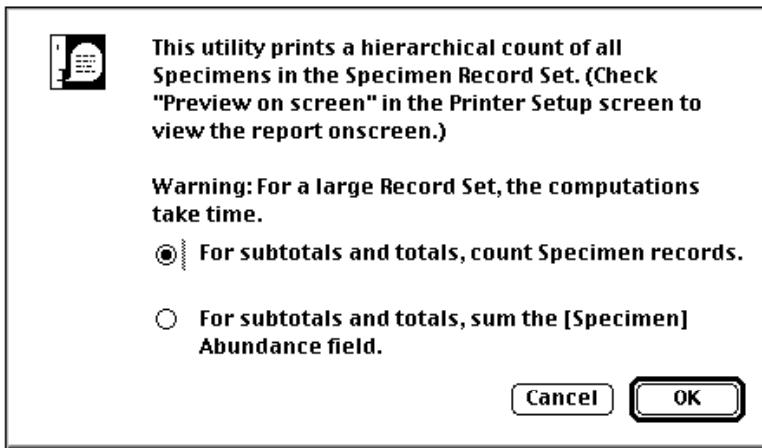
Printing a Specimen Count by Taxon Report

The Specimen Count by Taxon report provides quantitative information on the taxonomic breakdown of a Specimen Record Set. The report computes and displays the number of Specimen records for each taxon and rank.



To use this tool, follow these steps:

1. Choose “Specimen Count by Taxon” from the Special menu. An option screen appears.



2. Choose a summation option.

- **Option 1. “For subtotals and totals, count Specimen records.”** If you check this option (the default), values in the Abundance field of the Specimen table are ignored, and the Specimen records are simply enumerated.
- **Option 2. “For subtotals and totals, sum the [Specimen] Abundance field.”** If you check this option, values in the Abundance field of the Specimen table are summed for Specimen records in each taxonomic category.

NOTE: For information on the Abundance field of the Specimen table, see [Step 5 of the section “Entering Specimen Data: The ‘General’ Tab”](#) in Chapter 11.

3. Click the “OK” button.

You can use the screen preview option to display the report on the screen before (or instead of) printing it (see “[Printing and Previewing Procedures for Reports and Labels](#)” earlier in this chapter).

Designing and Printing Reports with the Quick Report Editor

The 4D Quick Report Editor is an “off the shelf” 4th Dimension utility described in Appendix E, “[The 4D Quick Report Editor](#).” But first, read the section below, “[Launching the 4D Quick Report Editor](#),” to get started.

NOTES:

- a. You can use the 4D Quick Report Editor to create reports for records in any Core table (see “[Core Tables](#)” in Chapter 3), specifying fields from that table and any of its parent tables. Fields in child tables cannot be used. Because there may be many child records linked to each parent record, the Quick Report Editor has no way to determine which record to access.
 - b. The Quick Report Editor can also be used to export text flatfiles. See “[Exporting Custom Flatfiles](#)” in Chapter 27. If you wish to create a graph from a Quick Report, export the report as a flatfile, then use another application (e.g., Microsoft Excel) to create the graph.
-

Launching the 4D Quick Report Editor

To launch the Quick Report Editor for printing a report, see “[Printing a Standard or Custom Report Based on the Records in a Record Listing Screen](#),” earlier in this chapter. For detailed help in setting up the Quick Report Editor, see Appendix E, “[The 4D Quick Report Editor](#).”

Left Margins in Quick Reports

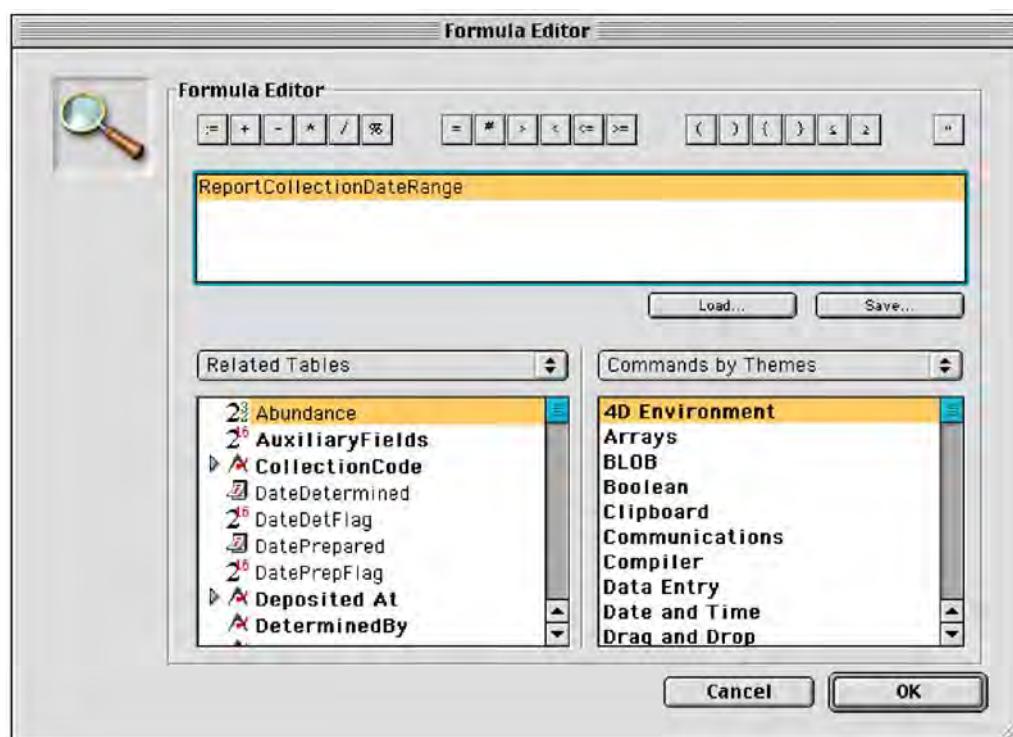
In the Quick Report Editor, you can explicitly control the size of Headers and Footers (see “[Adding Page Headers and Footers](#)” in Appendix E), but there is no obvious way to leave a wide left margin (for binding, for example). To do, simply insert a blank first column of the desired width.

Special Biota Date, Georeference, and Agent Formats in Quick Reports

When you use the Quick Report Editor to create custom reports (using the “Print” button, with the “Design and print a special report” option, in Record Listing screens) or to export custom flatfiles (using the “Export Custom Flatfile” tool in the Im/Export menu), you may wish to include certain data in special Biota formats. These formats include Partial Dates (month and year only, or year only), Collection Date Range, and Latitude/Longitude in Degrees/Minutes/Seconds format.

In addition, linking to the Personnel table from the Specimen or Collection table requires special commands to allow Personnel records linked to “agent” fields ([Specimen]PreparedBy, [Specimen]DeterminedBy, and [Collection]CollectedBy) to be included in reports based on the Specimen or Collection table.

You can do all these things easily by inserting very simple commands in the Formula Editor. You access the Formula Editor by adding a new column to a Quick Report, or by double-clicking an existing column. Here is an example for the special Biota command “ReportCollectionDateRange.”



Here are the special commands:

- **Georeference commands**
 - ◊ ReportLatitude
 - ◊ ReportLongitude
- **Date commands**
 - ◊ ReportCollectionDateRange
 - ◊ ReportDateCollected
 - ◊ ReportDateDetermined
 - ◊ ReportDatePrepared

Note: The format of all Date commands (International vs. U.S. format), is controlled by the Date setting in your operating system. See “[Date Formats in Biota: U.S. and International Formats](#)” in Chapter 9.

- **Agent commands**
 - ◊ ReportPreparatorFirstName
 - ◊ ReportPreparatorLastName
 - ◊ ReportDeterminerFirstName
 - ◊ ReportDeterminerLastName
 - ◊ ReportCollectorFirstName
 - ◊ ReportCollectorLastName
 - ◊ ReportCollectorLink. This special command can be entered in the Formula Editor in a hidden column (choose “Hide” from the Edit menu in the Quick Report Editor) to give full access to all fields of the Personnel record for a Collector in subsequent columns (to the right of the hidden column).

Chapter 15

Printing Labels

Biota provides several special tools (in the Labels menu) for producing labels for specimens, collections, and species. You can print labels directly from Biota on plain, acid-free paper or, for slide labels, adhesive-backed, acid-free paper. Alternatively, you can export label data to text files, where you can format and duplicate the label text with a word processing or spreadsheet application to suit your personal or institutional preferences.

WARNING: Biota preformatted labels use the Arial and Helvetica fonts, depending on the label type. If you do not have the appropriate font installed (in the printer's memory as well as on your computer, for some printers), the layout of labels will probably not be correct, depending on what font is substituted for Arial or Helvetica.

Printing and Previewing Procedures for Labels

For all printed labels, Biota presents the same series of screens and options when you are ready to preview and print. Because the procedures are identical for Reports, please consult “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14, “Reports.” That section outlines the steps to take once you have chosen the label options you want, following the instructions in the appropriate section of this chapter.

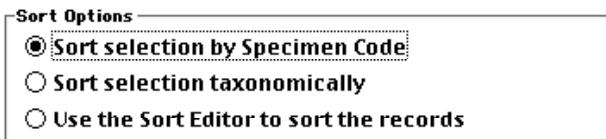
Label Option Windows

Each Label tool in Biota presents an option window, giving you control over certain features of the labels to be produced. Because most of the option sets recur in option windows for several different label tools, it makes sense to describe them just once, in this section.

Options that apply to only one or two kinds of labels are discussed in the section on the particular tool or tools to which they apply.

Sort Options

- **Option 1: Sort selection by Record Code or Key field.** This is the default option for all label tools. For all Specimen labels (both locality and determination labels), you can choose to sort by Specimen Code before printing them. For Collection labels, you can sort by Collection Code. With the Custom Label tool, which prints labels for any Core table, you can choose to sort by Key field (see “[Key Fields](#)” in Chapter 3).
- **Option 2: Sort the selection taxonomically.** For all specimen determination labels, you have the option of sorting Specimen records taxonomically before



printing the labels. The Specimen records are sorted by Specimen Code *within* species. Groups of records for the same species are sorted alphabetically by specific name, then these groups are sorted by genus, and so on. This option does not apply to locality labels or collection labels.

- **Option 3: Use the Sort Editor to sort the records.** For all label tools, you can choose to sort the records using the Sort Editor (see “[Sorting Records in Record Listing Screens](#)” in Chapter 10).

Data Options

- **Include Specimen Code on each label.** A checkbox for this option is offered for both locality and determination labels of all kinds. It is not exclusive of any other option, where offered.

Data Options
 Include Specimen Code on each label
- **Month format options.**
 - ◊ **Option 1: Use three-letter English abbreviations for Months** (Jan, Feb, Mar, Apr, etc.). This is the default option for all label tools.
 - ◊ **Option 2: Use Roman numerals for Months** (I, II, III, IV... for Jan, Feb, Mar, Apr...). In some disciplines, this style is preferred.
 In either case, partial dates (Month-Year or Year-only) and “intelligent” collection date ranges are exported or printed (see “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9).
- **Include Host Specimen name on each label.** A checkbox for this option is offered for collection labels (Host Specimen Code is an attribute of the Collection table; see Chapter 24, “[Host-Guest Relations](#)”) and for pin, slide, and vial Specimen locality labels. It is not exclusive of any other option, where offered. If you choose this option, Host Specimen data are checked case by case and are included only if present in individual Collection records. The data included in Host Specimen name are the host genus, specific name, and family.

Include Host Specimen name on each label
- **Include Family on each label.** A checkbox for this option is offered for slide and vial specimen determination labels (but not for pin determination labels, on which Family is not traditionally included) and for herbarium specimen labels. It is not exclusive of any other option, where offered.

Include Family on each label

Output Options

- **Send labels to printer.** With this option selected, you can preview and then print the labels (or cancel printing if the preview shows any problems.) Follow the directions in the section “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Output Options
 Send labels to printer
 Save labels as a text file

- **Save labels as a text file.** This option sends label data to a text file, where you can work with it in a word-processor. Biota exports some kinds of labels to tab-delimited text files and others to ordinary text files; see the individual sections for details.

Collection Labels

Labels produced from Biota Collection records (with fields from the parent Locality record) have several uses. When mass collections are made, such as with quadrats, traps, trawls, extractors, foggings, sweeps, and so on, many specimens share the same collection data. In whatever manner the collection (or lot) is stored until sorted and identified, it needs a collection label. Often, “residual” specimens need to remain in mass storage or in smaller groups, properly labeled, even after focal groups have been removed and specimens labeled individually.

In entomology, locality labels attached to specimens traditionally contain no information about the individual specimen (such as a Specimen Code or the equivalent) and provide only approximate geographical information. They are usually printed in large sets and applied to all specimens from a broadly defined locality (broadly, that is, compared with GIS/GPS standards, see “[Spatial Coordinates](#)” in Chapter 9).

Using Biota’s ability to export standard locality data (from Collection and parent Locality records) to disk file, entomologists (and others) can fine-tune the format, delete unwanted fields, and then produce as many copies of each label as needed for each set of data exported, using a word processing or spreadsheet application. The labels can then be printed on a laser printer or master sheets can be sent to a commercial printing service.

Information Included on Collection Labels

When you use the Collection Label tool, as described in the next section, Biota exports or prints the following fields from the Collection and Locality tables, for each record in the active Collection Record Set. The intention in choosing these fields for the tool was to be fairly inclusive, since you can delete extra information easily in a text file, whereas looking it up in the database to add it manually to label text is time-consuming.

- **Fields from the Collection record** (see “[Collection Input](#)” in Chapter 11)
 - ◊ Collection Code
 - ◊ Collected By
 - ◊ Date Collected or collection date range (see “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9)
 - ◊ Method
 - ◊ *Optional:* Site.
 - ◊ *Optional:* Host Genus, specific name (Species Name field), and Family (optional) (see “[Data Options](#),” earlier in this chapter)
- **Fields from the linked Locality record** (see “[Locality Input](#)” in Chapter 11)
 - ◊ Country
 - ◊ State/Province
 - ◊ Locality Name
 - ◊ District
 - ◊ Elevation

- ◊ Geographic coordinates: Latitude and Longitude in Degree/Minutes/Seconds (see “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9) and/or Alternate Coordinates (see “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9)

Below are three examples. In the second (a collection record for hummingbird flower mites taken from a plant specimen), Host Specimen data are included. An entry for District is included in the third label (*Sarapiquí*).

ECUADOR: Galápagos Islands Floreana Island Elev 10 m 1°17'0"S 90°26'0"W coll. C. Darwin 24 Sep 1832 Shotgun Collection Code: CD002	PERU: Cajamarca Cajamarca-Celendin rd. Elev 3080m 7°5'0"S 78°25'0"W coll. J. L. Luteyn 12 Feb 1985 Search Ex <i>Siphocampylus</i> <i>sanguineus</i> (Campanulaceae) Collection Code: JLL11314H	COSTA RICA: Heredia <i>Sarapiquí</i> La Selva Elev 150 m 10°26'0"N 84°1'0"W coll. J. T. Longino 9 Oct 1989 Search Collection Code: JTL03621
---	---	---

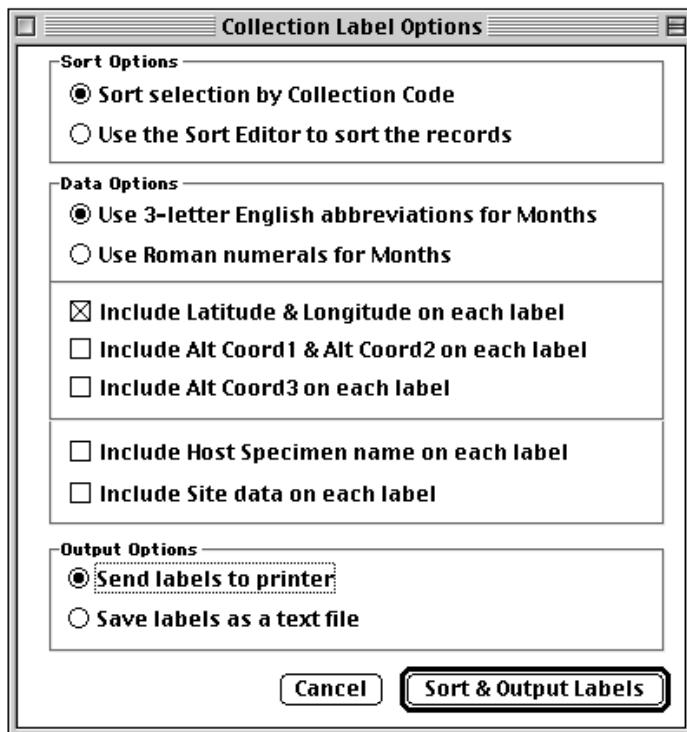
(The examples above are not actual labels, just the data that are printed or exported for each Collection record.)

If you choose the print option, rather than exporting to a text file, the printed labels carry the information shown above. Here is the middle example in printed format, shown at actual size.

PERU: Cajamarca Cajamarca-Celendin rd. Elev 3080m 7°5'0"S 78°25'0"W coll. J. L. Luteyn 12 Feb 1985 Search Ex <i>Siphocampylus</i> <i>sanguineus</i> (Campanulaceae) Collection Code: JLL11314H

Printing or Exporting Collection Labels: Step by Step

1. **Find the Collection records for which you wish to print labels or export label data**, using any of the tools in the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Declare these records to be the current Collection Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **From the Labels menu, choose “Collection Labels.”** The Collection label option screen appears.



4. Choose a Sort Option. See “[Sort Options](#)” earlier in this chapter for details.
5. Choose Data Options.
 - Month format option. See “[Data Options](#)” earlier in this chapter for details on Month formats.
 - Geographic coordinates options. You can include Latitude and Longitude in Degree/Minutes/Seconds (see “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9) and/or Alternate Coordinates (see “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9) on each label.

NOTE: If you have defined Aliases for the Alternate Coordinate fields, the Aliases will appear in the option screen by the checkboxes, instead of the default Alternate Coordinate field names.

- Host Specimen name option. See “[Data Options](#)” earlier in this chapter for details.
- Include Site data on each label. A checkbox for this option is offered for collection labels

NOTE: If you have defined an Alias for the Site field, the Alias will appear in the option screen by the checkbox instead of the default field name.

6. Choose an Output Option. See “[Output Options](#)” earlier in this chapter. Exported text files for Collection labels can be opened with any word-processing application.
7. Click the “Sort & Output” Labels button in the options window.

8. Follow the instructions in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Pin and Vial Specimen Locality Labels

Using tools from the Labels menu, Biota can print standard locality labels for pinned insect specimens as well as slightly larger (“vial”) locality labels for fluid-preserved specimens of arthropods, plants, and other taxa.

With the advent of GPS technology (see “[Spatial Coordinates](#)” in Chapter 9), individual specimen barcodes (Appendix K, “[Barcodes](#)”), and high quality laser and ink-jet printers, locality (or “collecting-event”) labels with information pertaining to individual specimens are now practical, if still not yet widely used in many disciplines.

Information Included on Pin and Vial Locality Label Text

When you use the Pin or Vial Locality Label tools, as described in the section “[Printing or Exporting Pin or Vial Specimen Locality Labels: Step by Step](#)” below, Biota prints the following fields from the Specimen, Collection, and Locality tables, for each record in the active Specimen Record Set.

- **Field from the Specimen record** (see “[Specimen Input](#)” in Chapter 11)
 - ◊ *Optional:* Specimen Code
- **Fields from the linked Collection record** (see “[Collection Input](#)” in Chapter 11)
 - ◊ Collected By
 - ◊ Date Collected or collection date range (see “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9)
 - ◊ *Optional:* Host Genus, specific name (Species Name field), and Family (optional) (see “[Data Options](#),” earlier in this chapter)
- **Fields from the linked Locality record** (see “[Locality Input](#)” in Chapter 11)
 - ◊ Country
 - ◊ State/Province
 - ◊ Locality Name
 - ◊ Elevation
 - ◊ Geographic coordinates: Latitude and Longitude in Degree/Minutes/Seconds (see “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9) or Alternate Coordinates (see “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9).

Here are some examples of pin locality labels, at their normal printed size. They have no printed borders, so they can be trimmed if you want. To make them even smaller, some printers have a setting for size reduction in “Print Setup” (Windows) or “Page Setup” (Mac OS) window.

COSTA RICA: Heredia La Selva Elev 150 m 10°26'0"N 84°1'10"W coll. J. T. Longino 22 Jan 1991 INBIOCRI0018459857	COSTA RICA: Heredia La Selva Elev 150 m 10°26'0"N 84°1'10"W coll. J. T. Longino 9 Oct 1989 INBIOCRI001459864
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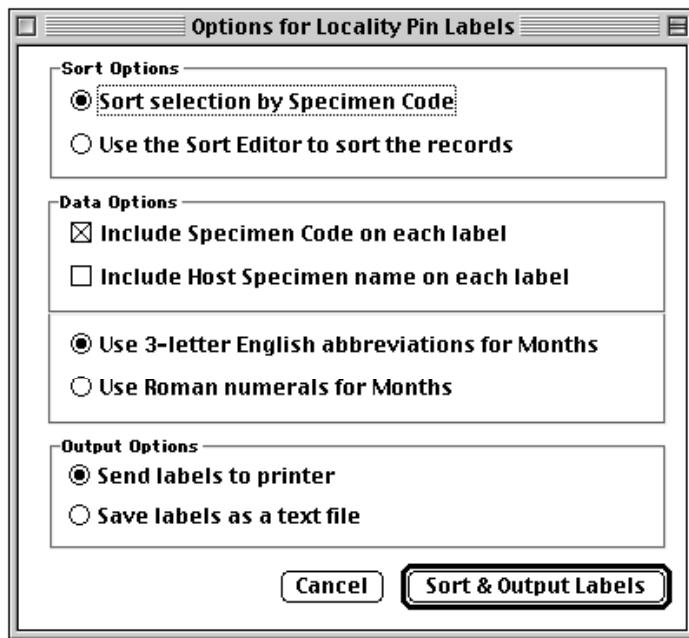
Below are vial locality labels, at their normal printed size, for the same collection data. They have printed borders.

COSTA RICA: Heredia La Selva Elev 150 m 10°26'0"N 84°1'0"W coll. J. T. Longino 22 Jan 1991 INBIOCRI001B459857	COSTA RICA: Heredia La Selva Elev 150 m 10°26'0"N 84°1'0"W coll. J. T. Longino 9 Oct 1989 INBIOCRI001459864
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Printing or Exporting Pin or Vial Specimen Locality Labels: Step by Step

1. **Find the Specimen records for which you wish to print labels or export label data**, using any of the tools in the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Declare these records to be the current Specimen Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **From the Labels menu, choose:**
 - ***Either:* “Pin Labels: Locality”**
 - ***Or:* “Vial Labels: Locality”**

In either case, Biota’s response depends on the current setting of the “Coordinate Display” option in the Coordinates tab of the Preferences screen (Special menu). If the “Show Alternate Coordinates” is active in the Preferences screen, an Alternative Coordinates option screen appears (see “[Latitude/Longitude and Alternate Coordinates on Labels or Reports and in Exported Text Files](#)” in Chapter 9), followed by the screen below. With any other “Coordinate Display” settings, the screen below appears immediately.



(The Label Options screen illustrated above is for Pin Locality labels. The Options screen for Vial Locality labels is identical.)

4. **Choose a Sort Option and Data Options.** See the section “[Label Option Windows](#)” earlier in this chapter.

5. **Choose an Output Option.** See “[Output Options](#)” earlier in this chapter. Exported text files for Pin or Vial Locality labels can be opened with any word-processing application.
6. **Click the “Sort & Output Labels” button** in the options window.
7. **Follow the instructions** in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Pin and Vial Specimen Determination Labels

Once determinations (identifications) have been entered in Biota for uniquely labeled specimens (identified by barcodes or by more traditional means), automatically printed *determination* labels are easy to produce. Using tools from the Labels menu, Biota can print standard determination labels for pinned insect specimens as well as slightly larger (“vial”) labels for fluid-preserved specimens of arthropods, plants, and other taxa.

Information Included in Pin and Vial Determination Label Text

When you use the Pin or Vial Determination Label tools, as described in the section “[Printing or Exporting Pin or Vial Specimen Determination Labels: Step by Step](#)” below, Biota prints the following fields from the Specimen, Species, and Genus tables, for each record in the active Specimen Record Set.

- **Fields from the Specimen record** (see “[Specimen Input](#)” in Chapter 11)
 - ◊ *Optional:* Specimen Code
 - ◊ Determined By
 - ◊ Year of “Date Determined” field
- **Fields from the linked Species record** (see “[Species Input](#)” in Chapter 11)
 - ◊ Genus
 - ◊ Specific name
 - ◊ Species Author (unless subspecies and/or variety recorded)
 - ◊ Subspecific name (if any)
 - ◊ Subspecies Author (if any, unless variety recorded)
 - ◊ Variety (if any)
 - ◊ Variety Author (if any)
- **Fields from the linked Genus record** (see “[Genus Input](#)” in Chapter 11)
 - ◊ Family (optional for vial labels, not available for pin labels)

Here are some examples of pin determination labels, at their normal printed size. They have no printed borders, so they can be trimmed if you want.

Strumigenys godmani Forel 1899 det. J. T. Longino 1992 INBIOCRI001B459857	Procydloceras impressus Forel 1899 det. J. T. Longino 1992 INBIOCRI001459864
---	--

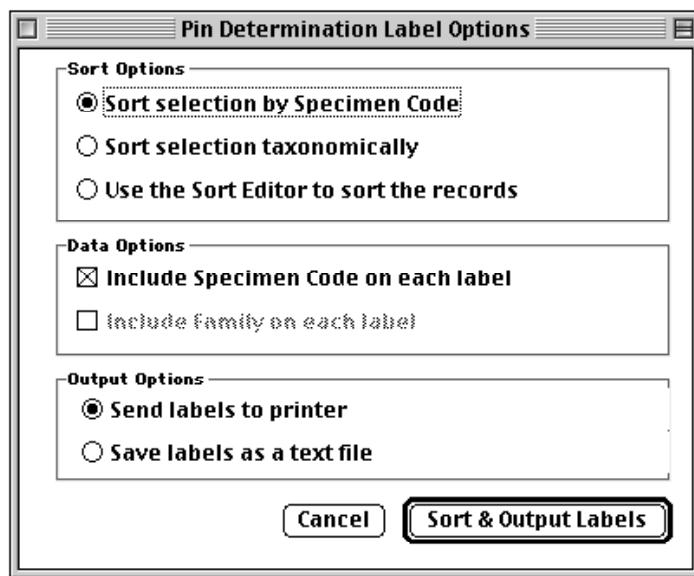
Below are vial determination labels, at their normal printed size, for the same specimen data. They have printed borders. The Family option has been included.

Strumigenys godmani Forel 1899 INBIOCR1001459857 FORMICIDAE	Procryptoceros impressus Forel 1899 det. J. T. Longino 1992 INBIOCR1001459864 FORMICIDAE
---	---

Printing Pin or Vial Specimen Determination Labels: Step by Step

1. **Find the Specimen records for which you wish to print labels or export label data**, using any of the tools in the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Declare these records the current Specimen Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **From the Labels menu, choose:**
 - ***Either:* “Pin Labels: Determination”**
 - ***Or:* “Vial Labels: Determination”**

In either case, the option screen that appears looks like the one below (with the appropriate window title).



4. **Choose a Sort Option and Data Options.** See the section “[Label Option Windows](#)” earlier in this chapter.
5. **Choose an Output Option.** See “[Output Options](#)” earlier in this chapter. Exported text files for Pin or Vial Determination labels can be opened with any word-processing application.
6. **Click the “Sort & Output Labels” button** in the options window.
7. **Follow the instructions** in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Slide Specimen Labels

Using tools from the Labels menu, Biota can print standard locality and determination labels for slide-mounted specimens. The precise format of these labels follows the acarological tradition (revealing Biota's ancestry), but this format may prove adequate for other small arthropods or parasites, and for organ or tissue specimens.

Individual locality labels have a long history for slide-mounted specimens in acarology and parasitology. With the advent of GPS technology (see “[Spatial Coordinates](#)” in Chapter 9), individual adhesive specimen barcodes (see Appendix K, “[Barcodes](#)”), laser and ink-jet printers, and high quality paper with permanent adhesive backing, printing precise locality slide labels for individual specimens—automatically, using Biota—saves an enormous amount of time over traditional methods.

Once determinations (identifications) have been entered in Biota for uniquely labeled specimens (identified by barcodes or by more traditional means), automatically printed determination labels are easy to produce and add to slides. (Barcode the slides first makes it easy to match up labels and specimens by Specimen Code.)

Information Included in Slide Specimen Label Text

Slide Locality Labels. When you use the Slide Label Locality tool, as described in the “Step by Step” section below, Biota prints the following fields from the Specimen, Collection, and Locality tables, for each record in the active Specimen Record Set:

- **Field from the Specimen record** (see “[Specimen Input](#)” in Chapter 11)
 - ◊ *Optional:* Specimen Code
- **Fields from the linked Collection record** (see “[Collection Input](#)” in Chapter 11)
 - ◊ Collected By
 - ◊ Date Collected or collection date range (see “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9)
 - ◊ *Optional:* Host Genus, specific name (Species Name field), and Family (optional) (see “[Data Options](#),” earlier in this chapter)
 - ◊ Source. The Source field is included only if the Host Specimen option is not checked, or if the Host Specimen option is checked, but a Specimen has no host record. The Source field is intended to be used for information such as “From soil core,” “Blacklight sample,” “In leaf litter.” (There is not enough space on slide labels for both the Source field and the Host Specimen data.)
- **Fields from the linked Locality record** (see “[Locality Input](#)” in Chapter 11)
 - ◊ Country
 - ◊ State/Province
 - ◊ Locality Name
 - ◊ Elevation
 - ◊ Geographic coordinates: Latitude and Longitude in Degree/Minutes/Seconds (see “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9) or Alternate Coordinates (see “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9).

Here are two pairs of slide locality labels, shown at normal printed size, that include Host Specimen information. The left pair are full-sized; the right pair leave room on the slide for a barcode label (see “[Printing or Exporting Slide Specimen Labels: Step by Step](#),” below).

JLL10953:05 ECUADOR Carchi Tulcán-El Caramelo rd. Elev. 3300m 0°45'0"N 77°40'0"W Ex Siphocampylus ecuadorensis (Campanulaceae) coll. J.L. Luteyn 10 Jan-6 Mar 1985	JLL11314:05 PERU Cajamarca Cajamarca-Celendin rd. Elev. 3080m 7°50'0"S 78°25'0"W Ex Siphocampylus sanguineus (Campanulaceae) coll. J.L. Luteyn 12 Feb 1985	JLL10953:05 ECUADOR Carchi Tulcán-El Caramelo rd. Elev. 3300m 0°45'0"N 77°40'0" W Ex Siphocampylus ecuadorensis (Campanulaceae) coll. J. L. Luteyn 10 Jan-6 Mar 1985	JLL11314:05 PERU Cajamarca Cajamarca-Celend in rd. Elev. 3080m 7°50'0"S 78°25'0"W Ex Siphocampylus sanguineus (Campanulaceae) coll. J. L. Luteyn 12 Feb 1985
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Slide Determination Labels. When you use the Slide Determination Label tool, as described in the section “[Printing or Exporting Slide Specimen Labels: Step by Step](#)” below, Biota prints the following fields from the Specimen, Species, and Genus tables, for each record in the active Specimen Record Set.

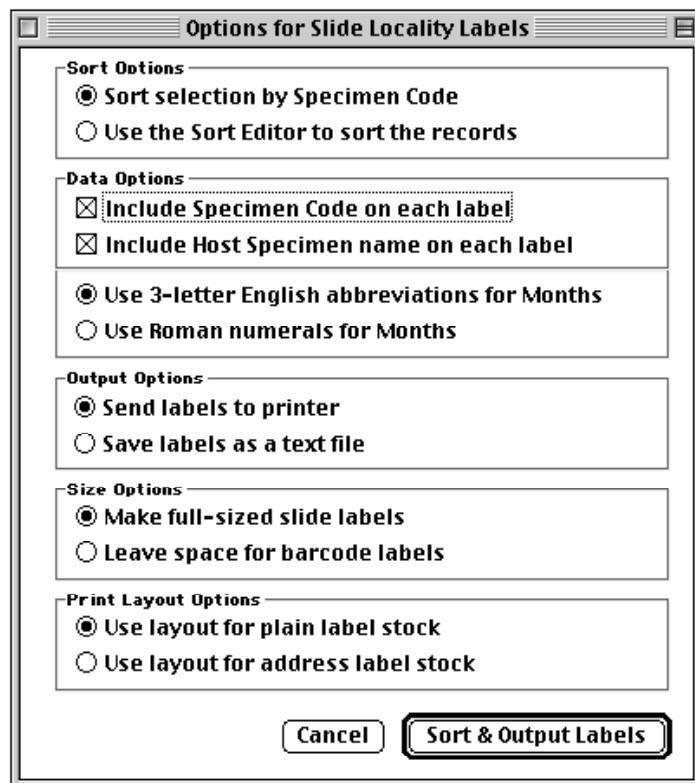
- **Fields from the Specimen record** (see “[Specimen Input](#)” in Chapter 11)
 - ◊ *Optional:* Specimen Code
 - ◊ Stage/Sex
 - ◊ Determined By
 - ◊ Year of “Date Determined” field
- **Fields from the linked Species record** (see “[Species Input](#)” in Chapter 11)
 - ◊ Genus
 - ◊ Specific name
 - ◊ Species Author (unless subspecies and/or variety recorded)
 - ◊ Subspecific name (if any)
 - ◊ Subspecies Author (if any, unless variety recorded)
 - ◊ Variety (if any)
 - ◊ Variety Author (if any)
- **Fields from the linked Genus record** (see “[Genus Input](#)” in Chapter 11)
 - ◊ Family (optional for vial labels, not available for pin labels)

Here is a pair of slide determination labels, with the Specimen Code and Family options included, shown at normal printed size.

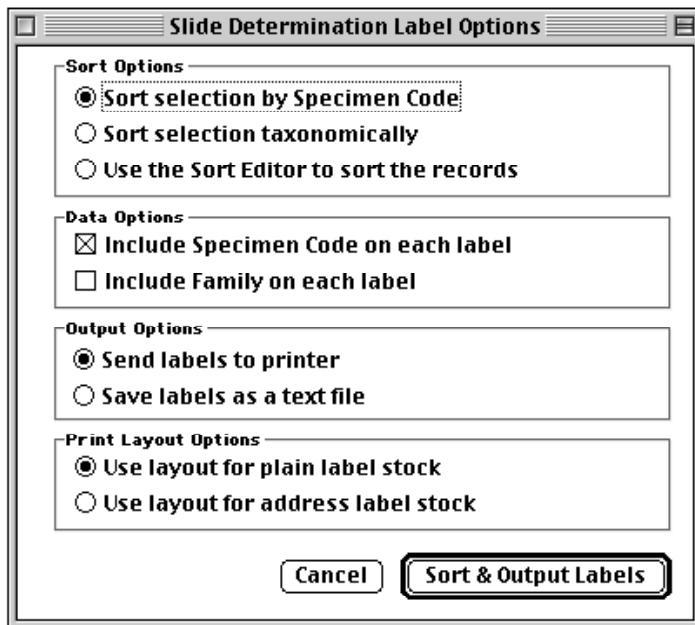
JLL10953:05 Tropicoseius steini sp. n. det. 1993 P. Naskrecki Protomymph ASCIDAE	JLL11314:05 Tropicoseius steini sp. n. det. 1993 P. Naskrecki Adult female ASCIDAE
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Printing or Exporting Slide Specimen Labels: Step by Step

1. **Find the Specimen records for which you wish to print labels or export label data**, using any of the tools in the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Declare these records the current Specimen Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **From the Labels menu, choose:**
 - ***Either: “Slide Labels: Locality.”*** Biota’s response depends on the current setting of the “Coordinate Display” option in the Coordinates tab of the Preferences screen (Special menu). If the “Show Alternate Coordinates” is active in the Preferences screen, an Alternative Coordinates option screen appears (see “[Latitude/Longitude and Alternate Coordinates on Labels or Reports and in Exported Text Files](#)” in Chapter 9), followed by the screen below. With any other “Coordinate Display” settings, the screen below appears immediately.



- **Or: “Slide Labels: Determination.”** The option screen below appears.



4. **Choose a Sort Option and Data Options.** See the section "[Label Option Windows](#)" earlier in this chapter.
5. **Choose an Output Option.** See "[Output Options](#)" earlier in this chapter. Exported text files for Slide Locality or Determination labels can be opened with any word-processing application.
6. **For slide Locality labels, choose a Size Option:**
 - **Either:** Make full-sized labels (22 mm by 22 mm).
 - **Or: Leave space for barcode labels.** In this case, the printed labels measure 22 mm by 16.5 mm, leaving room for a 22 mm by 8 mm barcode label (see Appendix K, "[Barcodes](#)") spanning the end of the slide, with the specimen centered on the slide.
7. **Choose a Layout Option.**
 - **Either: Use layout for plain label stock.** With this option checked, label layout is edge-to-edge, with unscored paper. Acid-free, permanent-adhesive-backed laser or inkjet printer paper is ideal (Avery 5165 or the equivalent).
 - **Or: Use layout for address label stock.** With this option checked, label layout is designed so that groups of three or four labels (the number depends on the Size Option) fit within each address label on prescored, adhesive-backed, address label stock for laser or inkjet printers (Avery 5160 or 5260 or the equivalent, 30 labels per sheet, each 1 in. by $2\frac{5}{8}$ in., 3 columns by 10 rows).

NOTES:

- a. Address label stock is expensive. Print out a draft set of labels on ordinary paper first to check the text and layout and to make sure the labels fit properly on the label stock. (Hold the stock in front of the paper-printed label sheet against a strong light to check the alignment.)
 - b. If you want to try out both layouts before buying special paper in quantity, most stationery and photocopy stores will sell you a few sheets of each kind.
-

WARNINGS:

- a. In a laser printer, never use any adhesive label stock not specifically intended for laser printers.
 - b. Use the single-sheet (manual) feed tray on your printer to feed label stock.
 - c. Be sure to open the “face up tray”—the direct exit tray of the printer. Label stock can cause serious (and very sticky) paper jams if forced to exit by the normal, “face-down” route.
-

8. Click the “Sort & Output Labels” button in the options window.
9. Follow the instructions in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Herbarium Specimen Labels

Biota can print standard herbarium specimen labels for dried, sheet-mounted specimens. Elements on the labels include both locality and determination data, as customary for herbarium labels. Numerous options allow flexibility regarding which elements are included on the labels, and for some elements, the fields they represent in the database. Multiple copies of each label can be printed for duplicate specimens.

Information Included in Herbarium Specimen Label Text

When you use the Herbarium Label tool, as described in the section “[Printing Herbarium Specimen Labels: Step by Step](#)” below, Biota prints the following fields from the Specimen, Collection, Locality, Species, Genus and Project tables, for each record in the active Specimen Record Set:

- **Fields from the Specimen (and Specimen Note) record** (see “[Specimen Input](#)” in Chapter 11)
 - ◊ *Optional:* Specimen Code
 - ◊ Determined By
 - ◊ Date Determined
 - ◊ *Options for Collector's field number:* Specimen Code, Stage/Sex, Medium, Storage, Specimen Custom 1, Specimen Custom 2
 - ◊ *Optional fields to include:* Determined By, Date Determined, Prepared By, Stage/Sex, Medium, Type Status, Specimen Custom 1, Specimen Custom 2
 - ◊ *Optional:* Text field of the first Specimen Note linked to the Specimen record, containing a field description of the plant (optional). See details below.

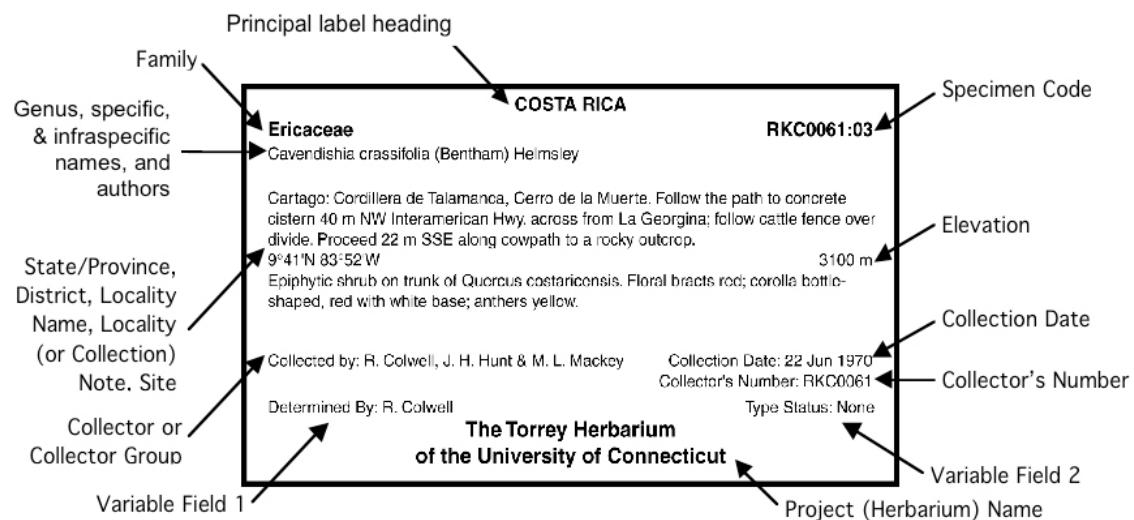
- **Fields from the linked Collection (and Collection Note) record** (see “[Collection Input](#)” in Chapter 11)
 - ◊ Collected By (See details in [the Note below](#) for treatment of Individual and Group Personnel records.)
 - ◊ Date Collected or collection date range (See “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9.)
 - ◊ *Options for Collector's field number:* Collection Code, Method, Source, Site
 - ◊ *Optional fields to include:* Collection Method, Site, Source
 - ◊ *Optional:* Site, as a component of Locality description, or as Collector's Field Number
 - ◊ *Optional:* Text field of the first Collection Note linked to the Collection record, containing details on the collecting site or locality. See details below.
- **Fields from the linked Locality (and Locality Notes) record** (see “[Locality Input](#)” in Chapter 11)
 - ◊ Country
 - ◊ State/Province
 - ◊ *Optional:* District (as label header)
 - ◊ Locality Name
 - ◊ Elevation
 - ◊ Geographic coordinates: Latitude and Longitude in Degree/Minutes/Seconds (see “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9) or Alternate Coordinates (see “[Alternate Coordinates \(Locality Table\)](#)” in Chapter 9).
 - ◊ *Optional fields to include:* Locality Code, Alternate Coordinates 1-3
 - ◊ *Optional:* Text field of the first Locality Note linked to the Locality record, containing details on the Locality. See details below.
- **Fields from the linked Species record** (see “[Species Input](#)” in Chapter 11)
 - ◊ Genus
 - ◊ Specific name
 - ◊ Species Author (unless subspecies and/or variety recorded)
 - ◊ Subspecific name (if any)
 - ◊ Subspecies Author (if any, unless variety recorded)
 - ◊ Variety (if any)
 - ◊ Variety Author (if any)
 - ◊ *Optional fields to include:* Species Code, Subgenus, Section, Common Name
- **Fields from the linked Genus record** (see “[Genus Input](#)” in Chapter 11)
 - ◊ *Optional:* Family
- **Fields from the linked Project record** (see “[Project Input](#)” in Chapter 16)
 - ◊ Project Name. This area displays the “Document Heading” field of the Active Project record.

NOTE:

The “Collected By” field is treated as follows for herbarium labels:

- **An individual collector:** If the [Personnel] Short Name entered in the [Collection] Collected By field represents an *Individual* Personnel record (see “[Personnel Input](#)” in Chapter 11), the Short Name itself is used for the “collector” element of the labels.
- **A group of collectors:** If the Short Name entered in the [Collection] Collected By field represents a *Group* Personnel record (see “[Personnel Input](#)” in Chapter 11), the Short Name for each member of the Group is included in the collector element of the labels. The order of individual names on the label follows the order displayed in the Group Editor when you click the “Edit Group” button in the Personnel input screen while the Group record is displayed. The names can be reordered using the Group Editor (see “[Displaying, Changing, or Reordering Group Membership for an Existing Group Personnel Record](#)” in Chapter 11).

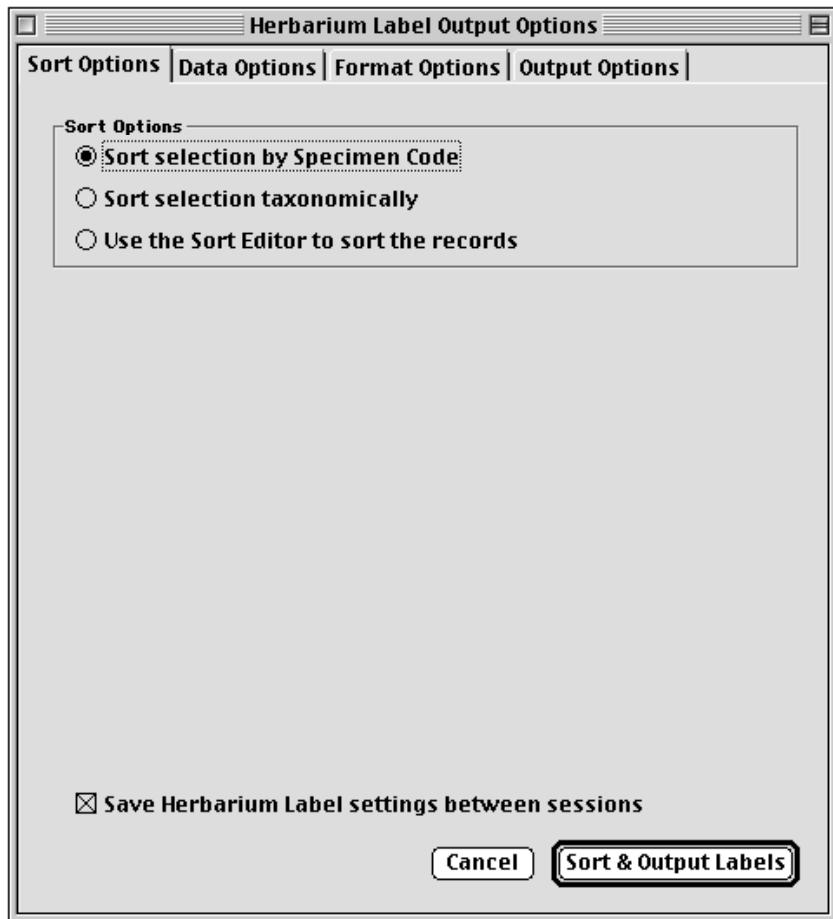
An herbarium label produced by Biota is shown below, with all elements labeled. The actual size of the label, when printed without reduction or enlargement, is 3 in. by 5 in. (7.6 by 12.5 cm is also available as an option.)



Printing or Exporting Herbarium Specimen Labels: Step by Step

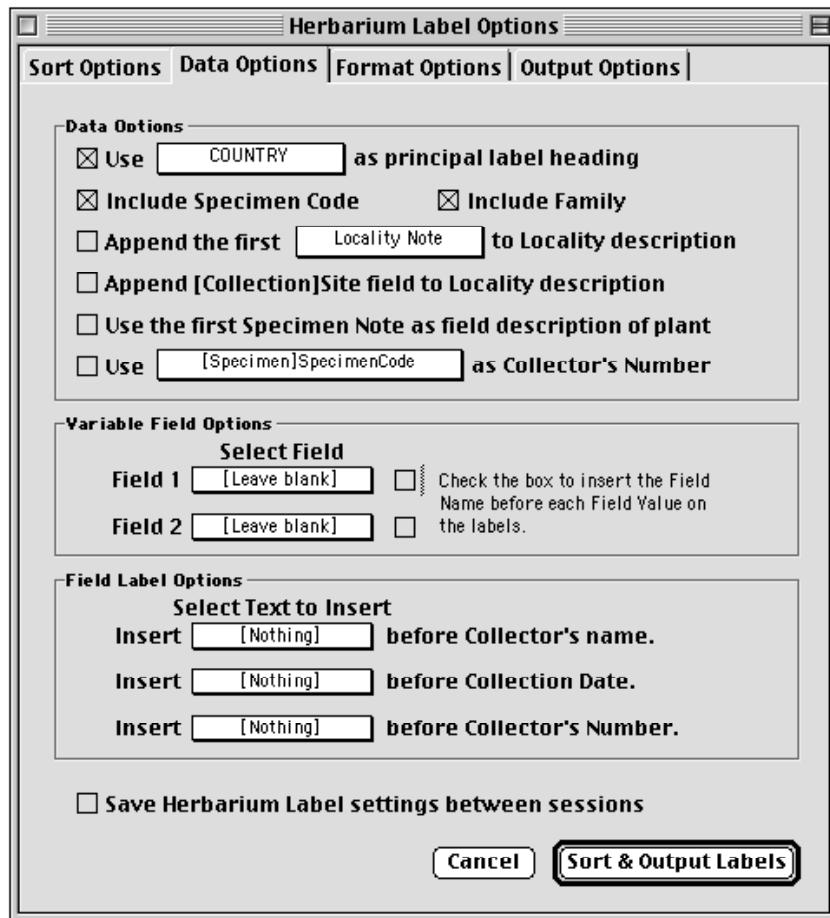
1. **Find the Specimen records for which you wish to print labels or export label data**, using any of the tools in the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Declare these records to be the current Specimen Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).

3. From the Labels menu, choose “Herbarium Labels” from the Labels menu.
The herbarium label option screen appears with the “Sort Options” tab displayed.



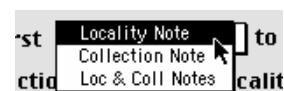
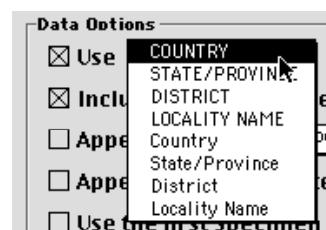
4. Choose a Sort Option. See the section “[Sort Options](#)” earlier in this chapter.

5. Click the “Data Options” tab. The tab is shown below.



6. Choose Data Options. (Each is independent of the others, and none need be checked.)

- **Use {COUNTRY} as principal label heading.** You can choose the principal heading for the labels from the popup list (indicated by curly brackets here) from the following fields in the Locality table: Country, State/Province, District, or Locality Name (all uppercase or mixed case). *Don't forget to check the checkbox as well as making a selection from the popup list.*
- **Include Specimen Code.** See “[Data Options](#)” earlier in this chapter.
- **Include Family.** See “[Data Options](#)” earlier in this chapter.
- **Append the first {Locality Note} to the Locality Description.** This option accommodates long locality descriptions and/or habitat descriptions on herbarium specimen labels. If you check this option, Biota will include the “Note Text” field from the first Note for either the Locality record, the Collection record, or both. (The first Note for a record is the Note with the



earliest Note Date). *Don't forget to check the checkbox as well as making a selection from the popup list.*

In all cases, the Note Text is appended to the string: [Locality] State/Province + [Locality] District + [Locality] Locality Name.

NOTE: In Biota 2.x, the “Locality Name” field itself can accommodate very long descriptions (up to 32,000 characters). This option and the next one are available in Biota 2 primarily to maintain backward compatibility with Biota 1.x Data Files, although you may find other reasons to use them.

- **Append [Collection] Site field to the Locality description.** If you check this option, whatever has been entered in the Site field of the Collection record will be appended to the State/Province, District, Locality Name string on the label.

If you check this option and also “Append the first {Locality Note} to the Locality Description” (see above), the order of Notes and the Site information depends on the Note selection.

- ◊ **If you select “Locality Note”** and also check “Append [Collection] Site field to the Locality Description,” the [Collection] Site value *follows* the Locality Note text.
- ◊ **If you select “Collection Note”** the [Collection] Site value *precedes* the Collection Note text, to maintain the correct hierarchy of information.
- ◊ **If you select “Loc & Coll Notes”** and also check “Append [Collection] Site field to the Locality Description,” [Collection] Site value is placed between the Locality Note text and the Collection Note text in the text string.

NOTE: In Biota 2.x, the “Locality Name” field itself can accommodate very long descriptions (up to 32,000 characters). This option and the previous one are available in Biota 2 primarily to maintain backward compatibility with Biota 1.x Data Files, although you may find other reasons to use them.

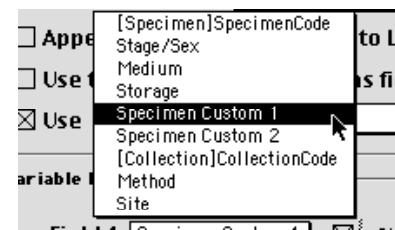
- **Use the first Specimen Note as field description of plant.** To accommodate the inclusion of a field description of the living material for each Specimen (habit, colors of floral structures, etc.), you can record the description as a Specimen Note for that Specimen record (see “[Notes Input](#)” in Chapter 11). Since each Specimen record can have any number of attached Notes (e.g., comments on the specimen by different botanists who have studied it), Biota needs some way to tell which note contains the field description in its Note Text field.

The convention Biota uses is a natural one: *the earliest Specimen Note, by Note Date, for each Specimen is assumed to contain a field description in its Note Text field.* Since field descriptions normally carry the date the specimen was collected, no earlier Note Date could be legitimate, in any case.

If you leave this option unchecked, if there are no Notes for a Specimen, or the earliest Note has a blank Note Text field, the field description of the plant is simply left blank on the label. If you need to print labels for a mixture of specimens, some of which have field descriptions in the earliest Specimen Note and some of which have other information in the earliest Note, you can either (1) print them in two sets, with this option checked for the set with field descriptions;

or (2) enter a Note with the collection date in the Note Date field but no entry in the Note Text field, for the specimens with that lack field descriptions.

- **Use {[Specimen] Specimen Code} as the Collector's Number.** The Collector's Field Number for the specimen is the link between the specimen and the collector's field notes. There are nine alternative fields you can use for the collector's number for the specimen, which Biota will include on herbarium labels if you check this option. Where you decide to keep track of Collector's Field Numbers in Biota depends on your collecting practices and data entry decisions.



Don't forget to check the checkbox in addition to making a selection from the popup list.

The options offered are:

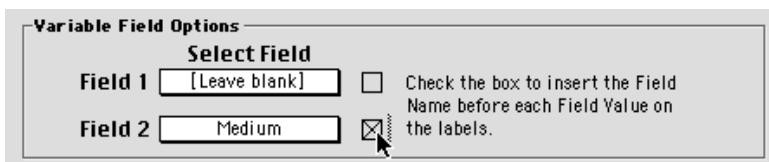
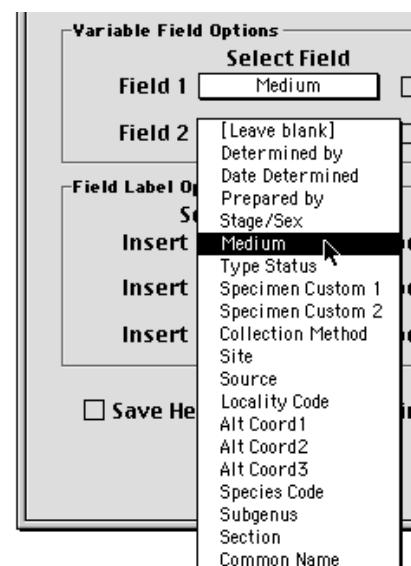
- ◊ **Fields in the Specimen record:** Specimen Code, Stage/Sex, Medium, Specimen Custom 1, and Specimen Custom 2.
- ◊ **Fields in the linked Collection record:** Collection Code, Method, or Site.

NOTE: You can change the name of any of these fields except Specimen Code and Collection Code to *Collector's Number* using a Field Alias. The Alias will appear in the popup list in place of the default field name. See Chapter 18, [“Renaming Fields.”](#)

7. **Choose Variable Field Options.** Using the popup field lists labeled “Field 1” and “Field 2” in this panel, you can add up to two fields of your choice to each specimen label, or leave the areas blank by selecting “[Leave blank].” The field options are illustrated at the right.

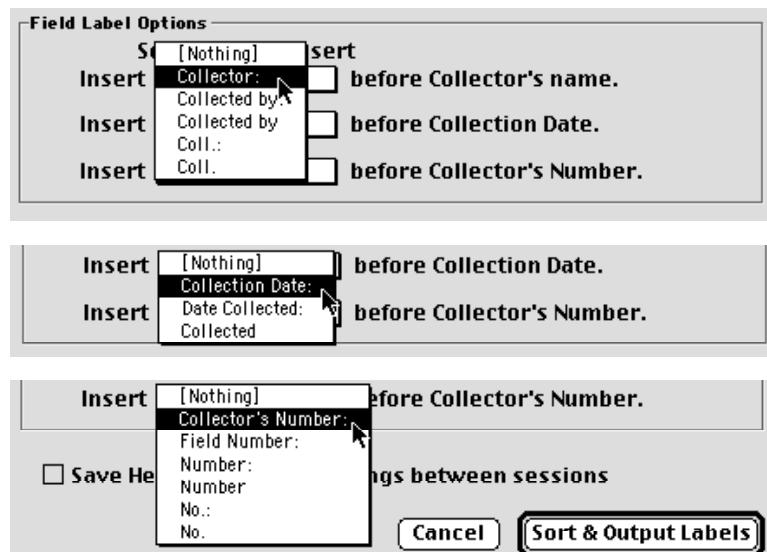
The fields you specify will appear just above the Project Name and just below the Collector's name (Field 1) and Date Collected (Field 2) in the herbarium labels, as illustrated in the introduction to the section [“Herbarium Specimen Labels.”](#)

Once you select a field from the list in the Variable Field popup, you can instruct Biota to insert the name of the field before its value on each specimen label by checking the checkbox next to the Field 1 or Field 2 popup list in the Variable Field Options panel, as illustrated below for the Medium field selected as Field 2.



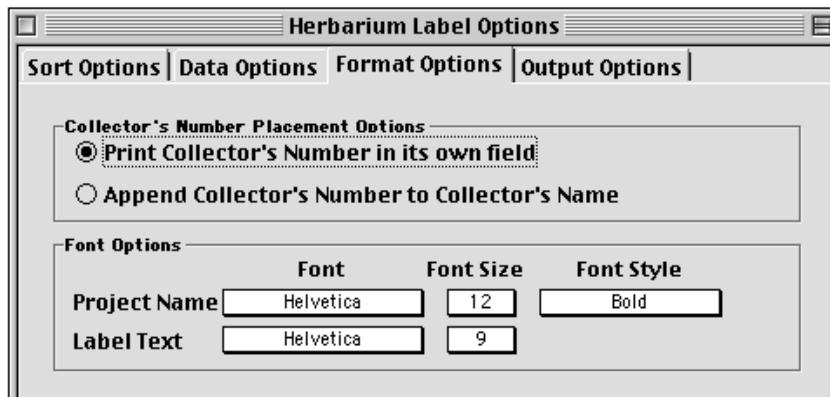
NOTE: If you have defined an Alias (see Chapter 18, “[Renaming Fields](#)”) for any of the fields in this list, the Alias will appear in place of the default field name in the field selection list shown above, as well as on the labels (as Field Name Labels) if you check the checkbox.

8. **Choose Field Label Options.** In this panel, you can choose field labels you wish to include on the herbarium specimen labels for the fields “Collector’s Name,” “Collection Date,” and for the field you have designated as the Collector’s Number—or select “[Nothing]” to omit field labels and print only the values for these fields. The options are illustrated in the popup lists, below.



NOTE: If you have enabled the Spanish option in the Language tab of the Preferences screen (Special menu), a series of Spanish field label options appears along with the English options illustrated above.

9. **Click the “Format Options” tab.** The tab is shown below.



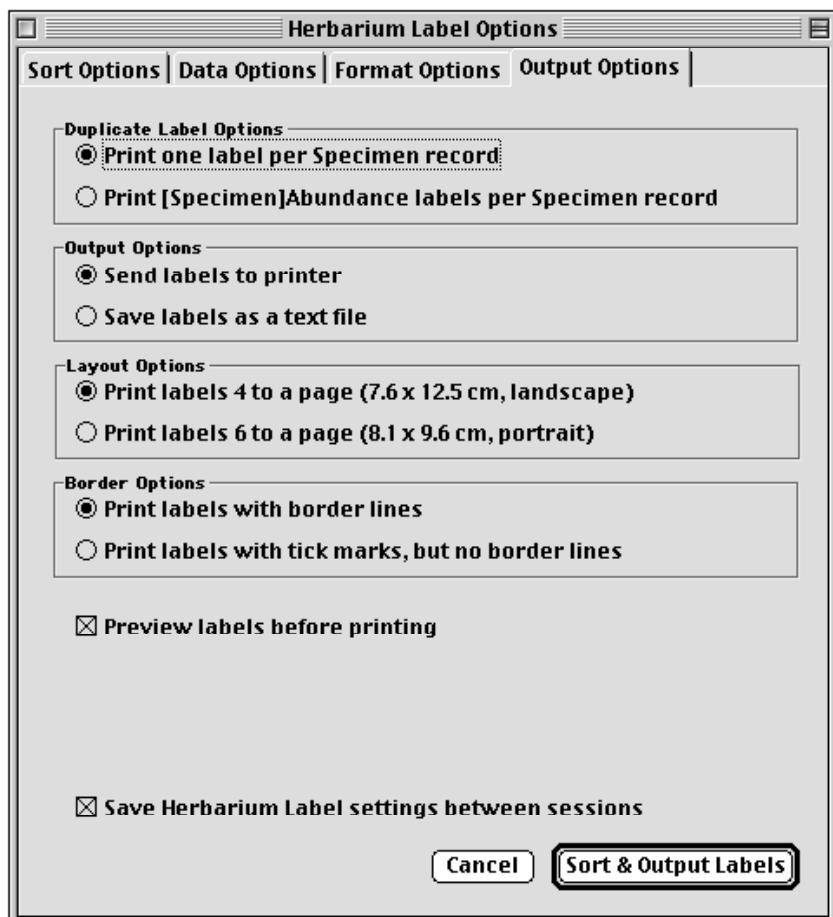
10. Choose a Collector's Number Placement Option.

- **Option 1: Print Collector's Number in its own field.** With this option selected, the Collector's Number appears, with the label specified in [Step 6](#), above, in a special field just below the Collection Date (as illustrated on the example label in the section, “[Information Included in Herbarium Specimen Label Text](#),” earlier in this chapter.)
- **Option 2: Append Collector's Number to Collector's name.** If you choose this option, the Collector's Number (specified in [Step 6](#), above) appears after the Collector's name in the Collector or Collector Group field on the label, preceded by the field label specified in [Step 8](#), above.

11. Choose Font Options. The settings in this panel control the appearance of the herbarium specimen labels.

- **The “Project Name” settings** control font, font size, and style for the herbarium, collection, or other name that appears at the bottom of each label. You enter the text for the Project Name field in the “Document Heading” field of the Active Project record. (See “[Entering Project Data: The General Tab](#)” in Chapter 16.)
- **The “Label Text” setting** controls the font used for the rest of the label layout. You can choose a sans serif font or a serif font. In either case, a 9-point font size is used, except that “Principal label heading” (see [Step 6](#), above) is set in 10-point bold (uppercase), Family is set in 10-point bold, and the Project Name is formatting is controlled separately (see above).

12. Click the “Output Options” tab. The tab is shown below.



13. Choose a Duplicate Label Option.

- **Option 1:** Print one herbarium label per Specimen record in the active Specimen Record Set.
- **Option 2: Print [Specimen] Abundance duplicate labels per Specimen Record.** With this option selected, Biota looks at the Abundance field for each record in the current Specimen Record Set. If the Abundance value in the record is 1 (the default for all new Specimen records, see “[Specimen Input](#)” in Chapter 11), one label is printed for that Specimen record. If the Abundance value is the number n , then n identical, duplicate labels are printed for the record.

NOTE: If no label is printed for a record in the current Specimen Record Set, under Option 2, the record probably has a zero in the Abundance field. Change it to 1 for one label, or to the number n for n labels.

14. Choose an Output Option. See “[Output Options](#)” earlier in this chapter. Exported text files for Herbarium Specimen labels are in tab-delimited format. They can be opened with any spreadsheet or word-processing application.

NOTE: You can use Microsoft Word Mail Merge tools (or the equivalent in another application) to design your own labels, using the exported delimited text file to provide the input fields.

15. Choose a Layout Option.

- **Option 1: Print labels 4 to a page (7.6 x 12.5 cm, landscape).** This option offers maximum space for long locality names and field descriptions.
- **Option 2: Print labels 6 to a page (8.1 x 9.6 cm, portrait).** This option allows less space for long locality names and field descriptions.

NOTE: You can also increase the amount of text that will fit on herbarium labels by reducing the Font Size in the Font Options panel of the Format Options tab (see [Step 11](#), above).

16. Choose a Border Option.

- **Option 1: Print labels with border lines.** If you choose this option, Biota prints a simple, fine line border around each label.
- **Option 2: Print labels with tick marks, but no border lines.** If you choose this option, Biota prints very fine tick marks outside the area of the labels as a guide for cutting the labels apart after printing.

17. Choose a Preview option. If you check the “Preview labels before printing” checkbox, Biota automatically sets the Preview option in the “Print” window for your active printer. See “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.**18. Choose a Save settings option.** If you check the “Save Herbarium Settings between sessions” checkbox, Biota saves your current option settings not only between uses of the Herbarium Labels tool within the current Biota work session, but stores them (transparently) in your Data File until changed in a later session.

19. Click the “Sort & Print Labels” button in the options window.
20. Follow the instructions in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Species Labels

Species Labels are used to identify conspecific sets of specimens in collections. They may be used to label unit trays in entomological collections or species folders in herbaria, for example.

Information Included on Species Labels

When you use the Species Label tool, as described in the next section, Biota prints the following fields from the Species table.

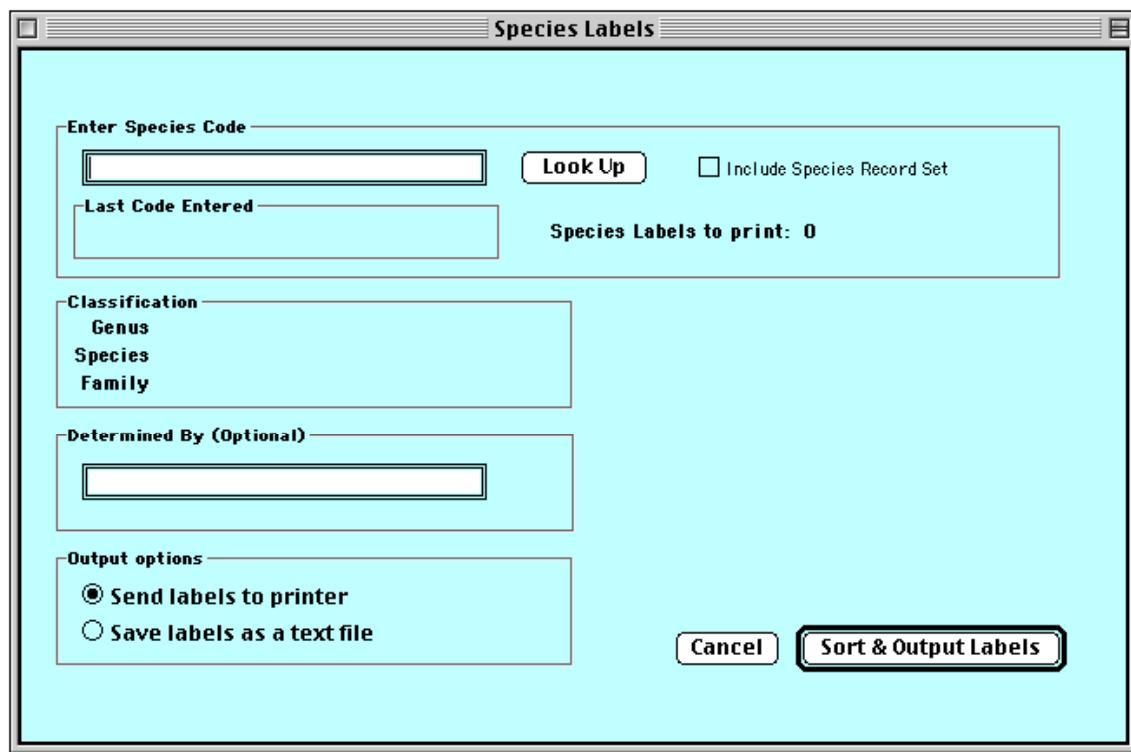
- **Fields from the Species record** (see “[Species Input](#)” in Chapter 11)
 - ◊ Species Code
 - ◊ Genus
 - ◊ Specific name
 - ◊ Species Author (unless subspecies and/or variety recorded)
 - ◊ Subspecific name (if any)
 - ◊ Subspecies Author (if any, unless variety recorded)
 - ◊ Variety (if any)
 - ◊ Variety Author (if any)
- **Field from the Personnel table.** As an option, you can include an additional line to show who determined the particular set of specimens that you intend to label with a Species label:
 - ◊ Personnel Short Name field for the determiner (optional)

Here are three examples of Species labels (determination option not included).

Cactospiza heliopterus (Snodgrass & Heller) 1901 Sp. Code: cactheli	Strumigenys godmani Forel 1899 Sp. Code:	Cavendishia crassifolia (Bentham) Hemsley Sp. Code:
---	---	--

Printing Species Labels: Step by Step

- From the Labels menu, choose Species Labels. The Species Labels setup screen appears.



- Define the set of Species records for which to print labels. There are three different ways to specify which species to include in a print run of Species Labels. *These methods can be used in any combination.*

- Species Record Set method.**
 - Find the Species records** for which you wish to print labels, using any of the tools in the Find menu (see Chapter 12, “[Finding and Updating Records](#)”).
 - Declare these records the current Species Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
 - Click the “Include Species Record Set” checkbox** in the Species Labels setup screen to set this option.



- **Species Code entry method.**

- In the Enter Species Code box, enter a Species Code. You can enter a full Species Code—manually or with a barcode reader (see Appendix K, “[Barcodes](#)”), or enter a partial code and use the wildcard entry method (see “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7).
- Press the TAB key.** The “Last Code Entered” display area now shows the Species Code you entered and the Classification panel shows information for the record found.

The screenshot shows a software interface for entering species codes. At the top, there is a label "Enter Species Code" above a text input field containing the text "pluan". Below this is a label "Last Code Entered" followed by a display area containing the text "pluan".

The screenshot shows a software interface for entering species codes. At the top, there is a label "Enter Species Code" above a text input field. Below this is a label "Last Code Entered" followed by a display area containing the text "pluangu". At the bottom, there is a "Classification" section with the following details:
Genus: Plutarchia
Species: angulata
Family: Ericaceae

- Repeat with additional Species Codes.

- **“Look Up Species” method.**

- Click the “Look Up” button. Use the techniques described for this tool in [Step 2, Method 5 of the section “Entering Specimen Data: The ‘General’ Tab”](#) in Chapter 11, to find and enter a Species Code.
 - Repeat with additional Species Codes. After each entry, the previous Code will be displayed in the “Last code entry” box.
- Enter a determiner’s name (optional). Use the techniques described in [Step 1 of “Entering Specimen Data: The ‘Determination’ Tab”](#) in Chapter 11 to find and enter the Short Name of a determiner. The name will be included on every Species label in this print run.
 - Choose an Output Option. See “[Output Options](#)” earlier in this chapter. Exported text files for Species labels are in tab-delimited format. They can be opened with any spreadsheet or word-processing application.

The screenshot shows a software interface for looking up species. It features a "Look Up" button with a cursor pointing at it, and a checkbox labeled "Include Species Record Set" which is checked.

The screenshot shows a software interface for determining by. It features a label "Determined By (Optional)" above a text input field containing the text "c. darwin".

NOTE: You can use Microsoft Word Mail Merge tools (or the equivalent in another application) to design your own labels, using the exported delimited text file to provide the input fields.

5. Click the “Sort & Print Labels” button in the Species Labels window. The labels will be sorted taxonomically (see “[Sort Options](#)” earlier in this chapter).
6. Follow the instructions in “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14.

Designing and Printing Custom Labels

Inevitably, the format of the standard labels produced by the tools of the Labels menu will not meet everyone’s specialized label needs. In many cases, you may be able to meet your requirements using the “Save labels as a text file” Output Option (see “[Output Options](#)” earlier in this chapter) to export the label date to a text file, where you can format, modify, or delete label text as you wish, or include additional data.

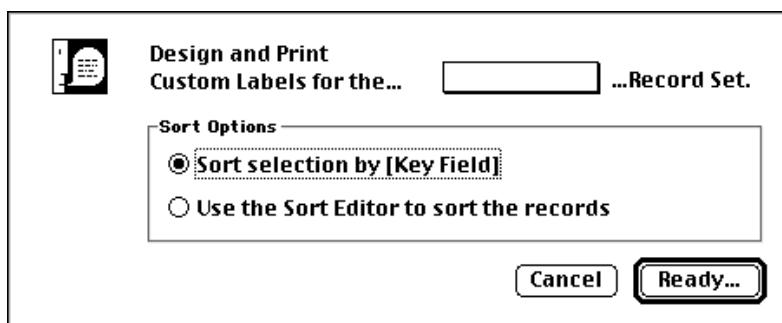
More generally, you can use the Export Editor (see Chapter 27, “[Exporting Data by Tables and Fields](#)”) to export data to a text file from any one table at a time, or the Quick Report Editor (see “[Exporting Custom Flatfiles](#)” in Chapter 27) to export data for fields from related tables. Microsoft Word or other applications have tools you can use to edit and format the data in the exported text file, as you require, before you print the labels.

For specialized labels of any kind, including those that require fields from related (child or parent) tables, consider The 4D Label Wizard, the “off the shelf” 4th Dimension utility described in Appendix D, “[The 4D Label Wizard](#).” But first, read the section below, “[Launching the 4D Label Wizard](#),” to get started.

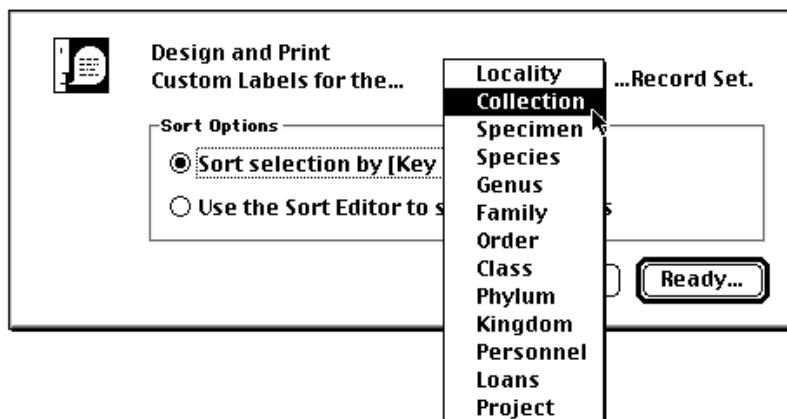
NOTE: You can use the 4D Label Wizard to make labels for records in any Core table (see “[Core Tables](#)” in Chapter 3), specifying fields from that table and any of its *parent* tables. Fields in child tables cannot to be used, because there may be many child records linked to each parent record so the Label Wizard has no way to determine which record to access.

Launching the 4D Label Wizard

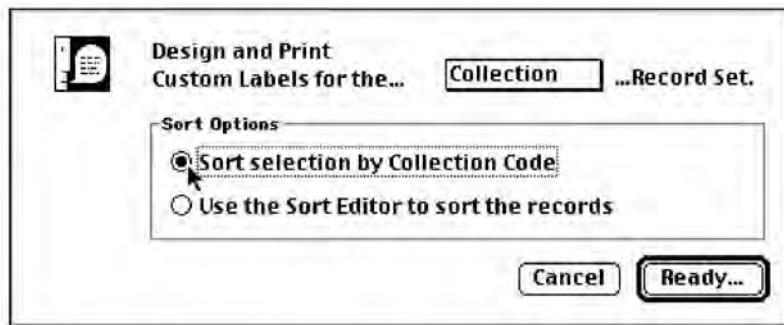
1. Find the records for which you want to print labels, and declare them the Record Set for that table (see “[The Record Set Options Screen](#)” in Chapter 3).
2. From the Labels menu, choose “Design & Print Custom Labels.” A table selection and option screen appears.



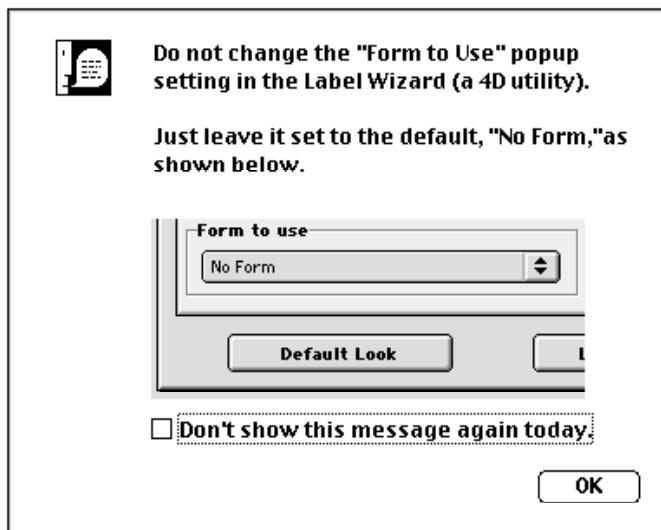
- Click and hold on the table selection popup list, then select the table for which you want to print labels.



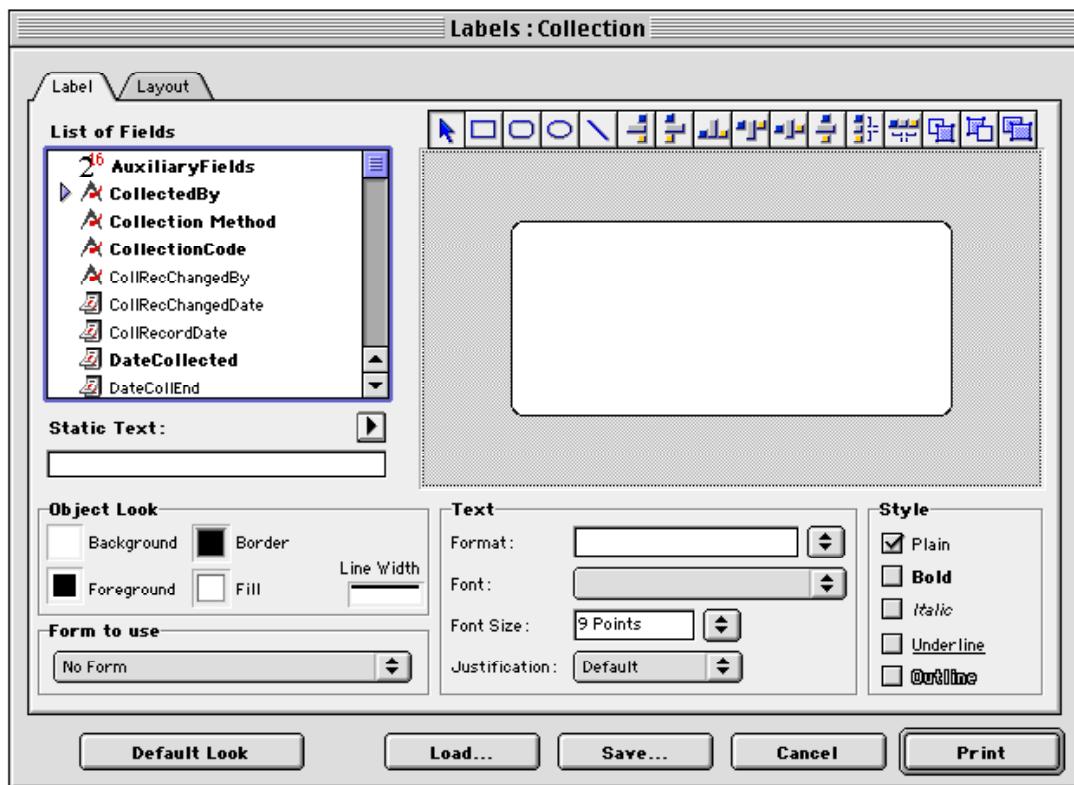
- Choose a Sort Option (See "[Sort Options](#)" earlier in this chapter).



- Click the "Ready" button in the table selection window. A message appears regarding a popup setting in the 4D Label Wizard that must be left set to the default. To bypass the warning for the rest of the current Biota session, click the "Don't show this message again today" checkbox.



6. Click the “OK” button in the message screen. The 4D Label Wizard appears.



7. Follow instructions in Appendix D, [“The 4D Label Wizard.”](#)

NOTE: Because Appendix D is based on a generic 4D document, the examples used in it do not refer to Biota.

Chapter 16

User-Defined Auxiliary Fields and the Project System

As your experience with software of other kinds will doubtless confirm, an application that is too narrow and inflexible is frustrating, whereas one that tries to do everything is ponderous and confusing. Biota is an attempt to strike the right balance between a lean, fast application that suits perfectly the needs of a few, and a jack-of-all trades application that suits no one well.

A relational database, by its nature, is confined within the limits of whatever relational structure the designer gives it. The challenge is to choose a structure that can accommodate a broad spectrum of uses, without greatly compromising the efficiency of the most common operations that users need to carry out.

This chapter and the next two in this Part explain in detail how you can customize Biota to meet special needs by adding Auxiliary Fields and defining Projects (this chapter), setting up Default Entries and Entry Choice Lists (pick lists) for data entry ([Chapter 17](#)), and renaming existing fields ([Chapter 18](#)). See also Chapter 8, “[Record Codes](#),” which explains how to set up custom prefixes for Record Codes.

Core Fields and Auxiliary Fields

In designing Biota’s relational structure (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”), the goal was to place essential and commonly used fields, called Core fields, in the Core tables (see “[Core Tables](#)” in Chapter 3). Inevitably, however, different people with different needs will find some existing fields needless and some needed fields lacking. Biota’s ability to re-name many Core fields with Field Aliases can solve some of these problems (see Chapter 18, “[Renaming Fields](#)”), but if you require more fields than exist in the Core tables (plus linked records in child tables, such as Notes and Images), you will need to create Auxiliary Fields.

Auxiliary Fields, in contrast to Core fields, are special fields that you create and name as you like. Core fields, however, are much faster to sort and to query. For this reason, in planning the way you will use Biota, *wherever possible, it is better to use Core fields, re-named or not, in preference to Auxiliary Fields.*

Any number of Auxiliary Fields can be created for the Species, Specimen, Collection, and Locality tables. The potential uses for Auxiliary Fields are endless, but here are just a few actual examples:

- **Systematists** use Species or Specimen Auxiliary Fields to record values for a character matrix. Biota can export Auxiliary Fields in the NEXUS format for direct use in MacClade¹ or PAUP².
- **Ecologists** use Collection Auxiliary Fields to record the habitat features or meteorological conditions of collection sites or live-organism observation sites. Plant ecologists use Specimen Auxiliary fields to record individual plant age and morphometric data (e.g., diameter at breast height).
- **Ethnobotanists** use Species Auxiliary fields to record uses of each species in matrix format.
- **Museums, herbaria, and reserves** use Species Auxiliary fields to record such ancillary data as conservation status and provenance.

How Auxiliary Fields Work

NOTE: Please do not skip this section. Auxiliary Fields are not complicated, but if you fail to understand how they work you will likely cause yourself needless problems.

Auxiliary Field Value Tables

Biota's Auxiliary Field system does not actually create "hard-wired" new fields in the Core tables. (There is no way to do that in a compiled database application.) Instead, data entered in an Auxiliary Field are kept in a special "triplet" format in a linked "Auxiliary Field Value Table" (either the *Specimen Field Value* table, the *Species Field Value* table, the *Collection Field Value* table, or the *Locality Field Value* table).

Suppose you create two Specimen Auxiliary Fields, one called "Bill Length" and the other called "Wing Length" for a Project on birds. Each time you enter a Bill Length or Wing Length value for a Specimen record, Biota creates a new record in the *Specimen Field Value* table, in the format: Specimen Code, Field Name, Field Value. (The Specimen Field Value table has only these three fields, hence the term *triplet*.)

Here are the records for Bill Length and Wing Length in the Specimen Field Value table, linked to the three parent Specimen records through the Specimen Code:

Specimen Code	Field Name	Field Value
SPM00634	Bill Length	0.86
SPM00634	Wing Length	6.31
SPM00635	Bill Length	0.78
SPM00635	Wing Length	6.63
SPM00636	Bill Length	0.82
SPM00636	Wing Length	6.57

¹ Maddison, W. P., and D. R. Maddison. 2000. *MacClade 4: Analysis of Phylogeny and Character Evolution*. Sunderland, MA: Sinauer Associates.

² Swofford, D. L. 2002. *PAUP*: Phylogenetic Analysis Using Parsimony (and Other Methods) 4.0*. Sunderland, MA: Sinauer Associates.

If you use statistical applications, you are probably already familiar with this alternative way of representing tabular data: *Row Index, Column Index, Value*. Even though it requires three entries for each Value, this format is a more memory-efficient way than setting out a full table for storing “sparse matrices”—tables that are mostly blanks or zeros. For this reason, you need not hesitate to add a new Auxiliary Field that will be used for only a small subset of the records in a Core table, for fear of adding unnecessarily to the size of the Data File. An Auxiliary Field “triplet” record is created only when you actually enter a *value* for an Auxiliary Field. Furthermore, using the Project system, you can control which Auxiliary Fields are available for input, displayed in output, or exported.

Auxiliary Field Name Tables

Linked to each Auxiliary Field Value table (e.g., the *Specimen Field Value* table) is a separate table that simply keeps a list of Auxiliary Field Names (e.g., the *Specimen Field Name* table; see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). Each of the four Auxiliary Field Name tables (the *Specimen Field Name* table, the *Species Field Name* table, the *Collection Field Name* table, or the *Locality Name Value* table) includes an Index field to keep track of the Auxiliary Field order you specify. Except for importing or exporting Auxiliary Field Names, you never need to bother with these tables; Biota does all the record-keeping automatically.

The “Auxiliary Fields” Field in Parent Tables

To keep track of how many Auxiliary Field Values are linked to each parent record, the Species, Specimen, Collection, and Locality tables each have a *field* called “Auxiliary Fields.” Biota automatically updates this field with the number of Field Value records currently linked to the parent record, for *all Projects combined* (see “Projects” later in this chapter). You cannot edit the “Auxiliary Fields” field directly.

Sorting Parent Records Based on Auxiliary Fields

Unfortunately, there is currently no tool for sorting parent records in the parent table Record Listing screen based on linked Auxiliary Field values. However:

- **You can sort parent records according to the *number* of linked Auxiliary Field Values**, simply by selecting the “Auxiliary Fields” field in the Sort Editor. (See “[Sorting Records in Record Listing Screens](#)” in Chapter 10 and “[The ‘Auxiliary Fields’ Field in Parent Tables](#)” earlier in this chapter.)
- **You can use the Query Editor to search for parent records** based on linked Auxiliary Field values. See “[Using the Query Editor with Auxiliary Field Values](#)” and “[Using the Query Editor with Auxiliary Field Values in Combination with Other Criteria](#)” in Chapter 12.

Creating, Editing, and Ordering Auxiliary Field Names

This section tells you how to create new Auxiliary Fields, change the order or name of existing Auxiliary Fields, and how to delete Auxiliary Field Names when you no longer want them. The next section explains how to enter, edit, and delete *values* in Auxiliary Fields.

Opening the Field Name Editor

You use the Field Name Editor to create, change, or delete Auxiliary Fields.

You can access the Field Name Editor directly from the “Aux Fields” tab of the Input screen for each Core table that supports Auxiliary Fields (Specimen, Collection, Locality, and Species). This method is described in the following section, “[Using the Field Name Editor](#).”

Alternatively, you can open the Field Name Editor from the “Auxiliary Field Set” tab of the Project Input screen (see “[Entering Project Data: The ‘Auxiliary Field Set’ Tab](#)” later in this chapter).

Using the Field Name Editor

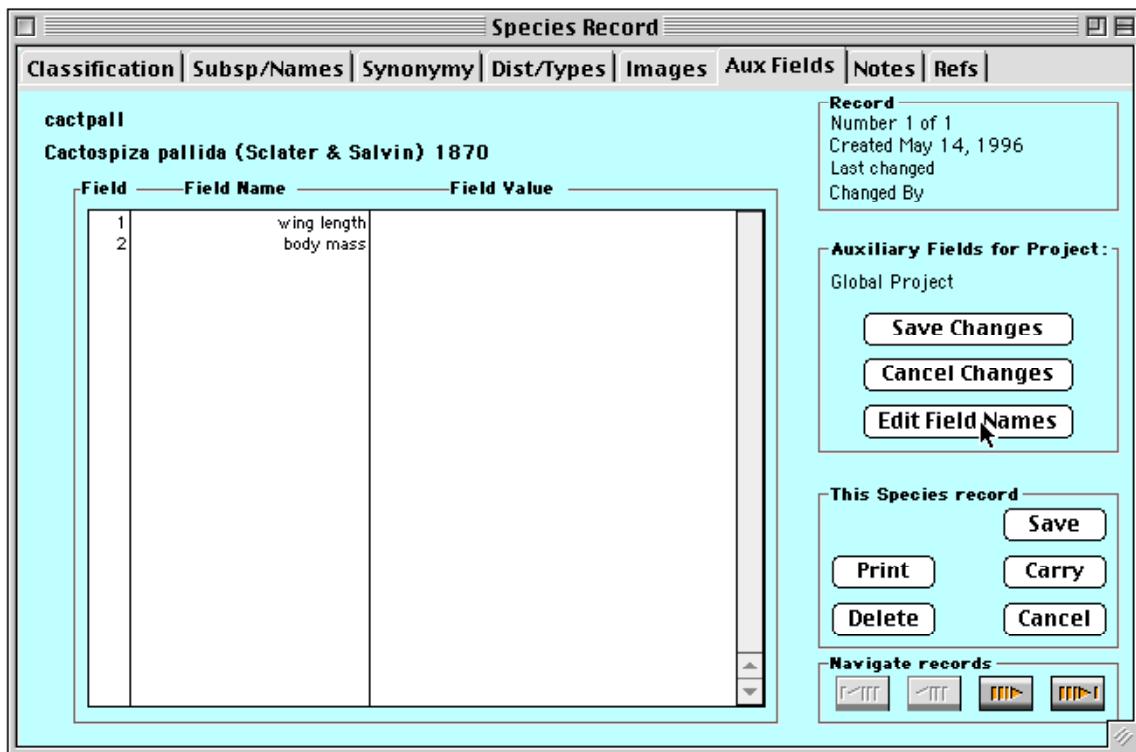
In this section, Species Auxiliary Fields will be used as an example, but the procedures are identical for Specimen, Collection, or Locality Auxiliary Fields.

1. **From the Input menu, choose Species** (or Specimen, Collection or Locality, depending on which table’s Auxiliary Fields you want to work with). The Species Input screen appears.
2. **Enter a Species Code.** Any value will do. You can even Cancel the Species record when you are finished modifying Species Auxiliary Field Names without losing the changes in Auxiliary Field Names.
3. **Click the Aux Fields (Auxiliary Fields) tab** in the Species Input screen.

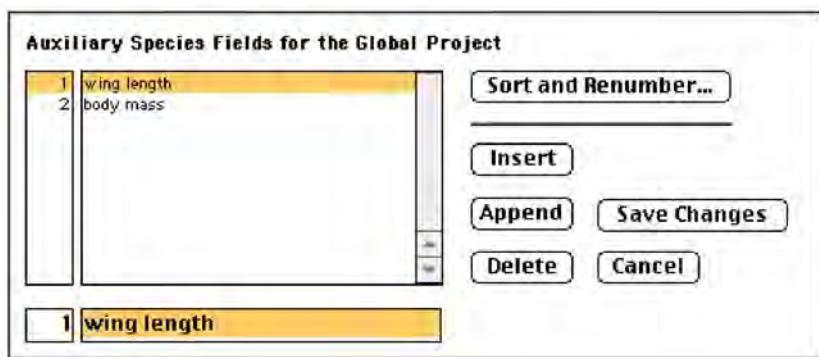


The Auxiliary Fields tab screen appears showing all Species Auxiliary Fields currently defined, together with spaces on the right for recording their value for this record. (No Species Auxiliary Fields are already defined if you are working with your own Data File and have not yet defined any.)

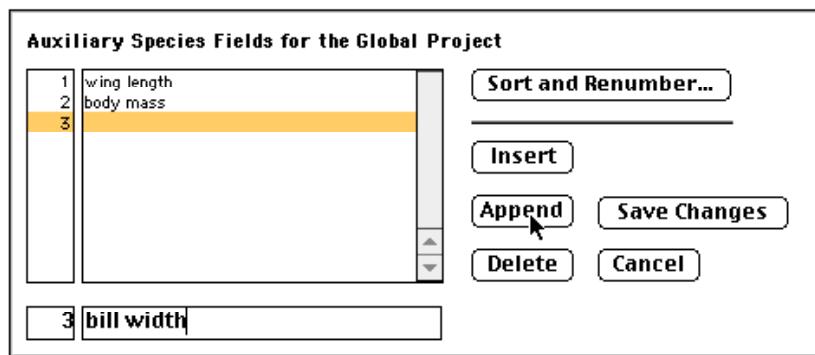
NOTE: If the Global Project is not currently selected as the Active Project, you will see only those Auxiliary Fields associated with the Active Project. To learn how to select the Global Project, see “[Using the Active Project Floating Window](#)” later in this chapter.



4. Open the **Field Name Editor** by clicking the “Edit Field Names” button, as shown above.
5. **Edit, append, insert, delete, re-order, or sort Field Names.**
 - To edit an existing **Field Name**, select the Field Name in the list, then edit it in the entry area at the bottom of the Field Editor window.



- To add a new Field Name at the end of the list, click the “Append” button, then enter the new Field Name in the entry area at the bottom of the Field Editor window, as shown below.

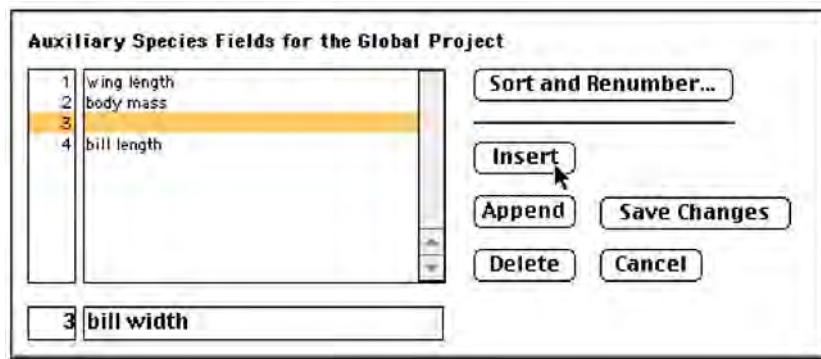


Auxiliary Field Names must be unique, within the set of Auxiliary Field Names for each Core table. If you try to enter a duplicate Auxiliary Field Name in the Field Name Editor, Biota displays the message shown here, and the name is not accepted.

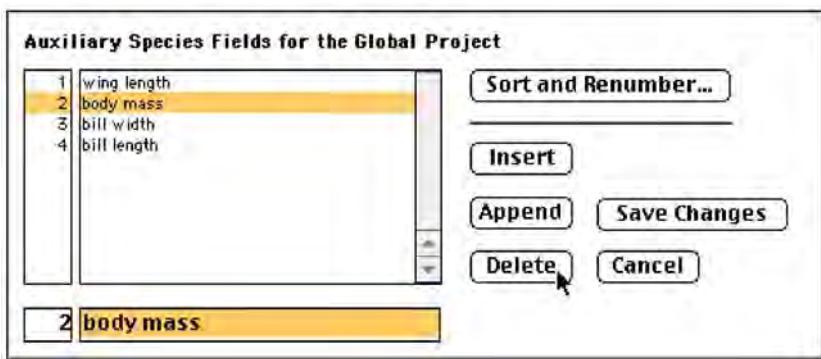


NOTE: Although you cannot create two Species Auxiliary Fields, both named Size, you could create a Species Auxiliary Field and a Specimen Auxiliary Field, both named Size. Of course, there is no restriction on repeated values for Auxiliary Fields in different records. For example, any number of Species can have the value Large for the Size field.

- To insert a new Field Name in the middle of the list, select the existing Field Name you want to follow the new Field Name, then click the “Insert” button and enter the new Field Name in the entry area at the bottom of the Field Editor window, as shown below.

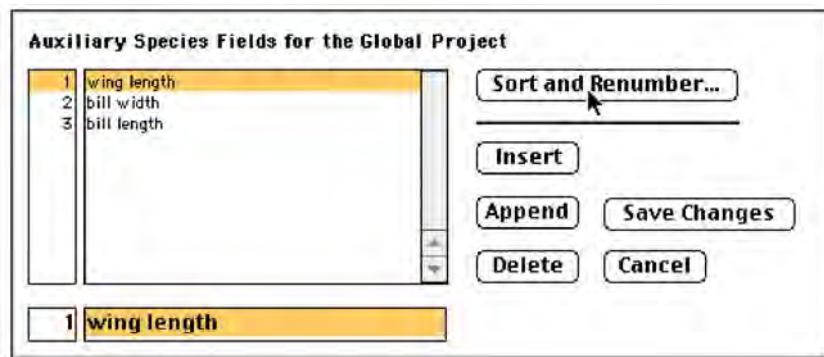


- To delete an existing Field Name, select it in the list, then click the “Delete” button.

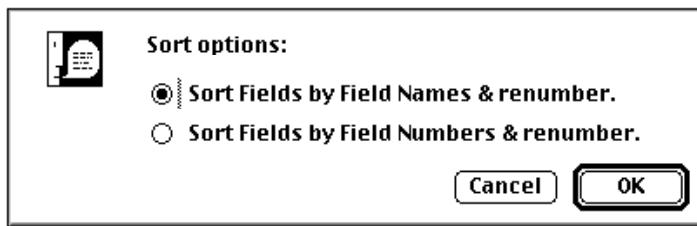


WARNING: Biota will post a warning when you attempt to delete a Field Name. If you confirm the deletion, not only the Field Name, but all Auxiliary Field Values for that Field, for all records that have them, will also be deleted. There is no way to undo this process.

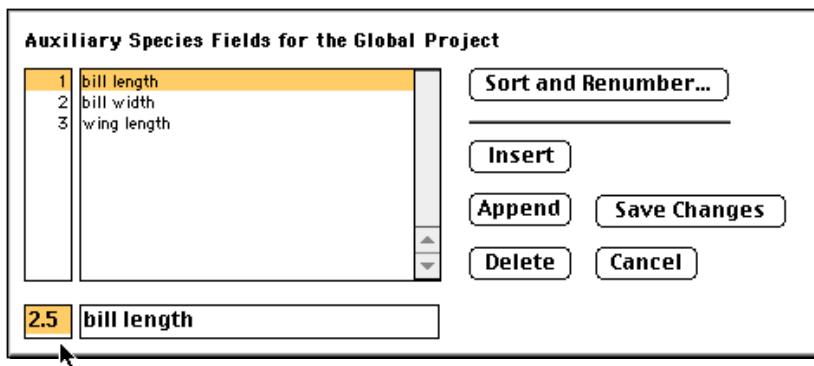
- To sort the Field Names alphabetically, click the “Sort and Renumber” button.



The Sort Option screen appears. Accept the default (“Sort Fields by Field Names & renumber”) by clicking the “OK” button.



- To change the order of the Field Names to a different (non-alphabetic order), edit the sort order numbers to match the desired order in the Number Entry Area of the Field Editor.



NOTE: You need *not* use consecutive numbers, or even integer numbers, as the fields are renumbered consecutively in the next step, based on the rank order of whatever temporary numbers you enter.

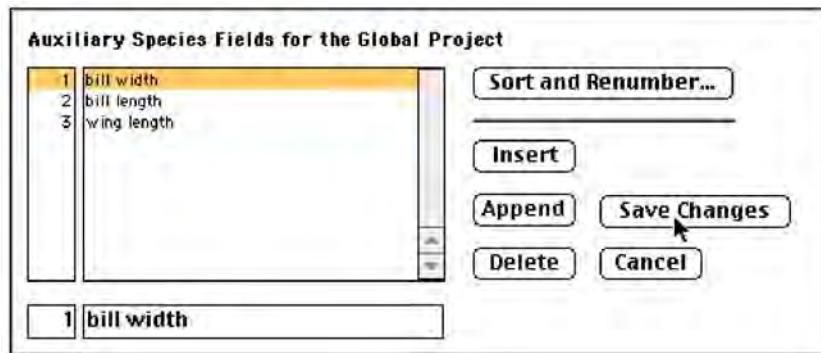
Now click the “Sort and Rerumber” button. The Sort Option screen appears. Choose “Sort Fields by Field Numbers & renumber” then click the “OK” button.



The fields are re-ordered and renumbered.



6. Click the “Save Changes” button in the Field Name Editor to accept the list of fields.



The Field Name Editor disappears, leaving the Aux Fields tab screen of the Species Input screen showing the new fields you created, edited, or re-ordered, ready for Auxiliary Field data entry for this Species record.

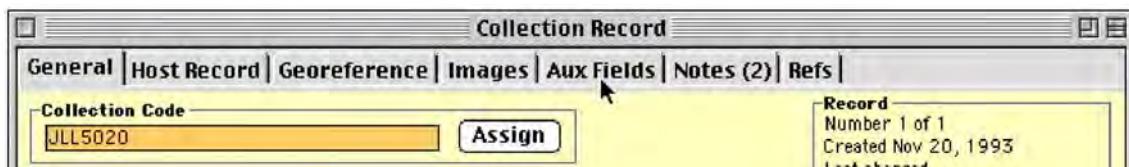
Entering and Displaying Data in Auxiliary Fields

Once you have defined the Auxiliary Field *Names* you want by using the Field Name Editor (see “[Creating, Editing, and Ordering Auxiliary Field Names](#)” earlier in this chapter), you are ready to enter Auxiliary Field *Values* (data) in your Auxiliary Fields.

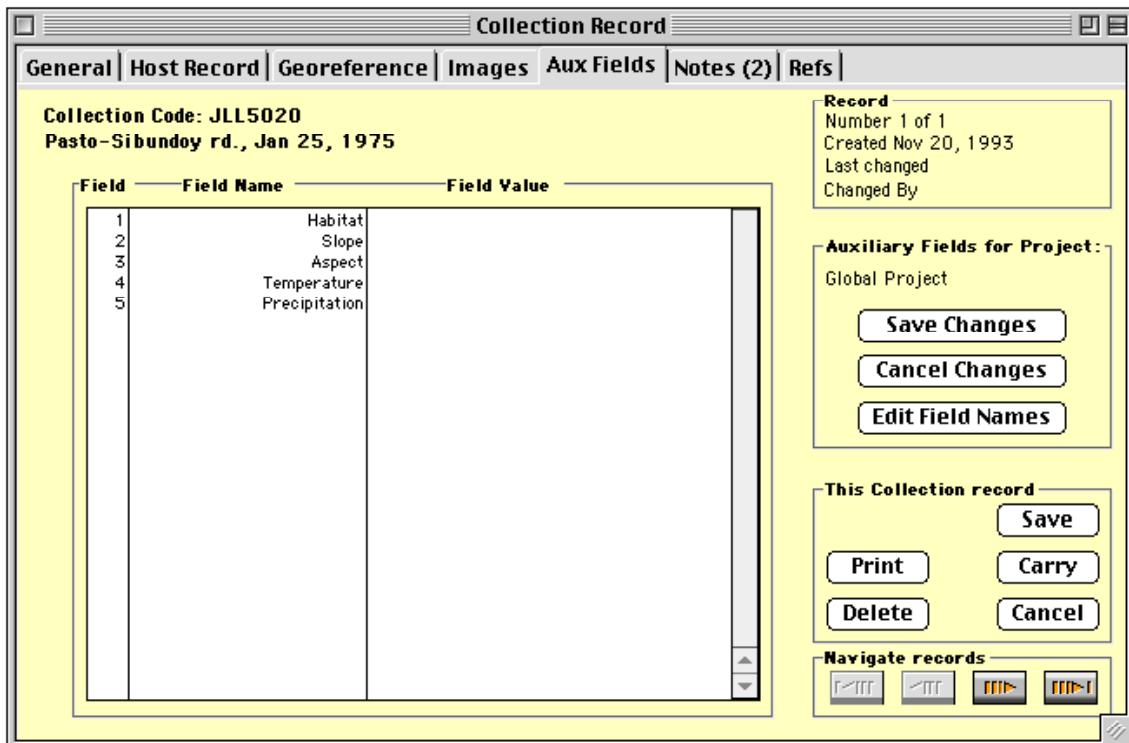
This section uses Collection Auxiliary Fields as an example, but the procedures are identical for Species, Specimen, or Locality Auxiliary Fields.

Entering New Data or Editing Data in Auxiliary Fields

1. **Display a new or existing Species, Specimen, Collection, or Locality record in the input screen**, using any tools from the Input menu (Chapter 11, “[Input—Table by Table](#)”) or the Find menu (Chapter 12, “[Finding and Updating Records](#)”).
2. **Click the Aux Fields tab.**



The Aux Fields tab screen appears showing all Collection Auxiliary Fields currently defined, together with spaces on the right for recording their value for this record. (To add or modify Auxiliary Field *Names*, see “[Creating, Editing, and Ordering Auxiliary Field Names](#)” earlier in this chapter.)

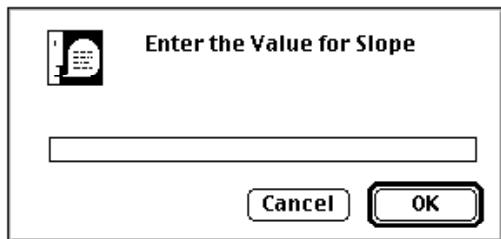


NOTE: If the Global Project is not currently selected as the Active Project, you will see only those Auxiliary Fields associated with the Active Project. To learn how to define Projects, see “[The Project System and Auxiliary Fields](#)” later in this chapter. To learn how to switch between Projects, see “[Using the Active Project Floating Window](#)” later in this chapter.

3. Click anywhere on the line for the field for which you want to enter (or edit) a value. (The “Habitat” field has just been clicked in the example, above.) The Field Value entry window appears.



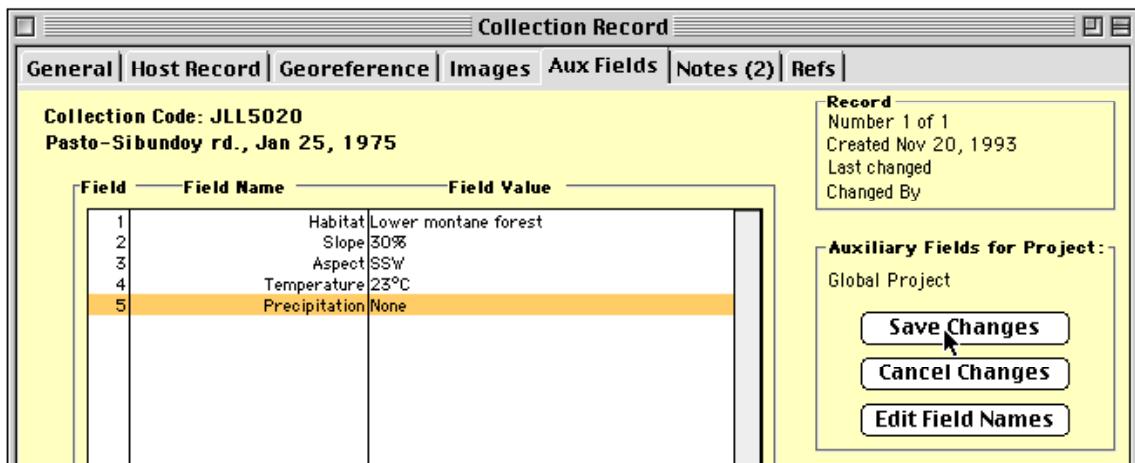
4. Enter a value (or edit the existing value), then click OK (or press the Return key). (The value “Lower montane forest” has been entered for the Habitat Auxiliary Field, in the example above.) The Field Value entry dialog reappears, ready for the Field Value for the next field in the Field Name list (the “slope” field in the example below).



5. If you want to enter or edit a value for this field, do so and click OK. This cycle continues until you reach the bottom of the Field Name list or until you click Cancel in the Field Value entry dialog.

NOTE: For non-sequential value entry, click on the line you want, make the entry or edit the existing value, then click Cancel when asked for a value for the next field.

6. When you have completed the entries and they appear as you wish in the Field Value list, click the “Save Changes” button in the Aux Fields tab screen.



NOTE: If you forget to click the “Save Changes” button before going to a different tab, moving to another record using the navigation buttons, Saving the record, or Carrying the record, Biota saves the new or revised Auxiliary Fields automatically. Therefore, if you make any changes you do not want to keep, be sure to click the “Cancel Changes” button on the Aux Fields tab screen.

- If you have finished working with the record, click the “Save” button for the parent record (the Collection record, in the example here).

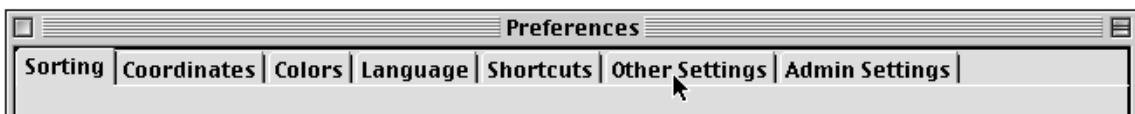


Carrying Auxiliary Fields

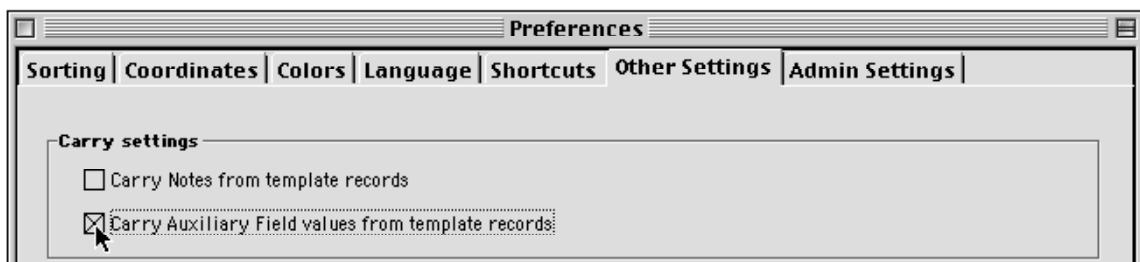
The “Carry” button in Biota Input screens allows you to use an existing record (or a record you have just created) as a template for a new record (see “[Using an Existing Record as a Template for a New Record](#)” in Chapter 10). As an option, you can choose to Carry (copy) all Auxiliary Field Values from the existing record to the new record (for the tables that support Auxiliary Fields).

To enable or disable this option:

- Choose Preferences from the Special menu. The Preferences screen appears.
- Click the “Other Settings” tab in the Preferences screen.



3. In the “Other Settings” screen, click the checkbox labeled “Carry Auxiliary Field Values from template records” to enable (check) or disable (unchecked) the Carry Auxiliary Field Values option. The default setting is disabled (unchecked).



4. Click the “Save” button in the Preferences screen.



Displaying Auxiliary Fields and Their Values for a Selection of Records

1. Display a selection of records for the Specimen, Collection, Locality, or Species table in the Record Listing screen for that table (see Chapter 12, “[Finding and Updating Records](#)”).

In this section, Collection records will be used as an illustration, but the procedures are identical for the other three tables.

The numbers in the “Aux” column (illustrated below) show how many Auxiliary Field Values have been entered from each parent table record (5 for each Collection record, in the example).

Aux Column

Collection Records

Double click a Collection to view or modify record

												Aux
JLL10573	J.L. Luteyn	May 15, 1984	Search	fr.Choco-Valle borde	Ansermanuevo	0	0					0 5
JLL12327	J.L. Luteyn	May 14, 1988	Search	Vereda Amarillas, S	Mpio.ElCairo,Correg. Boqu	0	0					0 5
JLL13393	J.L. Luteyn	Nov 23, 1989	Search	56-60km E Salcedo	Salcedo-Napo rd.	0	0					0 5
JLL14587	J.L. Luteyn	May 2, 1992	Search	5-30 km N Puyo	Puyo-Tena rd.	0	0					0 5
JLL14697	J.L. Luteyn	Oct 16, 1992	Search	9.5 km S Beza	Rd. to Puyo	0	0					0 5
JLL5020	J.L. Luteyn	Jan 25, 1975	Search	km 33-34	Pasto-Sibundoy rd.	0	0					0 5

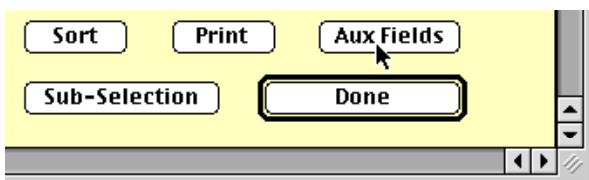
Var Field 1 Var Field 2

Change Var Fields Add Collection Sort Print Aux Fields

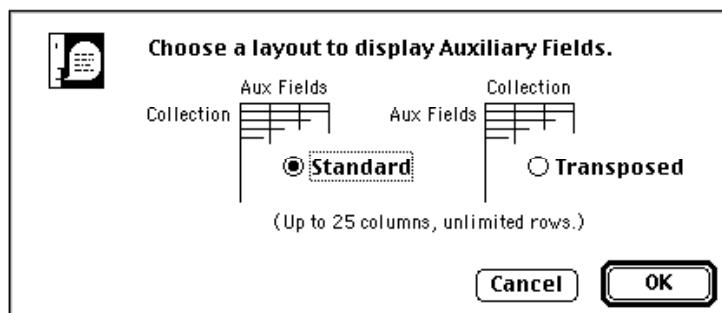
Display Images

Scroll Page Delete Selection Sub-Selection Done

2. Click the “Aux Fields” button at the bottom of the Record Listing screen.



An option window appears, offering two alternative display formats for the Auxiliary Fields for these Collection records.



3. Choose a display option.

- The **Standard option** (the default) displays the Auxiliary Fields in the same orientation as ordinary (Core) fields in the Record Listing screen—in the example, Collection records as rows, Auxiliary Fields as columns. See “[Displaying Auxiliary Fields in the Standard Format: Records as Rows, Auxiliary Fields as Columns](#)” later in this chapter.
- The **Transposed option** (right option button) displays the same information in a transposed format—in the example, it would display Auxiliary Fields as rows, Collection records as columns. See “[Displaying Auxiliary Fields in the Transposed Format: Auxiliary Fields as Rows, Records as Columns](#)” later in this chapter.

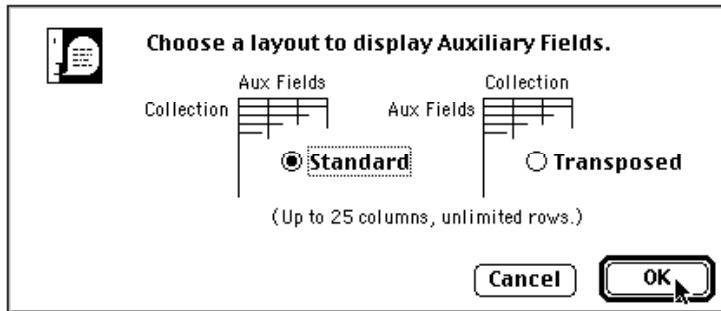
Although these Auxiliary Field display formats are limited to 25 columns, you will be able to examine all your data, regardless of the number of Auxiliary Fields you have defined and regardless of the number of records in the selection.

- **If you have defined 25 or fewer Auxiliary Fields and there 25 or fewer records in the current selection,** choose the option that makes more sense for the information you want to find or compare. (You may have to experiment a bit to know which is better for your purposes.)
- **If you have defined fewer than 25 Auxiliary Fields but there are more than 25 records in the current selection,** you will usually want to choose the Standard Auxiliary Fields display (the left option button). See “[Displaying Auxiliary Fields in the Standard Format: Records as Rows, Auxiliary Fields as Columns](#)” later in this chapter.

- If you have defined more than 25 Auxiliary Fields, but there are fewer than 25 records in the current selection, you will usually want to choose the Transposed Auxiliary Fields display (the right option button). See “[Displaying Auxiliary Fields in the Transposed Format: Auxiliary Fields as Rows, Records as Columns](#)” later in this chapter.
- If you have defined more than 25 Auxiliary Fields and there are more than 25 records in the current selection, choose the option that makes more sense for the information you want to find or compare.

Displaying Auxiliary Fields in the Standard Format: Records as Rows, Auxiliary Fields as Columns

1. Follow the instructions in the section “[Displaying Auxiliary Fields and Their Values for a Selection of Records](#)” earlier in this chapter.
2. In the display options window, make sure the Standard (left button) option is selected, and then click the “OK” button.



The selection of parent table records (Collection records, in the example) appears, with the corresponding values for Auxiliary Fields in labeled columns.

The window title is "Collection Records". It displays a table with 6 records. The columns are: Coll. Code, Date Coll., Locality Name, 1.Habitat, 2.Slope, and 3.Aspect. The data is as follows:

Coll. Code	Date Coll.	Locality Name	1.Habitat	2.Slope	3.Aspect
JLL10573	May 15, 1984	Ansermanuevo	Second growth montan	40%	NE
JLL12327	May 14, 1988	Mpio.El Cairo, Correg. Boquerón	Lower montane forest	15%	SSW
JLL13393	Nov 23, 1989	Salcedo-Napo rd.	Degraded cloud forest	10%	ESE
JLL14587	May 2, 1992	Puyo-Tena rd.	Montane forest	10%	SSW
JLL14697	Oct 16, 1992	Rd. to Puyo	Lower montane wet fo	35%	E
JLL5020	Jan 25, 1975	Pasto-Sibundoy rd.	Lower montane forest	30%	SSW

At the bottom are buttons: Sort, Print, Core Fields, Delete Selection, Sub-Selection, and Done.

In the example above, notice that only the first three Auxiliary Fields are visible (for Habitat, Slope, and Aspect).

3. To see the next set of Auxiliary fields (columns), click in the horizontal scroll bar (where the cursor arrow appears, above), or use the horizontal scroll arrows or “thumb-slider” to move to the right. The next set of fields appears (Temperature and Precipitation, in the example), along with the Record Code (Collection Code, in the example).

The screenshot shows a software window titled "Collection Records". The main area displays a table with six columns: "Collection Code", "4.Temperature", "5.Precipitation", and three empty columns. Below the table are several buttons: "Sort", "Print", "Core Fields", "Delete Selection", "Sub-Selection", and "Done". The window has scroll bars on the right side.

Collection Code	4.Temperature	5.Precipitation			
JLL10573	18°C	None			
JLL12327	21°C	Heavy rain			
JLL13393	16°C	Rain			
JLL14587	16°C	Light drizzle			
JLL14697	24°C	None			
JLL5020	23°C	None			

4. If not all Auxiliary Fields have been revealed, continue to move to the right in the display, using the horizontal scroll bar tools. Up to 25 Auxiliary Fields can be displayed.

NOTE: If you have a monitor wider than the display window, you can expand the window horizontally to see more Auxiliary Fields all at once, as shown below.

The screenshot shows the same software window with the horizontal scroll bar moved to the right, revealing additional columns of auxiliary fields. The table now includes columns for "Coll. Code", "Date Coll.", "Locality Name", "1.Habitat", "2.Slope", "3.Aspect", "Collection Code", "4.Temperature", and "5.Precipitation". The buttons at the bottom remain the same: "Sort", "Print", "Core Fields", "Delete Selection", "Sub-Selection", and "Done".

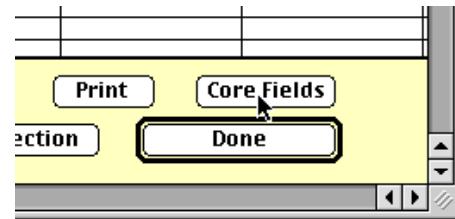
Double Click a Collection to View or Modify Record			6 Records			Double Click a Collection to View or Modify Record		
Coll. Code	Date Coll.	Locality Name	1.Habitat	2.Slope	3.Aspect	Collection Code	4.Temperature	5.Precipitation
JLL10573	May 15, 1984	Anzermanuevo	Second growth montan	40%	NE	JLL10573	18°C	None
JLL12327	May 14, 1988	Mpio. El Cairo, Correg. Boquerón	Lower montane forest	15%	SSW	JLL12327	21°C	Heavy rain
JLL13393	Nov 23, 1989	Salcedo-Napo rd.	Degraded cloud forest	10%	ESE	JLL13393	16°C	Rain
JLL14587	May 2, 1992	Puyo-Tena rd.	Montane forest	10%	SSW	JLL14587	16°C	Light drizzle
JLL14697	Oct 16, 1992	Rd. to Puyo	Lower montane wet fo	35%	E	JLL14697	24°C	None
JLL5020	Jan 25, 1975	Pasto-Sibundoy rd.	Lower montane forest	30%	SSW	JLL5020	23°C	None

5. To view all Auxiliary Fields for a record (or to edit them), double-click a row (a Collection record, in the example) in the Record Listing screen. The individual record appears in the standard Input screen (the Collection Input screen, in the

example). To edit or add Auxiliary Field values to the record displayed, follow the instructions in the section “[Entering New Data or Editing Data in Auxiliary Fields](#)” earlier in this chapter.

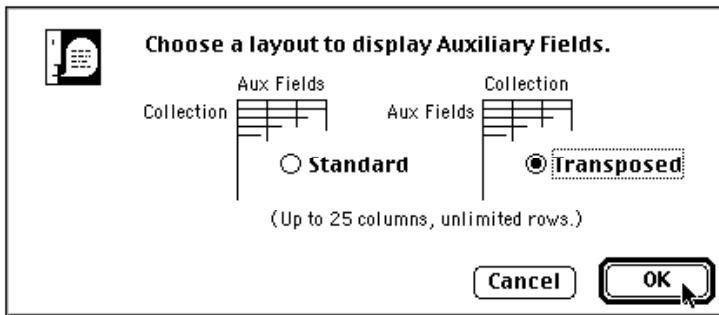
Note: With the parent record (Collection record, in the example) displayed in the Input screen, you can view (and edit) all Auxiliary Field Values for that record by clicking the Auxiliary Fields tab in the Input screen, even if you have defined more than 25 Auxiliary Fields.

6. When you are through using the Auxiliary Fields display screen, you can either dismiss the selection by clicking the “Done” button, or return to the normal Core Fields Record Listing screen to display the current selection of records by clicking the “Core Fields” button on the Auxiliary Fields display screen.

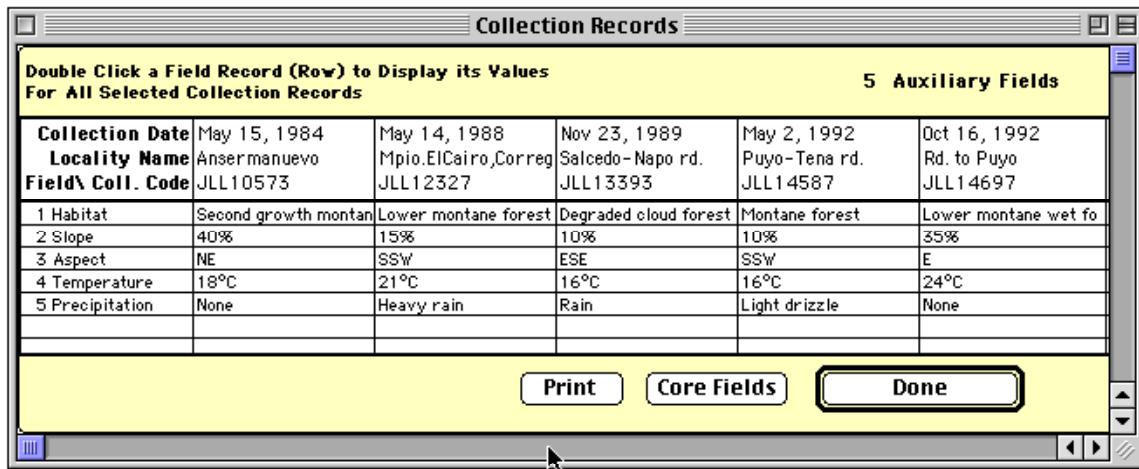


Displaying Auxiliary Fields in the Transposed Format: Auxiliary Fields as Rows, Records as Columns

1. Follow the instructions in the section, “[Displaying Auxiliary Fields and Their Values for a Selection of Records](#)” earlier in this chapter.
2. In the display options window, click the button for the “Transposed” format option, then click the “OK” button.

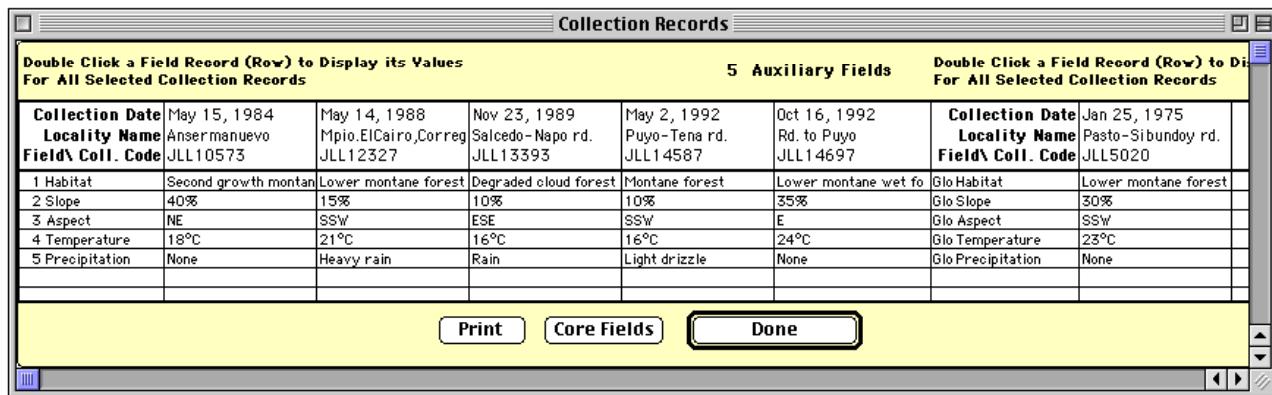


The selection of parent table records (Collection records, in the example) appears, with Auxiliary Field Names labeling the rows of the display and identifiers of the parent table records as column headings. (The identifier fields vary appropriately among for Species, Specimen, Collection, and Locality Auxiliary Fields.)

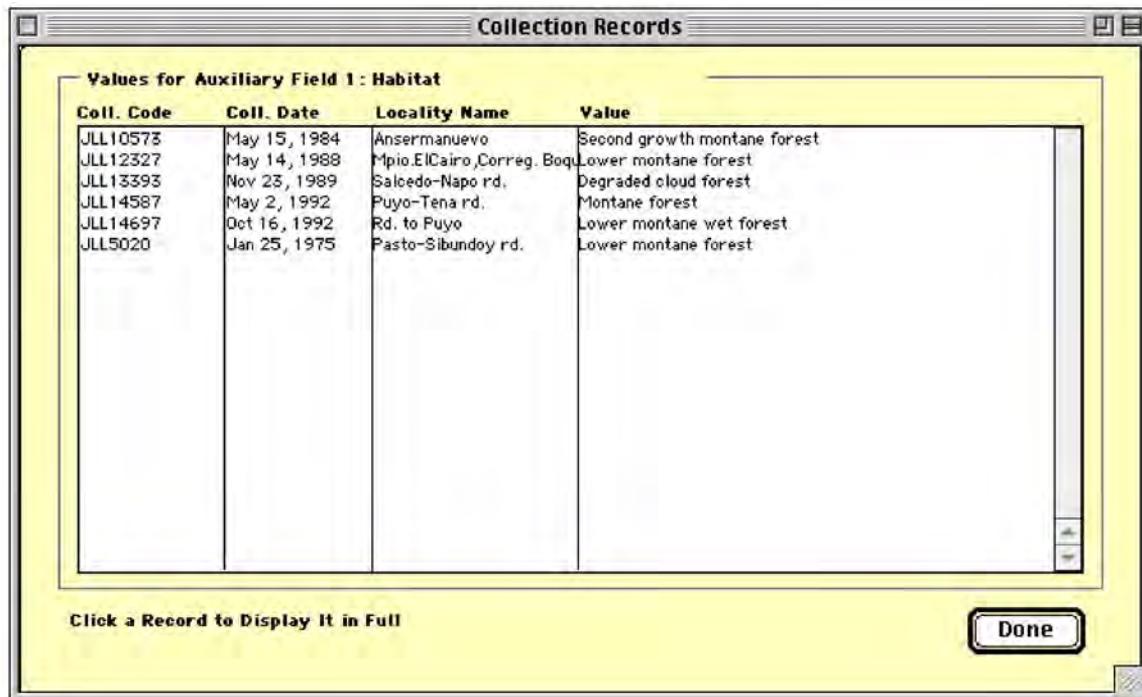


3. If not all columns (records) in the selection are visible, use the horizontal scroll bar to see additional columns.

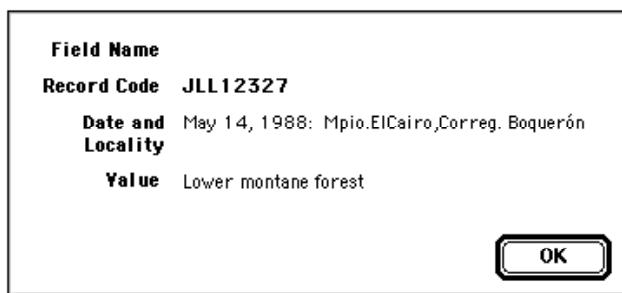
Note: If you have a monitor wider than the display window, you can open the window wider to see more Auxiliary Fields all at once, as shown below.



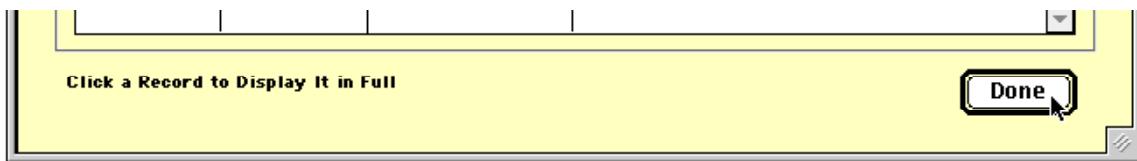
4. To view the Values for all Core records in the selection, for a given Auxiliary Field, double-click a row (a Collection Auxiliary Field, in the example). The Auxiliary Field expansion screen appears listing the Value for that Auxiliary Field ("Habitat" in the example below) for each parent table record (each Collection record, in the example) in the current selection, even if there are more than 25 parent table records in the selection.

**NOTES:**

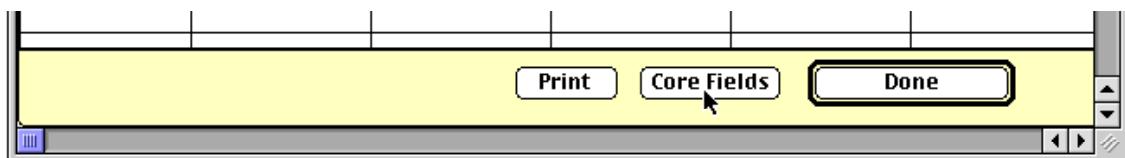
- a. This screen is available only with Transposed display format for Auxiliary Fields, not with the Standard format.
 - b. Auxiliary Field Values and Auxiliary Field Names cannot be edited in this screen. See "[Entering New Data or Editing Data in Auxiliary Fields](#)" earlier in this chapter for instructions on editing of adding Auxiliary Field data.
-
5. If an Auxiliary Field Value or an identifier field is too long to read fully in the display, you can double-click the record in the screen above, to display the information in full.



- Click the “Done” button at the bottom of the Auxiliary Field expansion screen, when you are through examining the values.



- When you are through using the Auxiliary Fields display screen, you can either dismiss the selection by clicking the “Done” button, or return to the Core Field display for the current selection of records by clicking the “Core Fields” button on the Auxiliary Fields display screen.



Printing Auxiliary Fields

You can print Auxiliary Fields and their values for a selection of parent table (Specimen, Species, Collection, or Locality) records in any of four formats: in matrix (row-by-column) format, either Standard or Transposed (see below); or in triplet format, either Standard or Transposed. (For details on these formats see “[Displaying Auxiliary Fields in the Standard Format: Records as Rows, Auxiliary Fields as Columns](#)” and “[Displaying Auxiliary Fields in the Transposed Format: Auxiliary Fields as Rows, Records as Columns](#)” earlier in this chapter).

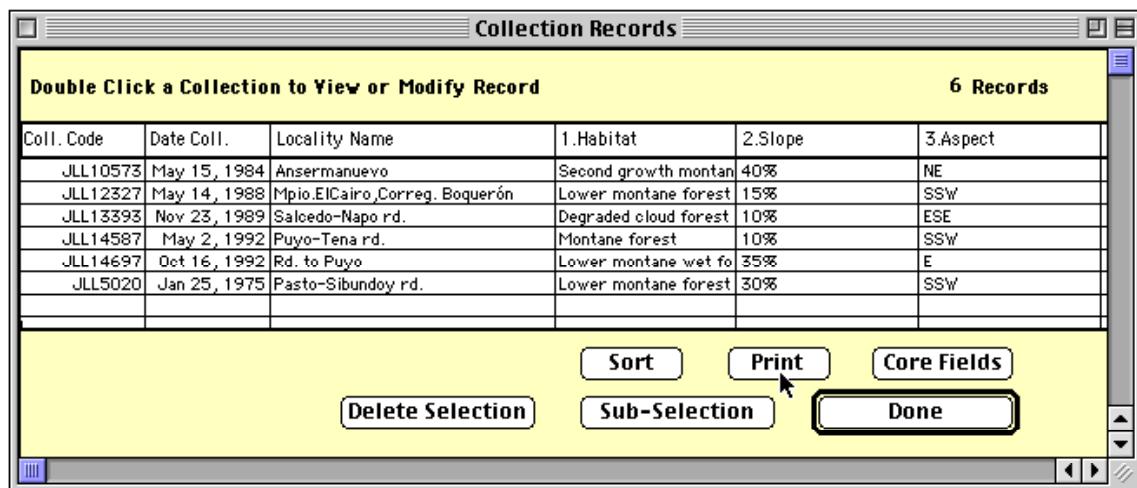
Printing Auxiliary Fields in Matrix (Row-by-Column) Format

The most flexible method for printing Auxiliary Field data is to export the Auxiliary Field Values to a text file in full matrix format (either Standard or Transposed), open the text file using a spreadsheet application (such as Microsoft Excel) or a text processing application (such as Microsoft Word), then format and print the data to suit your own needs. This is the method to use if you want to print Auxiliary Field data and Core Field data together for the same records.

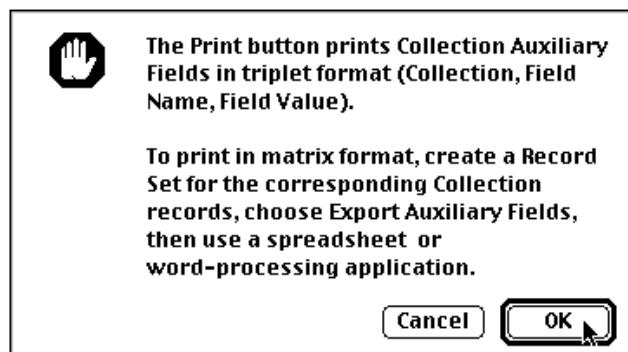
Biota does not provide a preformatted, printed report for Auxiliary Field data in matrix format. For help exporting Auxiliary Fields, see the section “[Exporting Auxiliary Field Values](#)” later in this chapter. For help exporting Core Field data, see Chapter 27, “[Exporting Data by Tables and Fields](#).”

Printing Auxiliary Fields in Standard Triplet Format (Record Code, Auxiliary Field Name, Auxiliary Field Value)

1. **Display Auxiliary Fields and their values** in the Standard Auxiliary Fields Record Listing screen, following the steps in the section “[Displaying Auxiliary Fields in the Standard Format: Records as Rows, Auxiliary Fields as Columns](#)” earlier in this chapter.



2. Click the “Print” button at the bottom of the screen (see above). A warning message appears, explaining that the data will be printed in triplet format.



3. Click the “OK” button in the warning window to proceed. The Page Setup window appears. (The appearance and options available in the Page Setup window depends on the printer and operating system you are using.)
4. Click the “OK” button in the Page Setup window. The Print window appears. (The appearance and options available in the Print window depends on the printer and operating system you are using.)

5. If you want to preview the printed report, click the “Preview on screen” checkbox in the lower-left corner of the Print window. (With some printers, you will need to select “4th Dimension” or “4D Engine” from a popup menu to find the “Preview on screen” checkbox.)

Collection Auxiliary Fields					Global Project
Collection Code	Collected By	Locality Name	FieldName	FieldValue	
JLL10573	J.L. Luteyn	Ansemanuevo	Precipitation	None	
			Habitat	Second growth montane fore	
			Temperature	18°C	
			Aspect	NE	
			Slope	40%	
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerón	Precipitation	Heavy rain	
			Habitat	Lower montane forest	
			Temperature	21°C	
			Aspect	SSW	
			Slope	15%	
JLL13393	J.L. Luteyn	Salcedo-Napo rd.	Precipitation	Rain	
			Temperature	16°C	
			Aspect	ESE	
			Slope	10%	
			Habitat	Degraded cloud forest	

Printing Auxiliary Fields in Transposed Triplet Format (Auxiliary Field Name, Record Code, Auxiliary Field Value)

1. Display Auxiliary Fields and their values in the Standard Auxiliary Fields Record Listing screen, following the steps in the section “[Displaying Auxiliary Fields in the Transposed Format: Auxiliary Fields as Rows, Records as Columns](#)” earlier in this chapter.

The screenshot shows a software window titled "Collection Records". A message at the top says "Double Click a Field Record (Row) to Display its Values For All Selected Collection Records". To the right, it says "5 Auxiliary Fields". Below this, there are two tables. The first table has columns for "Collection Date", "Locality Name", and "Field\ Coll. Code". It lists five rows corresponding to the collection records JLL14697, JLL5020, JLL13393, JLL12327, and JLL14587. The second table contains five rows of auxiliary field data, each with five columns: "1 Habitat", "2 Slope", "3 Aspect", "4 Temperature", and "5 Precipitation". The data values correspond to the entries in the first table. At the bottom of the window are three buttons: "Print", "Core Fields", and "Done".

Collection Date	Oct 16, 1992	Jan 25, 1975	Nov 23, 1989	May 14, 1988	May 2, 1992
Locality Name	Rd. to Puyo	Pasto-Sibundoy rd.	Salcedo-Napo rd.	Mpio.ElCairo,Correg.	Puyo-Tena rd.
Field\ Coll. Code	JLL14697	JLL5020	JLL13393	JLL12327	JLL14587
1 Habitat	Lower montane wet fo	Lower montane forest	Degraded cloud forest	Lower montane forest	Montane forest
2 Slope	35%	30%	10%	15%	10%
3 Aspect	E	SSW	ESE	SSW	SSW
4 Temperature	24°C	23°C	16°C	21°C	16°C
5 Precipitation	None	None	Rain	Heavy rain	Light drizzle

2. Click the “Print” button at the bottom of the display (see above). A warning window appears, explaining that the data will be printed in triplet format.



3. Follow [Steps 3 through 5](#) in the section “[Printing Auxiliary Fields in Standard Triplet Format \(Record Code, Auxiliary Field Name, Auxiliary Field Value\)](#)” earlier in this chapter. The report appears in the preview screen or is printed on paper.

Collection Auxiliary Fields					Global Project
FieldName	Collection Code	Collected By	LocalityName	FieldValue	
Precipitation					
JLL10573	J.L. Luteyn	Ansermanuevo	None		
JLL10573	J.L. Luteyn	Ansermanuevo	Second growth montane fore		
JLL10573	J.L. Luteyn	Ansermanuevo	18°C		
JLL10573	J.L. Luteyn	Ansermanuevo	NE		
JLL10573	J.L. Luteyn	Ansermanuevo	40%		
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerd	Heavy rain		
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerd	Lower montane forest		
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerd	21°C		
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerd	SSW		
JLL12327	J.L. Luteyn	Mpio.ElCairo,Correg. Boquerd	15%		
JLL13393	J.L. Luteyn	Salcedo-Napo rd.	Rain		
JLL13393	J.L. Luteyn	Salcedo-Napo rd.	16°C		
JLL13393	J.L. Luteyn	Salcedo-Napo rd.	ESE		
JLL13393	J.L. Luteyn	Salcedo-Napo rd.	10%		

Exporting Auxiliary Field Values

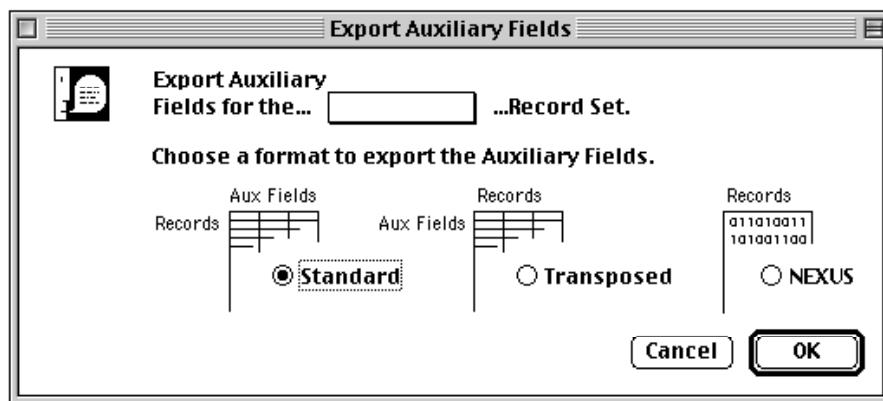
Like data in any other table in Biota, the data in the four Auxiliary Field Value tables (Spcm Field Value, Spp Field Value, Coll Field Value, and Loc Field Value) can be exported directly to a text file using the Export Editor (see Chapter 27, “[Exporting Data by Tables and Fields](#)”). In fact, if you are moving Auxiliary Fields data between Biota Data Files, you *must* use this method to create a text file in a format suitable for the Import Editor to import the text file into another Biota Data File.

The information in Auxiliary Fields appears internally in triplet format rather than in columns and rows (see “[How Auxiliary Fields Work](#),” earlier in this chapter, and Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). Therefore Biota offers special tools for exporting Auxiliary Field Values in matrix form, with a choice among several different formats, as detailed below.

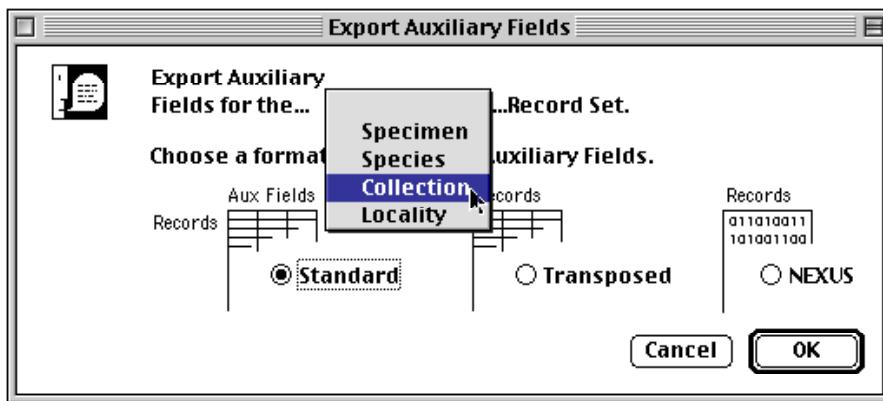
1. Establish a Record Set composed of the parent table records whose Auxiliary Field Values you wish to export. (See “[Record Sets](#)” in Chapter 3 if you need help declaring Record Sets.)

Suppose, for example, that you want to export values for the Collection Auxiliary Fields records used as an illustration earlier in this chapter, and you have already declared the parent Collection records as the current Collection Record Set.

2. From the Im/Export menu, choose Export Auxiliary Fields. An option screen appears.



3. In the option window, click and hold on the table name popup list.



4. Select the name of the Core table for which you want to export Auxiliary Field Values. (“Collection” is selected, above.)
5. Select the output format you want, using one of the three option buttons:
 - Standard format (Records as rows, Auxiliary Fields as columns).
 - Transposed format (Auxiliary Fields as rows, records as columns).
 - NEXUS format (see “[Exporting Auxiliary Fields in the NEXUS Format](#)” later in this chapter).
6. Click the “OK” button in the option window. The Save File window for your operating system appears.

7. Enter a name for the text file and click the “Save” button (Macintosh) or “OK” button (Windows) in the Save File window.

A progress indicator appears, then a notice that the text file has been created successfully. (If an error comment appears, try again.)

Now you can view, edit, format, or print the text file using any spreadsheet or word processing application. Here is how the example data, in Standard format, would look in an exported text table:

COLLECTION\FIELD	Habitat	Slope	Aspect	Temperature	Precipitation
JLL14697	Lower montane wet forest	35%	E	24°C	None
JLL5020	Lower montane forest	30%	SSW	23°C	None
JLL13393	Degraded cloud forest	10%	ESE	16°C	Rain
JLL12327	Lower montane forest	15%	SSW	21°C	Heavy rain
JLL14587	Montane forest	10%	SSW	16°C	Light drizzle
JLL10573	Second growth montane forest	40%	NE	18°C	None

Exporting Auxiliary Fields in the NEXUS Format

Systematists can use Biota Auxiliary Fields to create character matrices for Species or Specimens, then export the matrices in NEXUS format. (Biota can also export matrices in NEXUS format for the Collection and Locality Auxiliary Fields).

Biota exports NEXUS files using the “STANDARD” NEXUS datatype only (not to be confused with Biota’s Standard Auxiliary Fields format). NEXUS files exported by Biota can be used without modification as input for MacClade³ PAUP⁴, or any other application that supports NEXUS input. You may want to edit the NEXUS documents that Biota exports, however, to modify the way they are used by these applications.

To export a NEXUS file, just follow the directions in the previous section (“[Exporting Auxiliary Field Values](#)” earlier in this chapter), but in step 4, click the “NEXUS” button in the Export Auxiliary Fields option window.

Below is an example of a NEXUS file exported by Biota for several Species records for hummingbird flower mites, from the BiotaDemo Data File that is distributed with Biota. Notice that any internal space characters in Auxiliary Field Names are automatically filled with the underline character, as required in the NEXUS standards. Please consult the NEXUS data standards documentation for an explanation of the various components of the file.

³ Maddison, W. P., and D. R. Maddison. 2000. *MacClade 4: Analysis of Phylogeny and Character Evolution*. Sunderland, MA: Sinauer Associates.

⁴ Swofford, D. L. 2002. *PAUP*: Phylogenetic Analysis Using Parsimony (and Other Methods)* 4.0. Sunderland, MA: Sinauer Associates.

NOTE: There is one important restriction. To export Auxiliary Field Values in NEXUS format, all Auxiliary Field Values in the set must be single-digit integers (0 through 9) or single alphabetic characters (A through Z).

If you attempt to export a longer value or a value with other characters in NEXUS format, Biota posts an error comment. Please note that this restriction does not apply to Auxiliary Field values in general, only to those exported in NEXUS format

```
#NEXUS

BEGIN TAXA;
  DIMENSIONS NTAX=5;
  TAXLABELS rhinrich rhinhaplo troperio tropfuent
  tropkressi;
END;

BEGIN CHARACTERS;
  DIMENSIONS NCHAR=11;
  FORMAT
    DATATYPE=STANDARD
    SYMBOLS=" 0 1 2"
  CHARSTATELABELS
    1 metapodal_plates,
    2 opisthoventral_setae,
    3 exopodal_plates,
    4 genital_shield,
    5 genital_setae,
    6 anal_shield,
    7 dorsal_shield,
    8 peritrematic_plates,
    9 setae_z1,
    10 podonotal_setae,
    11 coxa_IV_spur;
  MATRIX
    rhinrich 1 1 1 1 1 0 2 1 1 1 1
    rhinhaplo 1 0 1 1 1 0 2 1 0 1 1
    troperio 1 1 0 0 0 0 2 0 0 0 0
    tropfuent 1 1 0 0 0 0 2 0 0 0 1
    tropkressi 1 0 0 0 0 0 1 0 0 0 0 ;
END;
```

The Project System and Auxiliary Fields

Biota's Project System allows you to create, view, and edit different sets of Auxiliary Fields for different Projects that share the same Biota Data File. For example, a database for a protected area or reserve might include records for birds, plants, and other groups of organisms. The bird Species records might require Auxiliary Fields for "Egg Size," "Egg Length," and "Clutch Size," whereas the plant Species records might need Auxiliary Fields for "Breeding System," "Pollination Type," and "Habit." Obviously, the Bird Auxiliary Fields are meaningless for plant records, and Plant fields are meaningless for Bird records.

To handle this problem you can create a "Birds" Project and a "Plants" Project for the same Data File. Each Project specifies its own set of Auxiliary Fields that are visible only when the corresponding Project is chosen as the Active Project. Here is an outline of how the Project System works:

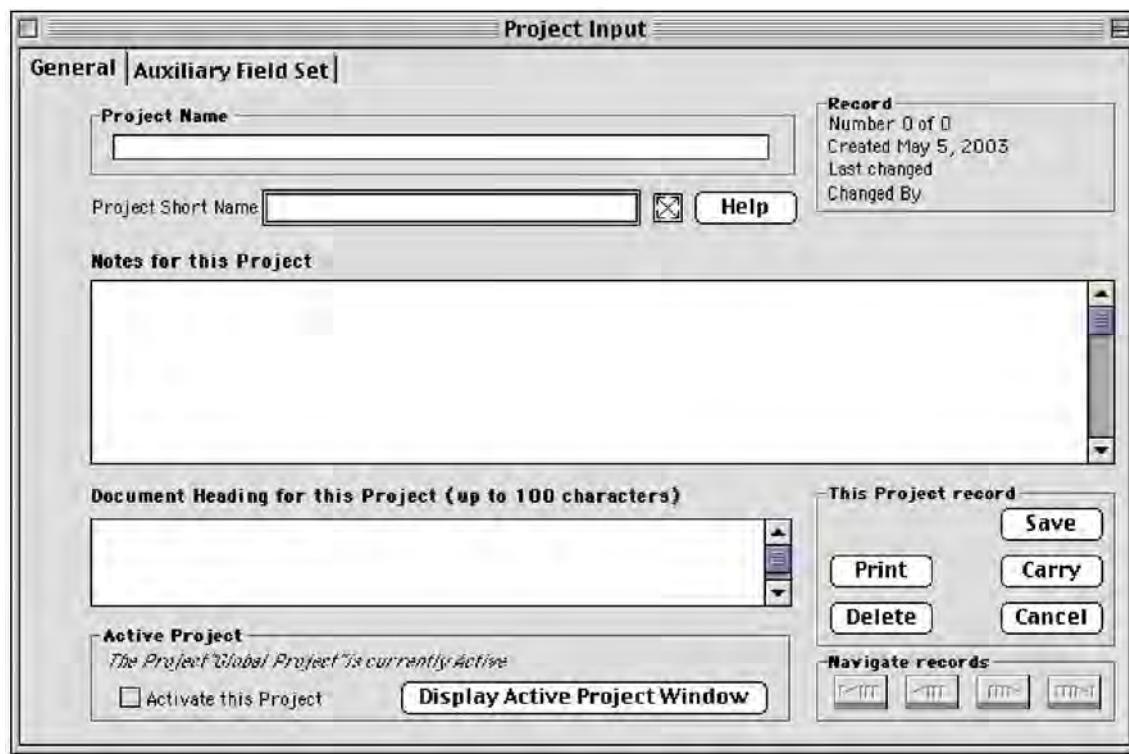
- **The Project Table** holds a record for each Project you create. The Project table is a Core Table (see "[Core Tables](#)" in Chapter 3) with its own Input screen and Record Listing Screen (see "[Project Input](#)" later in this chapter).
- **The AuxIndex Table** contains records that link Project records to Auxiliary Field Name records, to keep track of which Auxiliary Fields are used in which Projects. Biota creates and maintains these records automatically, based on the Auxiliary Fields you designate for each Project.
- **The Global Project record**, a special record that cannot be deleted, automatically includes all Auxiliary Fields. To include a particular Auxiliary Field in a Project or your own, you select it from the Global Project.
- **There is always one Active Project.** The Active Project specifies which Auxiliary Fields are visible in Species, Specimen, Collection, and Locality records. You can designate any Project (including the Global Project) as the Active Project, and easily activate a different Project in a floating window (see "[Using the Active Project Floating Window](#)" later in this chapter).
- **You can link each Project to a Personnel record** to record Project management or other personnel and to record contact information for the Project. See "[Personnel Input](#)" in Chapter 11 for information on Project-linked Personnel records, which may double as Group Personnel Records to link the individual Personnel record for Project participants.

NOTES TO USERS OF BIOTA 1.x:

- a. When you first open a Biota 1.x Data File with Biota 2.x, the Global Project record is automatically created, with all pre-existing Auxiliary Fields (if any) automatically included in it.
 - b. If you designated a particular Personnel record in a Biota 1.x Data File as the Project Record, Biota 2 automatically creates a Project record with the same name (in addition to the Global Project record), with all pre-existing Auxiliary Fields (if any) automatically assigned to both the Global Project and to your Biota 1.x Project.
-

Project Input

You can enter a new record in the Project Input screen by selecting Project from the Input menu or by clicking the “Add Project” button on the Specimen Project Listing screen. The Project Input screen has two tabs. Once you have entered a Project Short Name (the Key field, see “[Key Fields](#)” in Chapter 3), you can move between tabs. See “[Keyboard Shortcuts for Input Screen Tabs](#)” in Chapter 7 for information on using keyboard shortcuts to move between the tabs.



This section describes how to enter data in the General and Auxiliary Field Set tabs of the Project Input screen.

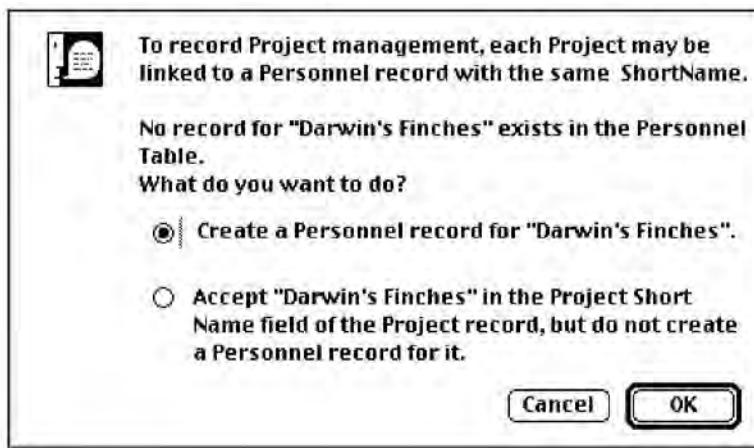
Entering Project Data: The “General” Tab

- Enter a Project Name.** The Project Name may be up to 80 characters in length.
When you tab to the Project Short Name field (or click in it), the Project Name you entered is copied there. The Project Name is an obligatory field.
- Shorten or alter the Project Short Name as you wish,** or leave it the same as the Project Name. (The Project Short Name may be up to 80 characters in length.)

The screenshot shows the 'General' tab with the 'Project Name' field containing 'Darwin's Finches'. The 'Project Short Name' field below it also contains 'Darwin's Finches'. Other fields and buttons are visible but not interacted with.

Because Project Short Name is the Key field for the Project table, it is an obligatory entry. All remaining entry areas (except Project Name) are optional.

The Project Short Name you enter must not duplicate the Project Short Name of any existing Project record, or you will receive an error message (see “[Duplicate Key Errors](#)” in Chapter 3 and Chapter 8, “[Record Codes](#)”).



Because this field is linked to the Short Name field of the Personnel table, the entry area has a double border. You can use any of the techniques for entering data in linking fields described in Chapter 7, “[Overview of Record Input Screens](#).” Unless a Personnel record already exists with a Personnel Short Name that matches the Project Short Name you have entered, Biota offers to create a linked Personnel record to record Project Personnel or contact data for the Project.

3. Enter Project Notes if you wish, up to 32,000 characters in length.

4. Enter a Project Document Heading if you wish, up to 100 characters in length. The Document Heading appears on Reports (see Chapter 14, “[Printing Reports](#)”), on Herbarium Labels (see “[Herbarium Labels](#)” in Chapter 15), and on Loan invoices (see “[Previewing, Printing, and Exporting Loan Records](#)” in Chapter 21).

5. To make the Project displayed in the Project Input screen the Active Project, check the “Activate this Project” checkbox at the bottom of the screen.

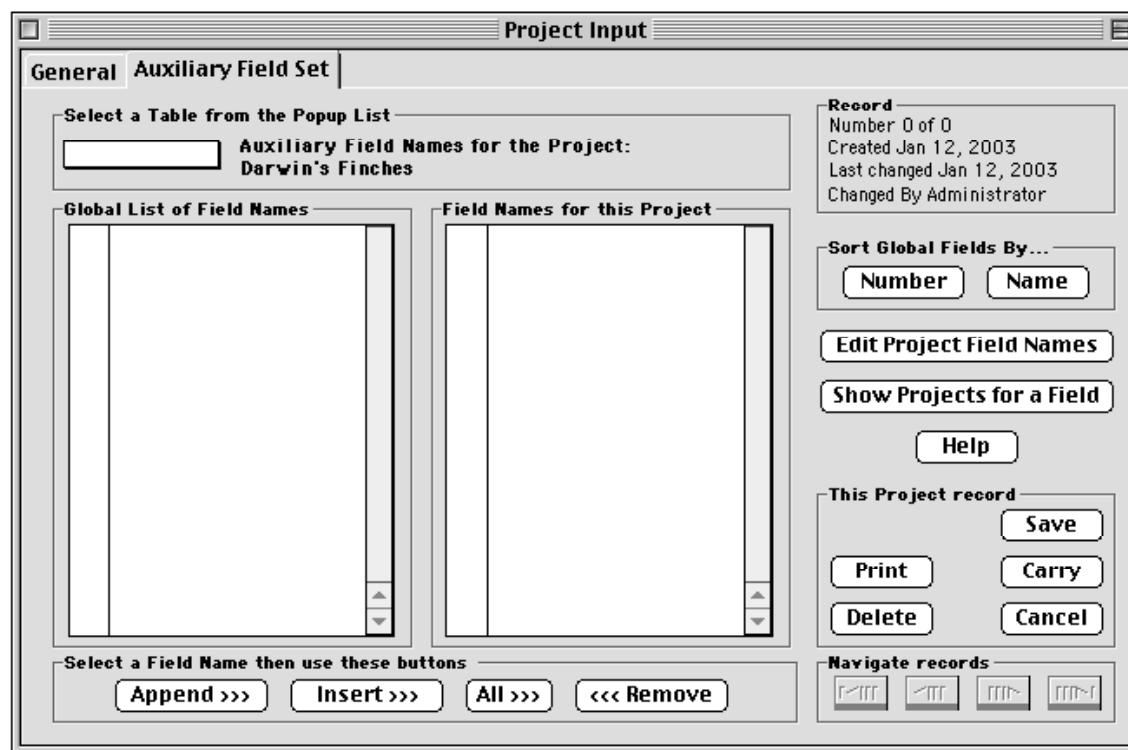
Note: You can also control which Project is activated using the popup list in the Active Project floating window itself. See [“Using the Active Project Floating Window”](#) later in this chapter.

6. To Display the Active Project floating window, click the “Display Active Project Window” button at the bottom of the screen. If the Active Project floating window is already being displayed, the button is disabled.

Note: You can also display or dismiss the Active Project floating window using the “Display Active Project Window” command in the Special menu.

Entering Project Data: The “Auxiliary Field Set” Tab

The Auxiliary Field Set tab of the Project Input screen manages the assignment of Auxiliary Fields to Projects.

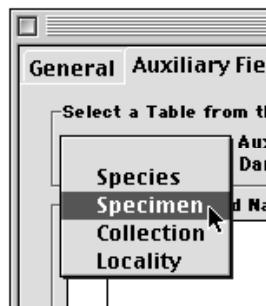


In addition, by clicking the “Edit Project Field Names” button on the Auxiliary Field Set tab (the button reads “Edit Global Field Names” for the Global Project), you can access the Field Name Editor from this tab to create new Auxiliary Fields or to re-name, re-order, or delete existing

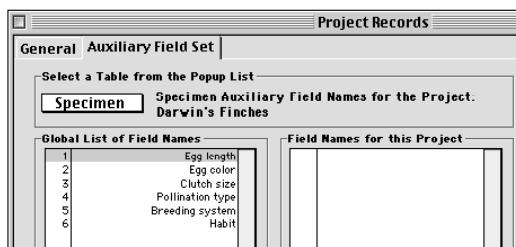


Auxiliary Fields. (For instructions on using the Field Name Editor, see “[Creating, Editing, and Ordering Auxiliary Field Names](#)” earlier in this chapter.)

1. Select a parent table from the popup list in the top panel of the tab: Species, Specimen, Collection or Locality.



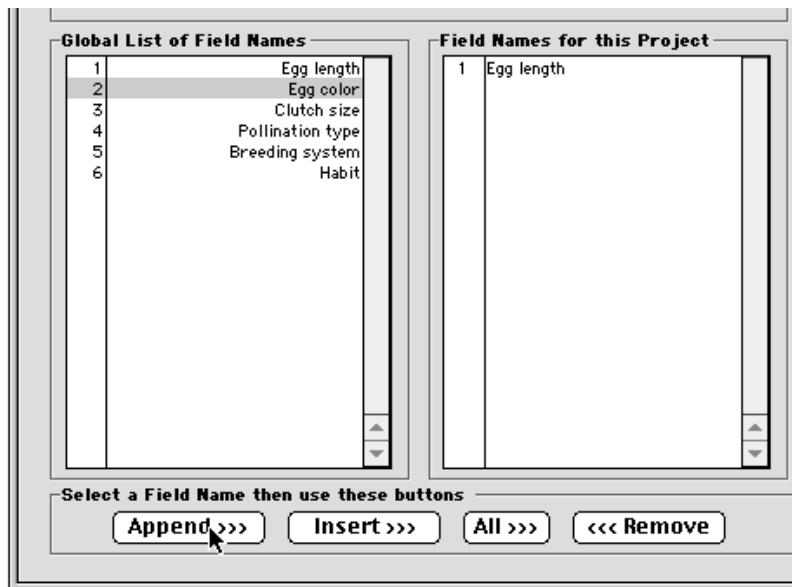
The Global List of Field Names for that table, if there are any, appears in the left panel, regardless of which Project record is open.



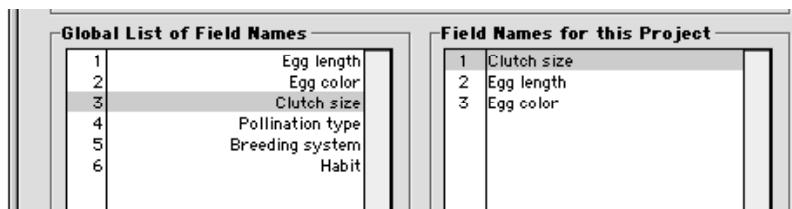
2. To sort fields in the “Global List of Field Names” panel by Number or by Field Name, click the appropriate button in the “Sort Global Field Names By...” panel.
3. To display a list of existing Projects that use a particular Field Name, select the Field Name in the “Global list of Field Names” panel, then click the “Show Projects for a Field” button.



4. To add an existing Auxiliary Field to the current Project, select it in the left panel (“Global List of Field Names”), then click the “Append” button. The Auxiliary Field name is copied (not moved) from the left panel to the right panel (“Field Names for this Project”). The next Auxiliary Field in the Global list is highlighted.



5. Continue using the “Append,” “Insert,” “All,” and “Remove” buttons to add more Auxiliary Fields to the Project or remove unwanted Fields. (To use the “Insert” button, first select the Field in the right panel before which you want to insert a selected Field from the left panel.)

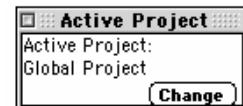


Henceforth, when this Project is selected, only those fields (and their values) that you have associated with this Project will appear in Record Listing Screens and Input Screens for the appropriate Parent Table (Specimen, Species, Collection, or Locality). Using this method, you can add or remove Field Names from any Project (except the Global Project) without affecting data for those fields.

Using the Active Project Floating Window

The Active Project specifies which Auxiliary Fields are visible in Species, Specimen, Collection, and Locality records.

Unless you have dismissed it or turned it off in the Preferences screen (see “[To Dismiss or Hide the Active Project Floating Window](#)” later in this chapter), the tiny Active Project Window is displayed in the upper left corner of your screen as a floating window (in front of any other open windows).

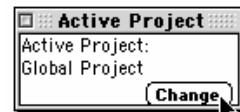


- **The Active Project Floating Window** specifies which of the existing Project records is currently activated. The Active Project specifies which Auxiliary Fields are visible in Species, Specimen, Collection and Locality records, and which Project name appears on certain reports and labels (see “Entering Project Data: The ‘General’ Tab” earlier in this chapter).
- **There is always one Active Project.**
- **You can designate any Project as the Active Project** (including the Global Project).

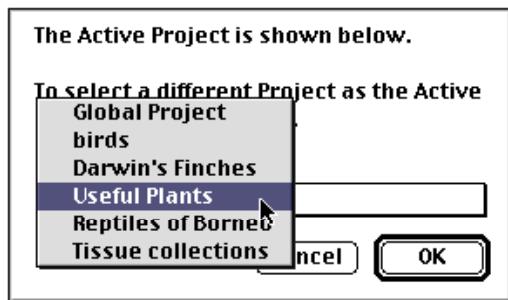
To Declare a Different Project to be the Active Project

1. Click the small “Change” button in the Active Project Floating Window.

The Project selection dialog appears.



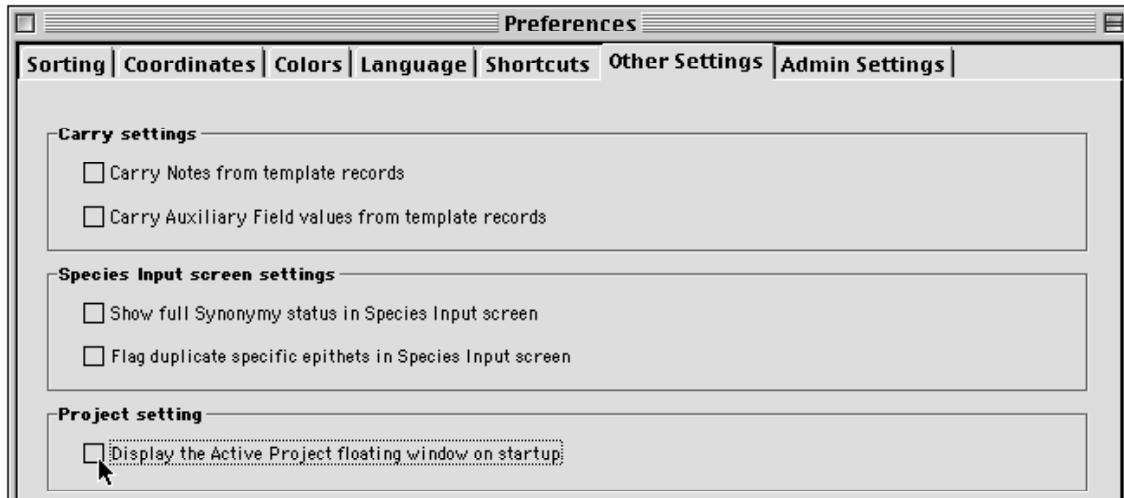
2. From the popup list, select the Project you want to activate.



NOTE: You can also control which Project is activated using the “Activate this Project” checkbox at the bottom of the General tab in the Project input screen. See “[Entering Project Data: The ‘General’ Tab](#)” earlier in this chapter.

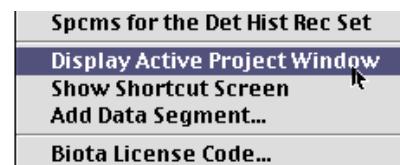
To Dismiss or Hide the Active Project Floating Window

- **To dismiss the Active Project Floating Window**, click its close box. The window will reappear next time you launch Biota. If you want to re-display it in the current session, see “[To Display the Active Project Floating Window](#)” later in this chapter.
- **To hide the Active Project Floating Window on startup**, choose Preferences from the Special menu, go to the “Other Settings” tab, then un-check the “Display the Active Project floating window on startup” checkbox and Save the Preferences.

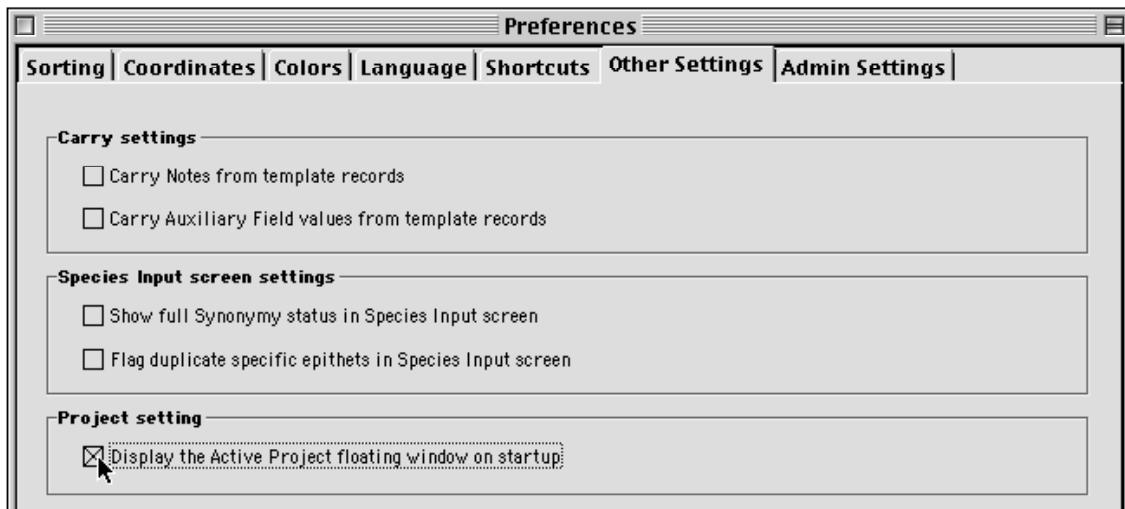


To Display the Active Project Floating Window

- **To display the Active Project Floating Window during the current Biota session**, choose “Display Active Project Window” from near the bottom of the Special menu.



- To display the Active Project Floating Window on startup, choose Preferences from the Special menu, go to the “Other Settings” tab, then check the “Display the Active Project floating window on startup” checkbox and Save the Preferences.



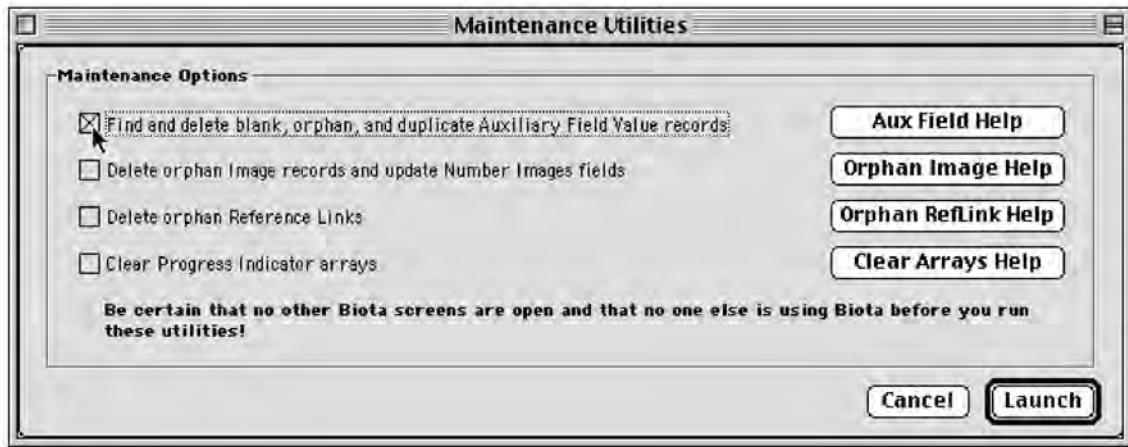
Maintaining and Repairing the Auxiliary Fields and Project Systems

Under normal operations, Biota correctly maintains links between parent records in the Specimen, Species, Collection, and Locality tables and records in the tables that contain information on Auxiliary Fields (the FieldValue andFieldName tables). In addition, Biota normally prevents duplication of RecordCode/FieldName combinations (ambiguous records) and correctly maintains the number of (non-blank) Auxiliary Field Values for each parent record in the AuxiliaryFields field of each parent record.

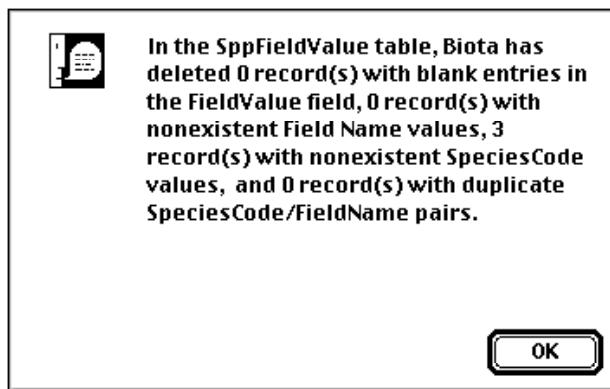
Power failures, system crashes, and incorrectly imported data, however, can produce anomalies. A record in a FieldValue table may become orphaned (either the RecordCode field or the FieldName field contains a nonexistent parent record value), a blank entry for FieldValue may appear, FieldValue records may be duplicated, or the AuxiliaryFields field of a parent record (a Specimen, Species, Collection, or Locality record) may indicate the wrong number of Auxiliary Field Values. In addition, the AuxIndex records that specify the Auxiliary Fields associated with each Project may sometimes be duplicated.

You can correct all these problems, without in any way affecting legitimate records, by running the Auxiliary Field/Project Maintenance Utility. Whereas none of these problems are very serious, it is recommended that you run this utility from time to time if you work with Auxiliary Fields and Projects (especially if you suspect problems) to “clean up” any orphan Field Value records and other anomalies.

1. To run the Auxiliary Field/Project Maintenance Utility, choose “Maintenance Utilities” from the Special menu. The option screen appears (next page).



2. Activate the option “Find and delete blank, orphan, and duplicate Auxiliary Field Value records.”
3. Click the “Launch” button. The utility presents a series of reports on its activities. Here is an example of a report from the Auxiliary Field Maintenance tool.



Chapter 17

Default Entries and Entry Choice Lists (Pick Lists)

This chapter explains how to set default values for data entry (see “[Setting Default Entries: Field Value Defaults](#)” later in this chapter), and how to set up Entry Choice Lists (pick lists) for data entry (see “[Using Entry Choice Lists](#)” later in this chapter). For automatic entry of Record Codes, see also Chapter 8, “[Record Codes](#),” which explains how to set up custom prefixes and counters for Record Codes.

Setting Default Entries: Field Value Defaults

Some fields in your database may require the very same entry for many or even all the records in a Data File. For fields likely to require default entries in the Specimen, Collection, and Locality tables, you can assign a *Field Value Default* that is entered in the data entry area for that field automatically whenever you create a new record. (You can select or erase the entry and replace it with an *ad hoc* one if you need to.)

If you need to select from *several* repetitive values for data entry in a field, see “[Using Entry Choice Lists](#)” later in this chapter

To Set Field Value Defaults

1. Choose “**Field Value Defaults**” from the **Special** menu. Screen 1 of the Set Field Value Defaults tool appears, showing default entries, if any, for fields in the Specimen table.

The screenshot shows the 'Set Field Value Defaults' dialog box. The title bar says 'Set Field Value Defaults'. The main area is titled 'Set the Value you want Biota to enter as the default for each Field (2 Screens)'. It lists fields under the 'Specimen Table' category:

Internal Field Name or Alias	Default Value
Prepared By	[Text Box]
Date Prepared	[Text Box] Mo: 0 Dy: 0 Yr: 00 Today
Determined By	[Text Box]
Date Determined	[Text Box] Mo: 0 Dy: 0 Yr: 00 Today
Stage/Sex	[Text Box]
Medium	[Text Box]
Storage	[Text Box]
Deposited	[Text Box]
Type Status	[Text Box]
Specimen Custom 1	[Text Box]
Specimen Custom 2	[Text Box]

At the bottom, it says 'Screen 1 of 2'. The footer has buttons: 'Alias Help', 'Clear Default Values', 'Cancel', 'Save', and 'Second Screen of Fields...'

Enter or edit the values for any listed fields in the Specimen table for which you want to enter default values.

Please note these important points:

- **If you have renamed any fields**, using the Core field Alias editor (see Chapter 18, “[Renaming Fields](#)”), then the Aliases, not the Internal Field Names, appear in the “Set Field Value Defaults” screens.
- **The “Prepared By” and “Determined By” entry areas**, with the double borders, are standard Biota wildcard lookup entries, linked to the Personnel table. (See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7 for information on wildcard entry techniques.)
- **The “Date Prepared” and “Date Determined” fields** each accept either full (DD/MM/YYYY) or partial (MM/YYYY or YYYY) dates. (See “[Partial Dates](#)” in Chapter 9.)

WARNING: Be careful how you use the “Deposited” field. If you use the Loans system, this field is used to store the Loan Code for specimens you have lent or borrowed. Entering your own collection name or institution name as a default entry value often makes sense for the entry of original data, however. If you later lend the specimens, the Loans system will automatically replace your collection name with the Loan Code for the new loan.

2. **Display the second screen of fields if necessary.** If you click the “Second Screen of Fields” button, the screen for Collection and Locality default entries appears.

Internal Field Name or Alias		Default Value					
[Collection]Locality Code							
Collection Table							
Collected By	<input type="text"/>						
Date Collected (or Date Started)	Mo:	0	Dy:	0	Yr:	00	<input type="button" value="Today"/>
Date Collection Completed (Optional)	Mo:	0	Dy:	0	Yr:	00	<input type="button" value="Today"/>
Site	<input type="text"/>						
Method	<input type="text"/>						
Source	<input type="text"/>						
Locality Table							
District	<input type="text"/>						
State/Province	<input type="text"/>						
Country	<input type="text"/>						

Screen 2 of 2

Alias Help Clear Default Values Cancel Save First Screen of Fields...

Please note these important points:

- **Entering a default Locality Code for Collection records** (the [Collection] Locality Code field) links all Collection records created while this default is set to the Locality record indicated in the default entry.
 - **The “Collected By” entry area**, with the double borders, is a standard Biota wildcard lookup entry, linked to the Personnel file. (See “[A Powerful Shortcut: Wildcard Data Entry for Linking Fields](#)” in Chapter 7 for information on wildcard entry techniques.)
 - **The “Date Collected” and “Date Collection Completed” entry areas** each accept either full (DD/MM/YYYY) or partial (MM/YYYY or YYYY) dates. (See “[Partial Dates](#)” in Chapter 9.)
3. Click the “Save” button on either screen to record the defaults in your Data File for both screens, once you are done entering default values in both screens.

NOTE: Field Value Defaults are recorded in the Lists table in your Biota Data File. See Appendix A, “[Biota Tables, Fields, and Relational Links](#)”

4. To clear all Field Value Defaults, click the “Clear Default Values” button at the bottom of either screen.



Using Entry Choice Lists

Some fields in your database will probably have a limited number of repetitive entries. Here are some common examples.

- **Authors** of Species, Subspecies, or Varieties.
- **Storage localities or Type designations** for Specimens.
- **Sex, life stage, or growth habit** for Specimens.
- **Collection Methods or Site characteristics** for Collection records.
- **Political entities** (Districts, States or Provinces, Countries) for Locality input.

For most non-linking fields in Biota you can activate and enter values in an *Entry Choice List* or *Pick List* (usually called simply a *Choice List* in this manual) that presents entry options in a floating window during data entry. Since Choice Lists eliminate misspellings, they are especially useful when someone else assists you in entering data.

Once you activate a Choice List for a field, the Choice List window appears automatically whenever you TAB or click into the entry area for that field during data input or revision. When the window appears, you can simply click an item on the List to enter it—or dismiss the List window (by pressing TAB or clicking the “Cancel” button in the Lists window) and then make a manual entry.

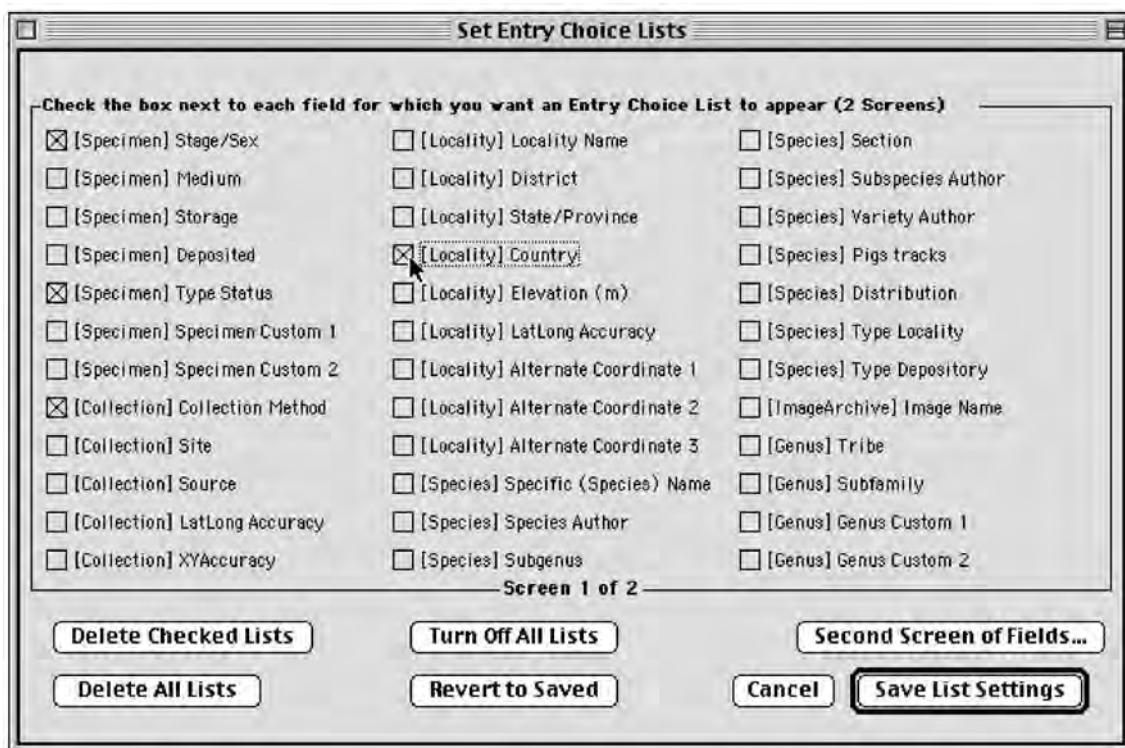
You construct each List by entering items with the List Editor, which is accessed from the List window itself by clicking the “Modify” button, as detailed below.

Between Biota sessions, the Lists you have created are kept as part of your Biota Data File in the List Items table (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”), not in the Biota application file. Saved Lists are preserved whether currently activated or not, until you change or erase them.

Each time you launch Biota, all activated Lists are loaded automatically from the Data File into the Biota application file. If you activate an existing List during a Biota session, the List is loaded and made available immediately.

Activating or Deactivating Choice Lists

1. Choose “Entry Choice Lists” from the Special menu. The List settings screen appears.



2. Set the activation state for each List.

- Click the empty checkbox next to the name of each field for which you want to activate an Entry Choice List. Table names appear in square brackets, followed by the field name.
- Click checked boxes to uncheck any List you wish to deactivate.

Note: Deactivating a List does not erase or change its entries. If you later reactivate the List, the entries appear just as they were last time the List was edited and saved.

3. For additional tables and fields, click the “Second Screen of Fields” button.

The second screen of options appears.



To return to the first screen of fields, click the “First Screen of Fields...” button.

4. Click the “Save List Settings” button to register the settings you have checked. Newly activated Lists will appear (and newly deactivated Lists stop appearing) the next time you use the appropriate Input screen. *Input screens already open are not affected.* Close any open Input screens and reopen them to activate changes in List settings. (It is not necessary to quit and restart Biota).
5. To deactivate all Lists, click the “Turn Off All Lists” button. *This action does not affect the content of the Lists.*

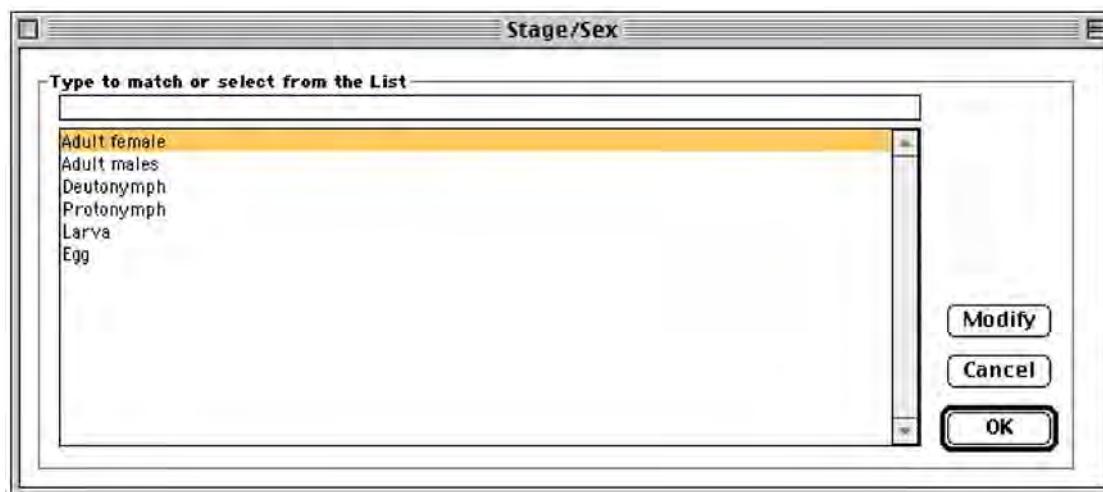


6. To restore all settings to their status when you opened the “Set Entry Choice Lists” screen, click the “Revert to Saved” button.

Adding, Deleting, Editing, or Re-ordering Items in a Choice List

Open the Input screen for the table that includes the List (field) you want to work on. You can do this by selecting the appropriate command from the Input menu (e.g., Input Specimens) or opening an existing record from an Record Listing screen (see Chapter 10, “[Working With Records in Record Listing and Input Screens](#)”).

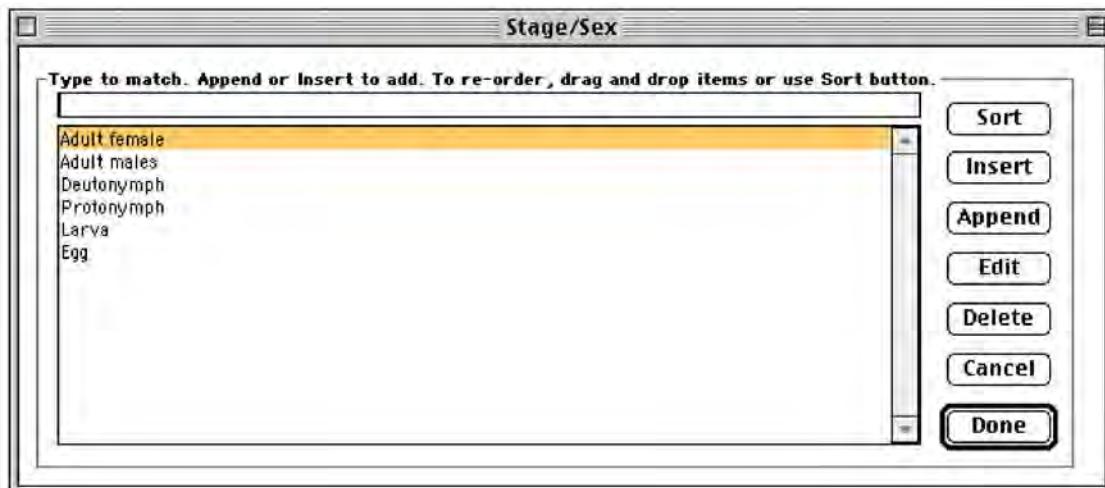
- Click in the entry area for the field.** The existing List, or an empty one, appears in a window titled with the name of the field (“Stage/Sex” in the example below).



NOTE: If no List appears, either the List has not been activated (see “[Activating or Deactivating Choice Lists](#)” earlier in this chapter), or the field does not support Entry Choice Lists.

- To open the List Editor, click the “Modify” button in the Choices window (above).

The buttons of the List Editor appear at the right side of the List window.



You use the buttons in the List Editor to Sort, Insert, Append, Edit, or Delete items in the Choice List for this field. You can change the order of List items by dragging and dropping them in the List Editor window.

Each field for which a List can be activated in the Entry Choice List screen (see “[Activating or Deactivating Choice Lists](#)” earlier in this chapter) has its own set of List items.

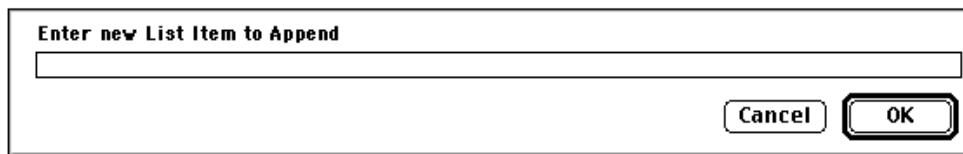
NOTE: To edit Lists, you must have Administrative access privileges. Otherwise, Biota posts an explanatory message when you click the “Modify” button.



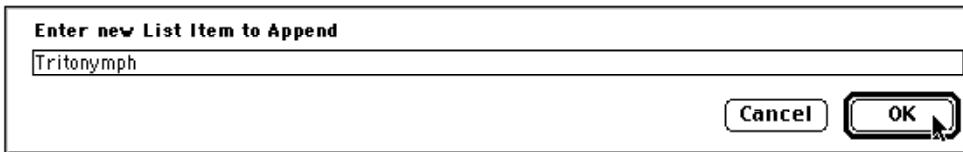
3. **To add a new item at the end of the existing List, click the “Append” button. Alternatively, you can use the keyboard shortcut, CTRL–N (Windows) or COMMAND–N (⌘–N) (Mac OS).**



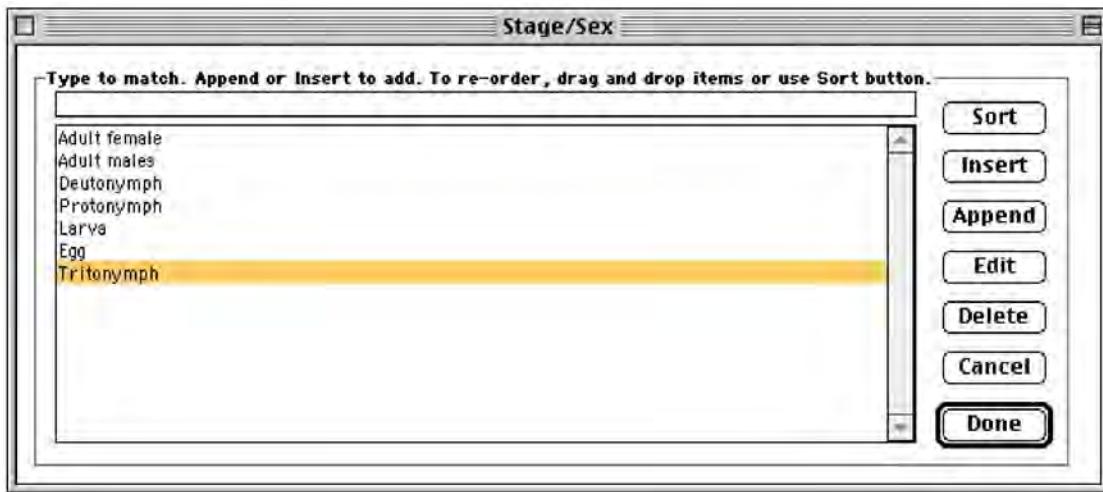
The List Item editing window appears.



4. **Enter the text for the new item and click the “OK” button in the List Item editing window.**



The item is added at the end of the List.

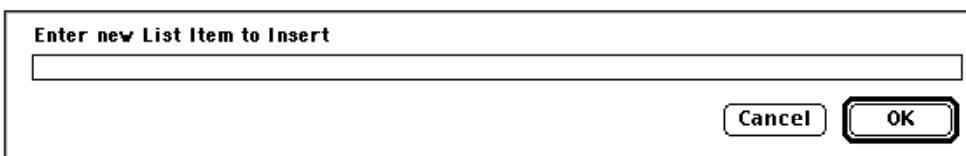


NOTE: Each List may have one blank list item. The blank item can be useful as a default (first) entry. Placing a blank item in the first position in the List makes it easy to enter a blank as the default (if that is something you often need to do), or to enter a blank and then change it to an ad hoc entry for which there is no List item. On the other hand, if you don't want blanks or ad hoc entries in your records, don't offer a blank item.

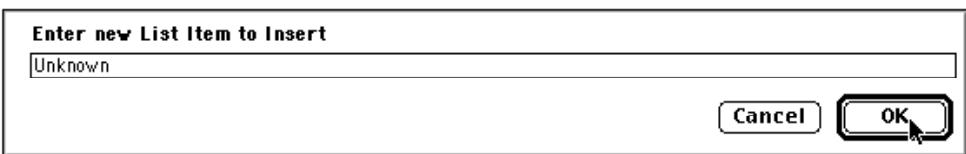
5. To insert a new item between two existing items, select the item in the existing list that you want to *follow* the new item, then click the “Insert” button. Alternatively, you can use the keyboard shortcut, CTRL-i (Windows) or COMMAND-i (⌘-i) (Mac OS).



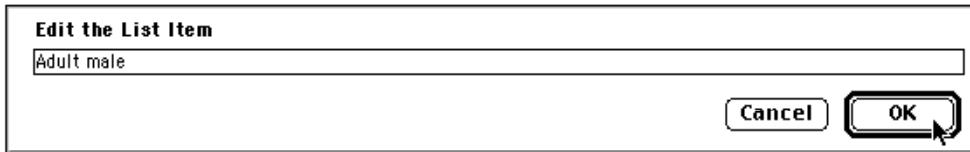
The List Item editing window appears.



6. Enter the text for the new item then click the “OK” button in the List Item editing window to insert the item in the list.

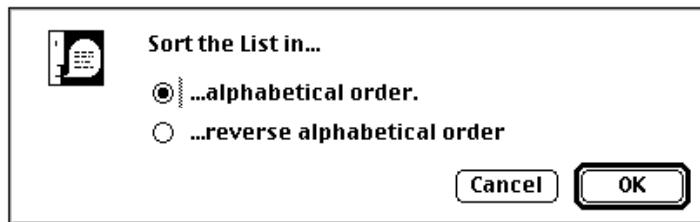


7. To edit an existing item, select the item to be modified, then click the “Edit” button to display the item to be edited in the List Item editing window. Edit the item then click the “OK” button.

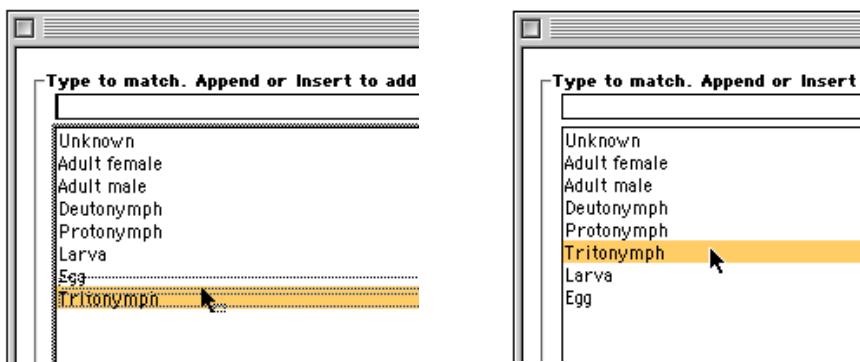


NOTE: The List Editor is not case-sensitive. Thus, if you want to change the case of an existing item in the ListItems table, you must delete the old version of the item (e.g., “canada”) before entering the new or corrected item (e.g., “Canada”). Otherwise, Biota will consider the new item to be a duplicate, and will not accept it.

8. To delete an existing item or a new item you don't want, click on the item to be deleted to select it, then click the “Delete” button. Alternatively, you can use the keyboard shortcut, CTRL-D (Windows) or COMMAND-D (⌘-D) (Mac OS). (A blank item can also be deleted.)
9. To sort the items alphabetically, click the “Sort” button. An option screen appears offering alphabetical or reverse alphabetical order.



10. To change the order of List items non-alphabetically, drag and drop items to re-order them as you wish.



11. To undo changes made in a List and dismiss the List Editor, without recording any changes you have made, click the “Cancel” button in the List Editor. The List Editor disappears and the List is restored to its previous state.
12. When a List is set as you wish, click the “Done” button in the List Editor window to record the changes. The List Editor buttons disappear.



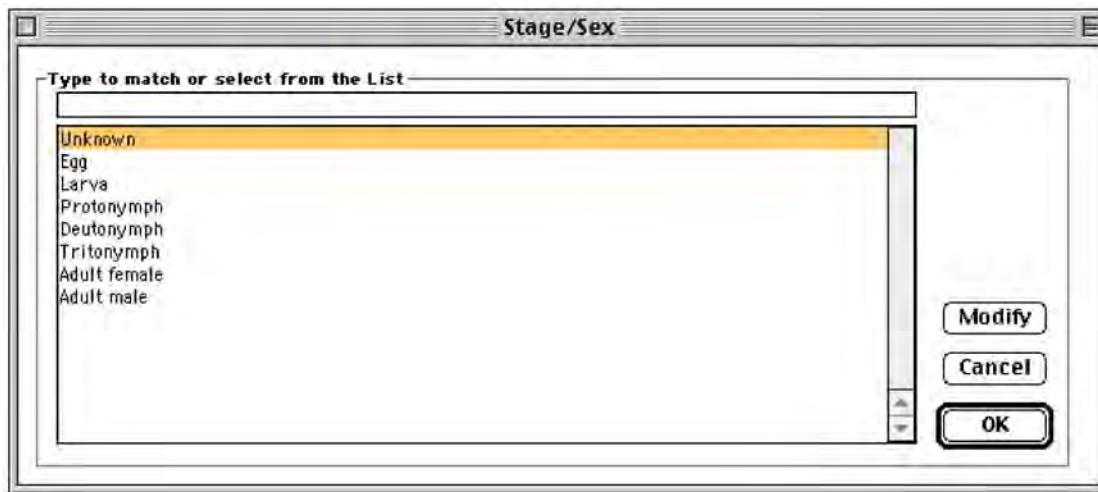
Using an Entry Choice List to Enter Data in a Record

Once you have activated an Entry Choice List (see “Activating or Deactivating Choice Lists” earlier in this chapter) and entered the items you want in the List (see “[Adding, Deleting, Editing, or Re-ordering Items in a Choice List](#)” earlier in this chapter), you are ready to use the List to enter values in records.

Open the Input screen for the table that includes the List (field) you want to work on. You can do this by selecting the appropriate command from the Input menu (e.g., Input Specimens) or opening an existing record from a Record Listing screen (see Chapter 10, “[Working With Records in Record Listing and Input Screens](#)”).



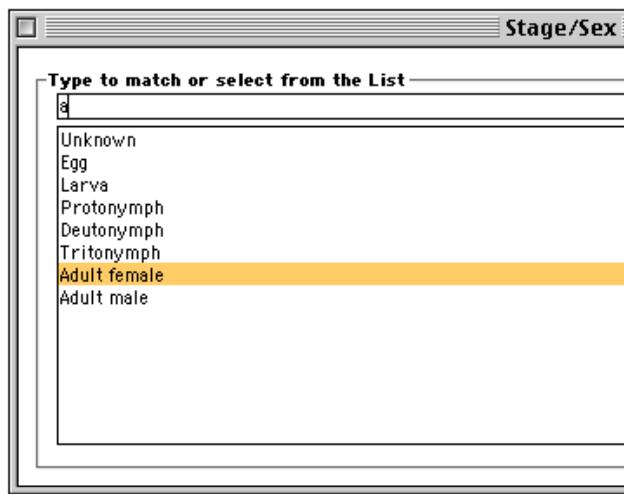
1. Display a new or existing record in the Input Screen for a table. (See Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”)
2. Tab into or click on a field for which an Entry Choice List has been enabled. The List window appears, titled with the name of the field (“Stage/Sex” in the example below).



3. To enter an item from the Choices window:

- If the item you want is already highlighted, simply press the ENTER key (Windows) or the RETURN key (Mac OS), or click the “OK” button in the Entry Choice List window. The Entry Choice List window is dismissed and the value is entered in the Input screen.
- To choose an item from the list:
 - ◊ Either: In the List, click on the item you want. The Entry Choice List window is dismissed and the value is entered in the Input screen.

- ◊ **Or:** Type the first letter or first few letters of the item in the entry area at the top of the Entry Choice List window (labeled “Type to match or select from the list”) until the item you want is highlighted in the list.



(In the example above, the letter **a** has been typed, which automatically highlights the first entry that begins with **a**: “Adult female.”)

Now press the ENTER key (Windows) or the RETURN key (Mac OS), or click the “OK” button in the Entry Choice List window. The Entry Choice List window is dismissed and the selected value is entered in the Input screen.

4. **To manually enter an item not shown in the Entry Choice List window,** click the “Cancel” button in the Entry Choice List window (*not* the “Cancel” button of the Input Screen!) to dismiss the Entry Choice List window, then enter the special item manually in the field.

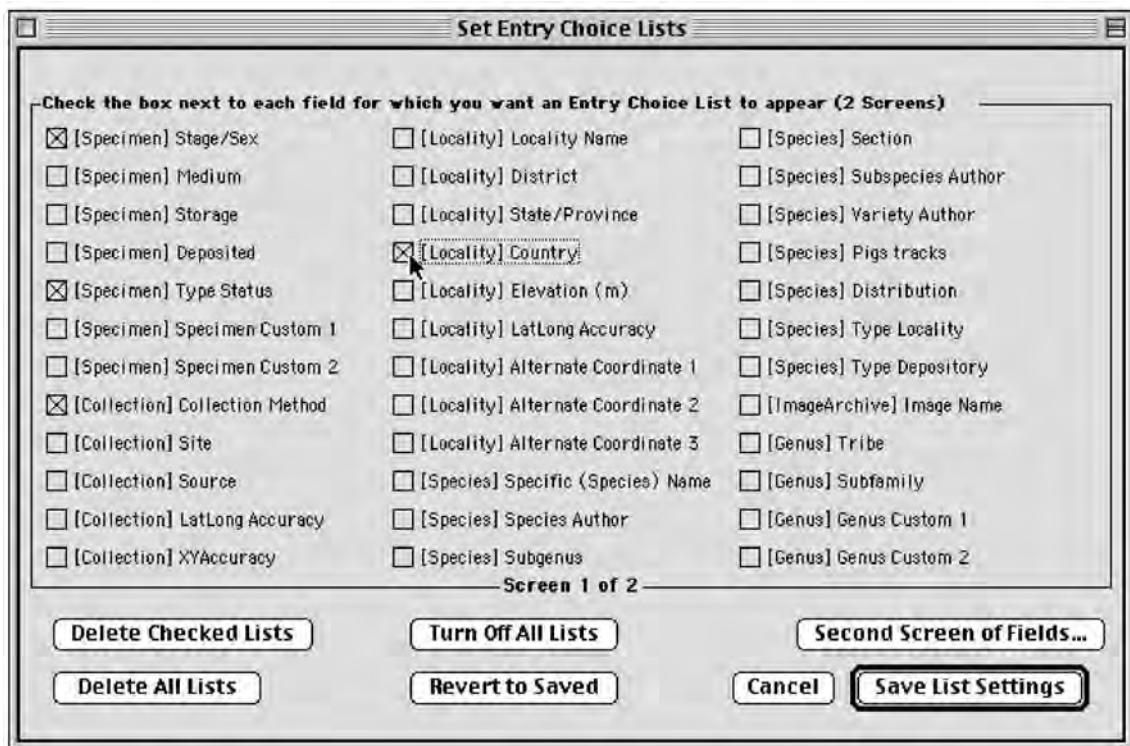
NOTE: Each List will accept one blank List Items entry. If you have a field (that supports Lists) for which blank entries are common, consider making the blank List Item the first (default) entry in the List.

5. **To stop an Entry Choice List from appearing,** you must deactivate the Choice List. See “[Activating or Deactivating Choice Lists](#)” earlier in this chapter.

Deleting All the Items in an Entry Choice List or Lists

Sometimes you may wish to delete all the items in an Entry Choice List at once. For example, you might first export all the items in the List to a text file (using the Export Editor, see Chapter 27, “[Exporting Data by Tables and Fields](#)”), delete them all from the Biota Data File, then edit them in the text file in some way and re-import the edited items to the same Biota Data File.

1. Choose “Entry Choice Lists” from the Special menu. The List settings screen appears.



2. Set the deletion status for each List.
 - Click the empty checkbox next to the name of each field for which you want to *delete the entire contents* of its Entry Choice List. Table names appear in square brackets, followed by the field name.
 - Click checked boxes to uncheck any List you want to *leave unchanged*.
3. For additional tables and fields, click the “Second Screen of Fields...” button.

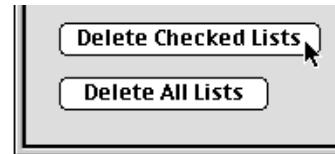


The second screen of options appears.



To return to the first screen of fields, click the “First Screen of Fields...” button.

4. **To permanently delete the entire contents of all checked Entry Choice Lists,** click the “Delete Checked Lists” button. Biota requests confirmation and warns you that the action cannot be undone, even using the “Revert to Saved” button.



5. **To permanently delete the entire contents of all Entry Choice Lists, whether checked or not,** click the “Delete All Lists” button. Biota requests confirmation and warns you that the action cannot be undone, even using the “Revert to Saved” button.
6. **To dismiss the List settings screen without changing the previous activation status of Lists,** click the “Cancel” button.



Importing Choice List Data From a Text File

Sometimes data that you would like to place in a Biota Entry Choice List are available as text files (e.g., lists of geographical names or authors of taxa) that you would like to import into Biota. Or, for a long Entry Choice List that you create yourself, it may be more convenient to create the List items in a spreadsheet application, then import the data into Biota.

This section explains how to format and import data to populate Entry Choice Lists using Biota’s Import Editor (see Chapter 28, “[Importing Data by Tables and Fields](#)”).

All List items are stored in Biota in a table called (appropriately enough) “ListItems.” (The activation status of Entry Choice Lists, on the other hand, is recorded in a separate table, called “Lists.” (See Appendix A, [“Biota Tables, Fields, and Relational Links.”](#))

The ListItems table has four fields. To import data into the ListItems table, you must prepare a delimited text file (in Excel, for example) with four columns that match these fields. Here are the fields, in alphabetical order.

- **FieldName (required, alphanumeric):** In this field, you must enter the name of the field for which you want to import List items. The field name must correspond to a field name in the Lists table, Appendix A, [“Biota Tables, Fields, and Relational Links.”](#)

Do not add any spaces to the field name (e.g., enter “CommonName” not “Common Name”). Do not include the table name. If the FieldName entry does not match a legitimate field, Biota posts an error message.

NOTE: You must use the “internal” field name, as indicated in the Lists table, Appendix A, [“Biota Tables, Fields, and Relational Links.”](#) If you have set up any Aliases, and are not sure which internal field name corresponds to an Alias, select “Core Field Aliases” from the Special menu, then click the “Display Current Aliases” button. (See Chapter 18, [“Renaming Fields”](#) for details.)

- **Item (required, alphanumeric):** In this field, you enter the value of each List item (e.g., geographical names). Each entry may be up to 80 characters in length.

Each item should be unique. If you try to import two or more duplicate items, or an item in the file to be imported matches an item already in the Lists table (for the same field in the same table), Biota simply skips the duplicate item and does not import it.

NOTE: The Import Editor is not case-sensitive. Thus, if you want to change the case of an item in the ListItems table, you must delete the old version of the item (e.g., “canada”) before importing (or manually entering) the new or corrected item (e.g., “Canada”). Otherwise, Biota will consider the new item to be a duplicate, and will not import it (or accept it, if entered manually.)

- **ItemNumber (required, integer):** In this field, you may enter an integer to indicate the order in which you want the List items to appear in the Entry Choice List. ItemNumber entries need not be consecutive or even unique, but you must include this field as a column in the text file to be imported.
- **Table (required, integer):** In this field, you must enter a code number for the table to which the field designated in FieldName (above) belongs. The table code numbers appear below. If you try to import a FieldName and Table number that do not correspond to a field that supports Entry Choice Lists, Biota posts an error message.

Table Number	Table Name
0	Species
1	Specimen
2	Collection
3	Locality
4	Genus
5	Family
6	Order
7	Class
8	Phylum
9	Kingdom
10	ImageArchive

Here is an example of a small, mixed-table text file set up for import into the ListItems table.

FieldName	Item	ItemNumber	Table
SpeciesAuthor	E. W. Baker	1	0
SpeciesAuthor	A. Berlese	2	0
StageSex	Adult female	1	1
StageSex	Adult male	2	1
Method	Tullgren extractor	1	2
Method	Hand collected	2	2
Country	Colombia	1	3
Country	Ecuador	2	3

Note: The column headings in the text file are not required. If you use them, be sure to check the “Column Headings: Ignore first record of text file” checkbox in the Import Editor.

Once the text file is read for importing into Biota, follow the instructions in Chapter 28, “[Importing Data](#).” (Select “ListItems” as the table, then click the “All” button to set up the fields in the order indicated above.)

Transferring Choice Lists to a Different Biota Data File

If you have only a few short Entry Choice Lists, it will not take long to recreate them in a new or existing Biota Data File. Long or complex Lists, however, are worth transferring all at once.

Two different tables are involved in keeping track of Entry Choice Lists:

- **The Lists table.** In the Lists table, Biota keeps track of the activation status of each Entry Choice List: enabled or not enabled. This requires only a single record in the Lists table, which has a field corresponding to each List-capable field in the Biota data structure.

NOTE: The Lists table has exactly three records at all times, even in a new, “empty” Biota Data File. The first two records contain long and short Core Field Aliases (respectively), if any have been established, for re-namable fields in the data structure (see Chapter 18, “[Renaming Fields](#)” and Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

The third record contains the activation settings for Entry Choice Lists. Thus, if you transfer the records of the Lists file from one Biota Data File to another, all Aliases will be transferred, along with the Lists activation status record.

- **The ListItems table.** In the ListItems table, Biota keeps track of the values for all Entry Choice Lists, along with information on which field and table they apply to and their ordering within list. See “[Importing Choice List Data From a Text File](#),” earlier in this chapter, for details.

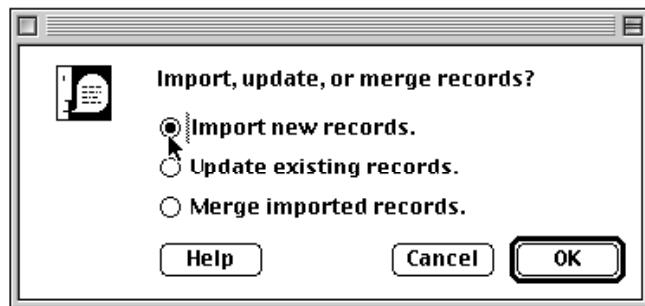
You cannot view or edit the Lists or ListItems tables directly, but they can easily be exported and imported between Biota Data Files. Here is how to do it:

1. **Launch Biota and open the “donor file”—**the existing Biota Data File from which you want to transfer Entry Choice Lists and List Settings. Press and hold the ALT key (Windows) or the OPTION key (Macintosh) while launching Biota to display the Open File window so you can select the correct Data File. If the user password system has been activated, press and hold the key while clicking the “Connect” button in the Password window, to display the Open File window for your operating system.
2. **From the Im/Export menu, choose Export by Tables and Fields.** The Export Editor appears. (See Chapter 27, “[Exporting Data by Tables and Fields](#)” for a detailed introduction to the Export Editor.)
3. **Choose Lists or ListItems from the Table Name popup list.** The fields for the selected table appear in the “Biota Field Names or Aliases” list in the lower-left panel of the Export Editor.
4. **Click the “All>>>” button.** All fields appear in the Text File Fields list on the lower right. 
5. **Click the “Export” button to launch the export.** The Save File window for your operating system appears. 
6. **Place and name the text file** that Biota will create for the Lists or ListItems table records.

7. **Edit the text file if necessary.** If you wish, you can now edit the exported Lists records using a text processing or spreadsheet application. Be sure to save the file as Tab-delimited Text if you edit it.
8. **Open the “receiving file”—**the new or existing Biota Data File into which you want to import the Lists and/or ListItems records. If you are using BiotaApp (not Biota4D) and you have sufficient available memory, you can open the receiving file using a duplicate copy of BiotaApp, if you have made one. Otherwise, close down the donor file and relaunch Biota.

Note: Be sure to press and hold the ALT key (Windows) or the OPTION key (Macintosh) while launching Biota, to bring up the Open File window. Otherwise, Biota will open the donor file again, if you have re-launched Biota.

- **If you want to create a new, blank Biota Data File,** click the “New” button in the Open File window (see “[Creating an Empty Biota Data File](#)” in Chapter 3).
 - **Otherwise, find the receiving file and open it.**
9. **From the Special menu, choose Import by Tables and Fields.** An option screen appears.



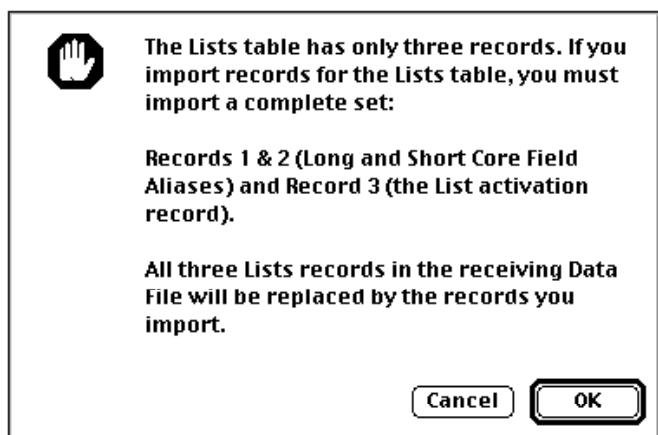
10. **Click OK to accept the default option “Import new records.”** The Import Editor appears. See Chapter 28, “[Importing Data](#)” for full details on using the Import Editor.
11. **Choose Lists or ListItems from the Table Name popup list.** The fields for the Lists table appear the “Biota Field Names or Aliases” list in the lower-left panel of the Export Editor.

WARNING: If you import the three records for the Lists table, Biota replaces the three existing Lists records with the ones you import—an action unique to Lists table importation. (For all other tables, existing records are never deleted using any import option.)

12. **Click the “All>>>” button** to enter all fields into the Text File Fields list on the lower right.



13. Click the “Import” button to launch the import. If you are importing the Lists table, a warning message appears. (The warning does not appear if you are importing records to the ListItems table.)



14. Find the text file you created for exported Lists or ListItems records and open it. The Import progress indicator appears.
15. If problems arise or Biota posts an error message, see "[Displays and Error Messages During Record Importing or Updating](#)" in Chapter 28. If all else fails, repeat the steps in this section.

Chapter 18

Re-naming Fields

This chapter explains how to re-name fields in Biota, by creating Core Field Aliases. Biota displays and prints these Aliases in virtually every context, once you establish them, instead of the default (internal) name for the corresponding fields.

Core fields in Biota include all fields that belong to Biota's Core tables: Specimen, Collection, Locality, Species, and all higher taxon tables—plus Personnel, Projects, References and Loans (see "[Core Tables](#)" in Chapter 3).

Auxiliary Fields, in contrast to Core fields, are special fields that you create and name as you like (see Chapter 16, "[User-Defined Auxiliary Fields and the Project System](#)"). Core fields, however, are much faster to sort and query, so you should always use Core fields, renamed or not, in preference to Auxiliary Fields, wherever possible.

Each Core field has a default or *Internal Field Name*. An easily recognized version of each Internal Field Name is used to label input areas on Input screens and output columns on Record Listing screens, as well as in printed reports. For example, the Internal Field Name [Specimen] Specimen Code appears on the screen as "Specimen Code." The internal field [Locality] State Province appears on the screen in two forms. Where space permits, Biota displays "State/Province." Where space is tight, you will see "State/Prov." (Notice the convention used for writing Internal Field Names: [TableName] FieldName.)

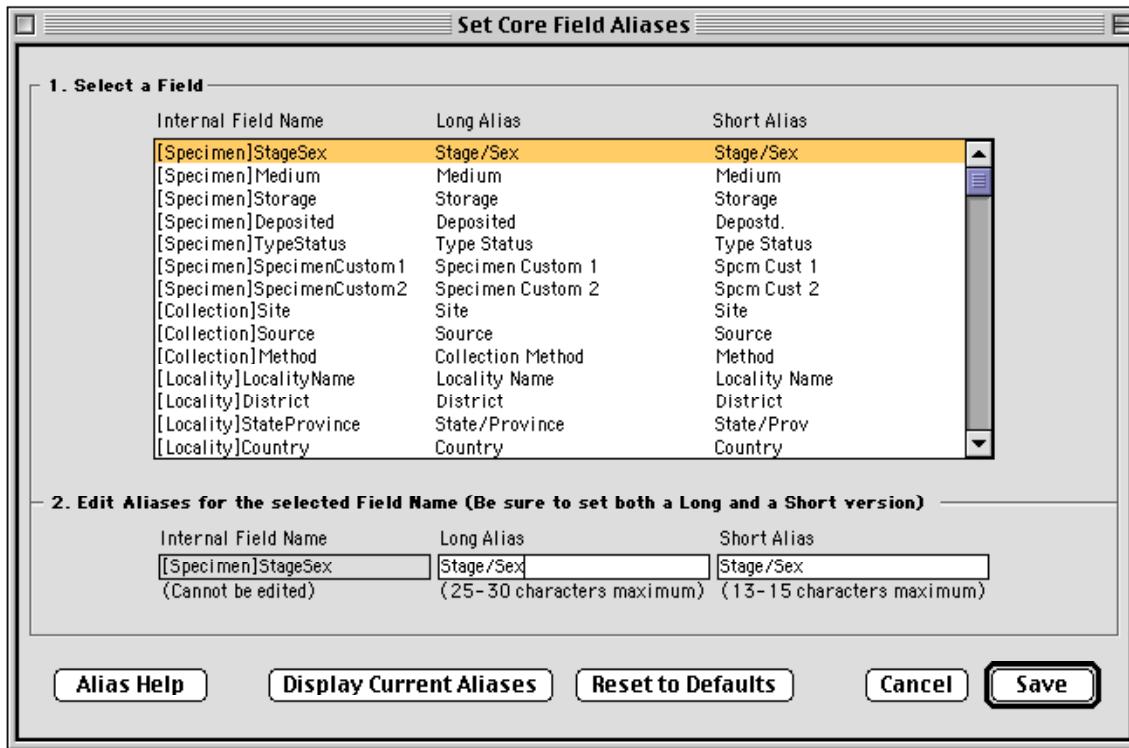
If your data entry, display, and reporting needs would be better served by renaming certain Core fields, you can use Biota's Core Field Alias system to do so very easily. For example, a plant ecologist, with no use for the [Species] TypeLocality field might want to rename the field "Growth Form." The new field name, Growth Form, is then called a *Core field Alias* (or just an *Alias*). It is an alias because Biota must still use the Internal Field Name "behind the scenes."

Core Field Aliases do not affect the *data* in the fields that aliases describe. You can change the field name later to something else (or back to the Internal Field Name) at any time without affecting Core Table record data.

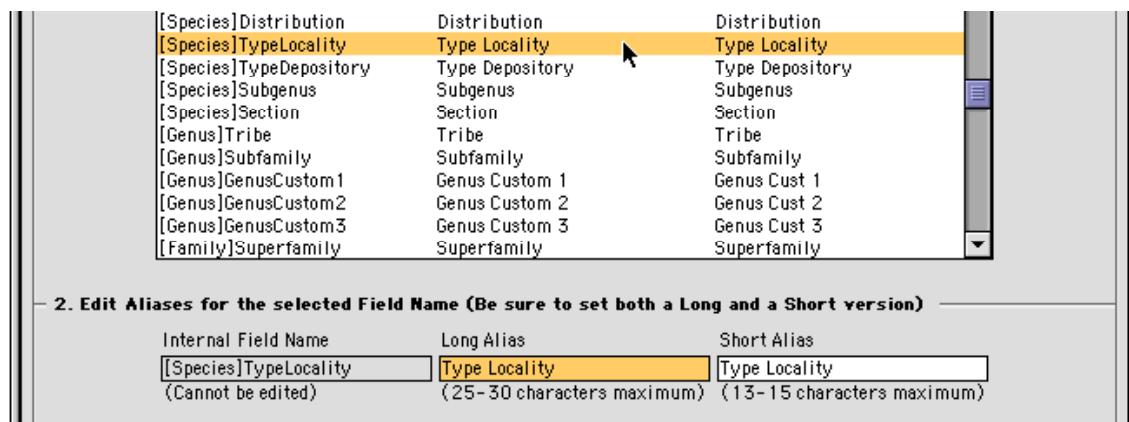
Renaming Core Fields: Setting Aliases

To re-name fields in Biota, take the following steps:

1. **From the Special menu, select "Core field Aliases."** The "Set Core field Aliases" window appears.



2. **Locate the field you want to rename.** Notice that the Internal Field Names (the left-hand column in the screen) follow the format: (TableName) FieldName.
3. **Click once on the field you want to rename in the list of fields.** The field name now appears in the entry areas in the lower panel of the window. (If you can't see the field you want, use the scroll bar to move down the list.)



The selected Internal Field Name ("Type Locality" in the exampled above) now appears in the entry areas in the lower panel of the window.

4. **Edit the Long Alias and Short Alias entries in the lower panel.** In Biota's screens and reports, the Long Alias (25–30 characters) appears where space permits, and the Short Alias (13–15 characters) otherwise. Be sure to define both.

— 2. Edit Aliases for the selected Field Name (Be sure to set both a Long and a Short version) —

Internal Field Name [Species]TypeLocality (Cannot be edited)	Long Alias Growth Form of Plant (25-30 characters maximum)	Short Alias Growth Form (13-15 characters maximum)
--	--	--

Note: You may have to experiment with the length of the Aliases after you see them in context in other screens. The number of characters that will fit depends on the exact letters used—e.g., “tillage” and “maximum” are each seven letters long, but differ substantially in the space they occupy in proportional fonts.

- When you have finished setting up all the Aliases you want, click the “Save” button in the “Set Core field Aliases” window.

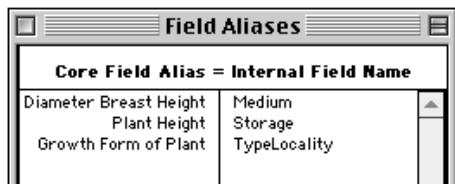


Checking Field Aliases

- From the Special menu, select “Core field Aliases.” The “Set Core field Aliases” window appears.
- Click the “Display Current Aliases” button.



If any Aliases have been defined and saved, a floating window appears, listing all current Core field Aliases and their Internal Field Name equivalents. (If no Aliases have been defined and saved, a message appears instead.)



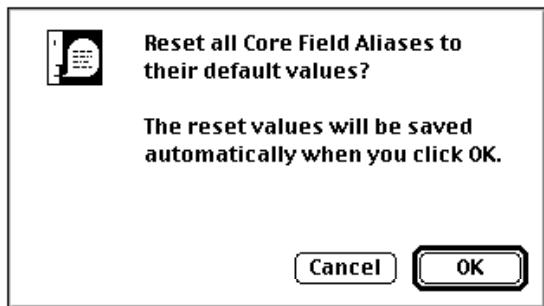
- To close the floating window, either click in the close box in the upper left corner or click the “Save” or “Cancel” button in the Set Core field Aliases window.

Clearing All Aliases and Resetting to Defaults

- From the Special menu, select “Core field Aliases.” The “Set Core field Aliases” window appears.
- Click the “Reset to Defaults” button.



A confirmation dialog appears.



3. Click the “OK” button if you want to proceed. All Aliases will be reset to the defaults that Biota uses when you first create a new Data File. These default values correspond closely with the Internal Field Names.

PART

6

Special Tools and Features

Chapter 19 **Images**

Biota incorporates a powerful and flexible set of tools for acquiring or importing, editing, archiving, comparing, and exporting images. You can link as many images as you wish to each record in the Species, Specimen, Collection or Locality table.

How Biota Works With Images

Special Components: QuickTime and QPix

Biota's image capabilities rely on two non-4D software components (the only non-4D components in Biota).

- **QuickTime.** Low-level image handling, including format conversions, compression, depth adjustment, and display, is handled by Apple QuickTime.

NOTE: You must have a recent version of QuickTime installed on your computer to use images in Biota. If you are not sure whether you have QuickTime or not, Biota will tell you if you need it. If the version you have is too old, Biota will notify you about that as well. Just click on the Image tab in the Input screen for the Species, Specimen, Collection or Locality table. You can also click the "Check QuickTime" button on any Image Input screen.

Check QuickTime

The latest version of QuickTime is available, gratis, from Apple for both Windows and Mac OS at www.apple.com/quicktime/download. Be sure to select the "Recommended" installation option.

- **QPix.** The second special image component is QPix (www.escape.gr), which integrates QuickTime into Biota through a special set of programming tools. QPix is automatically installed along with Biota (in the Win4DX or Mac4DX folder). If you use BiotaApp (the stand-alone version of Biota), the purchase price you paid for Biota includes a single-user license for QPix. In the case of Biota4D (the client-server version of Biota), you must purchase a separate QPix license based on the number of client connections you intend to use. (Write colwell@uconn.edu for details on how to purchase the QPix license for Biota4D.)

How and Where Images Are Archived

Biota can archive images in either of two ways:

- ***Either: Full image in an external file with a linked thumbnail in the Biota Data File.*** With this approach, you can store images in individual files, in virtually any file format you wish, compressed or not. When you link an image file to a Species, Specimen, Collection or Locality record, Biota creates a small thumbnail copy of the image and stores the thumbnail in the Biota Data File, along with path information to the original image file. When you use Zoom or editing tools in Biota, the original image is automatically accessed and displayed at full resolution.

NOTE: Biota keeps track of the location of linked external files by recording (in the Biota Data File) the “path” to the image file. This means that, if you move the image file to another folder, or relocate the folder that contains it, Biota will no longer be able to find the original file (for zooming, editing, changing file format, etc.).

To help ensure that linked image files remain where Biota expects them, ***you must place all linked image files somewhere inside the Biota application folder.*** You can create as many folders as you like to organize your images, at any number of levels, but all must be within the Biota Application folder.

- ***Or: Full image in the Biota Data File.*** With this alternative, Biota stores images directly in the Biota Data File, along with your text data. When you use Zoom or editing tools in Biota, the stored image is displayed at full resolution. With this option, if you import an image from an external image file, it does not matter where the that file is located.

ADVICE: High color depth, high-resolution image files can be extremely large. Storing many large images in a Biota Data File is *not* a good idea (even if they are compressed.) Archiving a single, high-depth color image in the Data File itself may enlarge the Data File more than saving hundreds of Specimen or Species records. The first approach (Full image in an external file with a linked thumbnail in the Biota Data File) allows you to leave image files of any size untouched, yet access them transparently from within Biota. Unless you intend to store only a few, relatively small images in the Biota Data File, *it is strongly recommended that you use the external file approach instead.* The only drawback is that (for obvious reasons), you cannot move the external image files to a different location and expect Biota to find them. You can always create a copy elsewhere, however.

WARNING TO BIOTA 1 USERS: In Biota 1, all images were stored in the Biota Data File. When you convert your Biota 1 Data Files to work with Biota 2, it is strongly advised that you first export the Image records to individual image files, then re-acquire them as thumbnails in the corresponding Biota 2 Data File. This process is very easy using special tools provided. See Appendix F, “[Updating Biota 1.x Data Files to Biota 2 Format](#),” for full details.

Image Sources

You can use images from a digital camera or download image files from Web pages or from ftp sites. You can scan drawings, photographs, illustrations in books, herbarium sheets, live plant specimens, or text documents using a flatbed scanner. You can capture video frames directly from a video camera, from videotape played on a VCR/VTR, or from other video storage technologies. If your image acquisition device is TWAIN compatible, you can acquire images directly from the device using Biota (see “[Acquiring an Image From a TWAIN-compliant Digital Device](#)” later in this chapter).

Some graphics and image editing applications store supplementary information with image files that provide special instructions for output devices such as a PostScript printer. This information “tags along” when you paste or import an image into Biota and is used when printing the picture to an appropriate output device.

Image Size and Shape

Unless you use Biota’s image editing tools, images in Biota are never enlarged, cropped, or changed in proportion.

Enlargement generally reduces image quality, cropping might remove an important feature you intended to illustrate, and “stretch to fit” changes in proportion are a surrealistic touch not usually approved by biologists attempting to document living things. If you need to enlarge, crop, proportion, touch up, or change the palette for an image, you can either use Biota’s onboard image editing tools (see “[Editing an Image](#)” later in this chapter) or use an application designed for those purposes before storing the image in a Biota Data File.

Image areas in Biota are uniformly about 3 by 4 in proportion, but they vary in absolute size from thumbnail display areas (100 by 133 pixels) to large format zoom screens (768 x 576 pixels). If the original image is smaller than the dimensions of a display area, the entire image is shown at its original size. If the original image is larger than a display area, it is *proportionally reduced* to the largest size that can be displayed in the display area, for display only. The digital archive retains the original resolution and size for the image.

Image Color Depth

Biota Image records accept images of any bit depth, including black and white (1 bit), gray scale (8 bit), or color (8, 16, 24, or 32 bit). As you know if you work with color image files, the bit depth of a color image greatly affects the amount of memory required to store the image on disk.

Image File Formats



An image file format specifies the algorithm used to translate the pattern and color of pixels in a screen image into digital form in a disk file. Many different image formats exist. Biota imports, archives, edits, exports, and interchanges all still image formats currently supported by QuickTime (see “[Special Components: QuickTime and QPix](#)” earlier in this chapter).

Export formats currently available (in QuickTime 6) are listed in the popup menu on the left. The list of import format supported by QuickTime 6 is somewhat longer, since certain formats are

proprietary, and may be read but not written. These additional import formats currently include GIF, FlashPix and QDGX.

Image Compression

Image compression algorithms, or codecs (for *compressor/decompressor*), allow image files to be stored in a fraction of the memory required by uncompressed image files. Biota supports all codecs supported by QuickTime (see “[Special Components: QuickTime and QPix](#)” earlier in this chapter), although not all are relevant to still images. The current list appears on the right. See “[Compressing an Image](#)” later in this chapter for instructions on image compression.

Animation
BMP
Cinepak
Component Video
DV - NTSC
DV - PAL
DVCPro - PAL
Graphics
H.261
H.263
Motion JPEG A
Motion JPEG B
MPEG-4 Video
None
<input checked="" type="checkbox"/> Photo - JPEG
Planar RGB
PNG
Sorenson Video
Sorenson Video 3
TGA
TIFF
Video

Creating a New Image Record in Biota

When you archive an image in Biota, you can bring the image (or its thumbnail representation and external link) into Biota by any of three different means: by pasting the image into Biota from the Clipboard, by importing the image from an image file, or by directly acquiring the image from an external device (scanner or camera). In all cases, start by taking the steps in the section immediately below (“Displaying an Image Input Screen”), then proceed to the appropriate section for the image-acquisition method you intend to use.

Displaying an Image Input Screen

1. From the Input menu, choose Specimen, Collection, Locality, or Species. The Input screen appears for the table you selected. The Species Input screen is illustrated here.

(In the case of Species records, you may instead create a new Species record “on the fly” from the Specimen Input screen. See “[“On-the-Fly’ Creation of Linked Records](#)” in Chapter 7. Likewise, Collection records may be created on the fly from the Specimen Input screen, and Locality records from the Collection Input screen.)

NOTE: Of course, Images can also be added at any time to an *existing* Specimen, Collection, Locality, or Species record (Chapter 12, “[Finding and Updating Records](#)”).

2. **Enter a Record Code.** If you need help with Record Codes, see Chapter 8, “[Record Codes](#).”
3. **Click the Images tab** to display the Images Input screen for the table. The keyboard shortcuts for the Image tab are CTRL-I for Windows or COMMAND-I (⌘-I) for Mac OS.



The Images Input screen for the table appears.

The screenshot shows the 'Species Input' window with the 'Images' tab selected. The window contains the following elements:

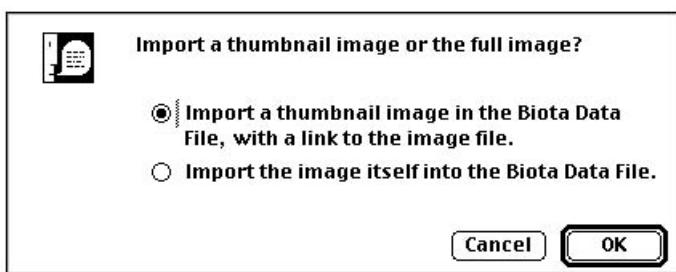
- Record:** Number 0 of 0, Created May 15, 2003, Last changed May 15, 2003, Changed By Administrator
- Image Note:** A large text area for entering notes about the image.
- Data for this Image:** A scrollable list area.
- Path:** A button to view the file path.
- Image Selection:** A preview area with a scroll bar and a 'Reorder images' button below it.
- Image Actions:** Buttons for 'Get new Image', 'Import from File', 'Send this Image', and 'Export to File'.
- This Image:** Buttons for Zoom, Edit, and Compress.
- This Image record:** Buttons for Print, Save, Delete, Cancel, and Zoom 4 Images.
- This Species record:** Buttons for Print, Save, Carry, Delete, and Cancel.
- Navigation:** Buttons for navigating between records.
- Check QuickTime:** A button to check if QuickTime is installed.

Importing an Image From an External File

NOTE: As an alternative to the method described in this section, you can also import images using the Image Console. See “[Acquiring and Editing Images in Biota Using the Image Console](#),” later in this chapter.

1. **Display an Image Input screen**, following the instructions in the section “[Displaying an Image Input screen](#)” earlier in this chapter.
2. **From the “Get new Image” popup list** in the Image Input screen (illustrated on the right), choose “Import from File.”

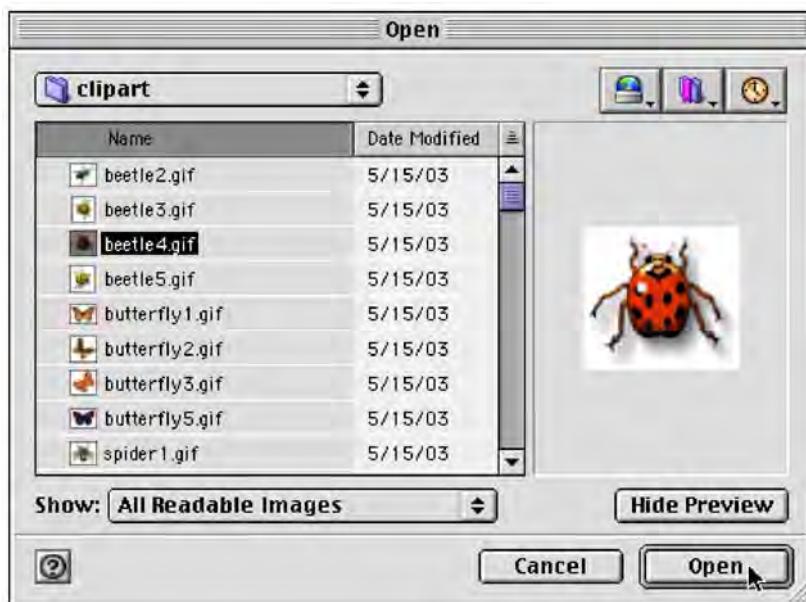
The Image Import options window appears (below).



Choose an option for importing the Image:

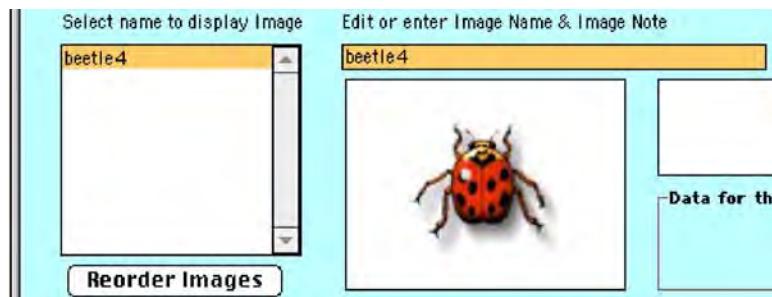
- **Either: Import a thumbnail image in the Biota Data File**, with a link to the image file.

Biota presents an Open Image screen. (The appearance of the screen depends on your operating system.)



- a. Choose an image to import and click the “Open” button (above).

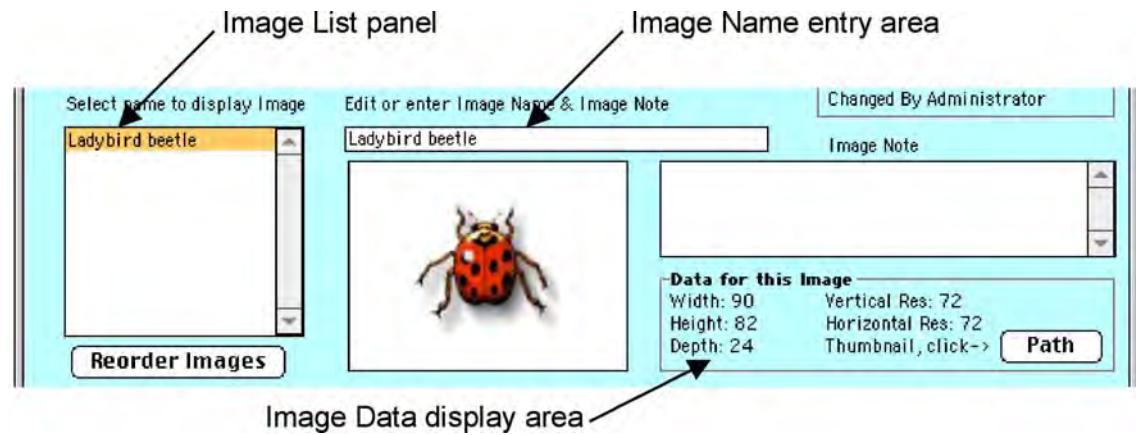
A thumbnail of the imported image appears in the Image display area, and the name of the external file now appears automatically in the Image Name entry area in the middle of the Image Input screen. The name also appears in the Image List panel at the left side of the Image Input screen.



- b. Change the name of the Image record in Biota if you wish, then click the TAB key to enter the Image Name.

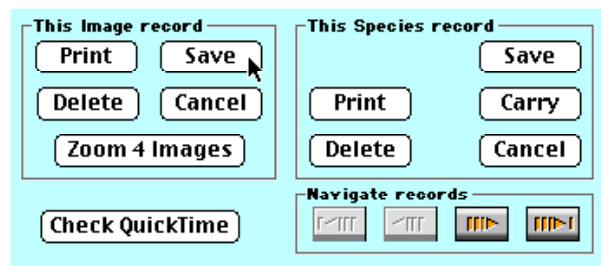
NOTE: The Image name that matches the file name is just a default suggestion. You may name the Image in the Biota Data File anything you want. It does not have to be the same as the corresponding external file to maintain the linkage between the two.

Size and resolution data for the saved thumbnail image appear in the Image Data display area on the right side of the Image Input screen, along with the designation “Thumbnail” to indicate that these data apply to the thumbnail image stored in the Biota Data File, not the image in the external file.



The “Path” button in the Image Data display area is enabled.

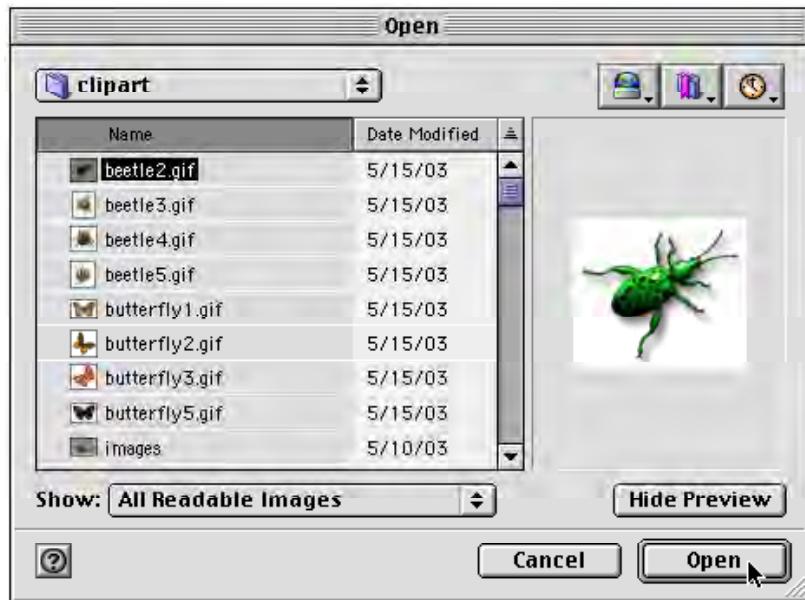
- c. Click the “Save” button in the pane titled “This Image record.” (Not the “Save” button for the parent record, although this action will also allow you to save the Image.)



- d. To display the path to the saved Image file, click the “Path” button in the Image Data display area. The path information is displayed in a separate window. (You might need this information to find the external file if you want to work with it in another application.)

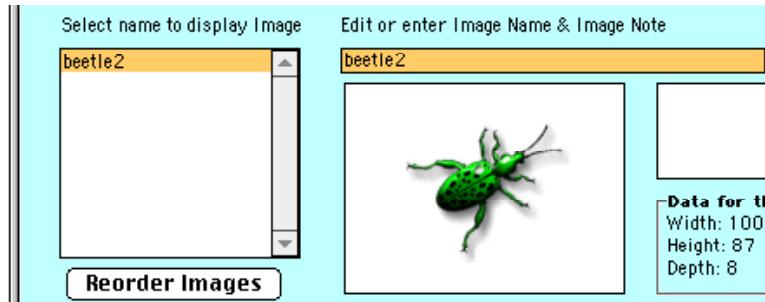


- Or: Import the image itself into the Biota Data File.
- Biota presents an Open Image screen. (The appearance of the screen depends on your operating system.)



- a. Choose an image to import and click the “Open” button (above).

A thumbnail of the imported image appears in the Image display area, and the name of the external file now appears automatically in the Image Name entry area in the middle of the Image Input screen. The name also appears in the Image List panel at the left side of the Image Input screen.

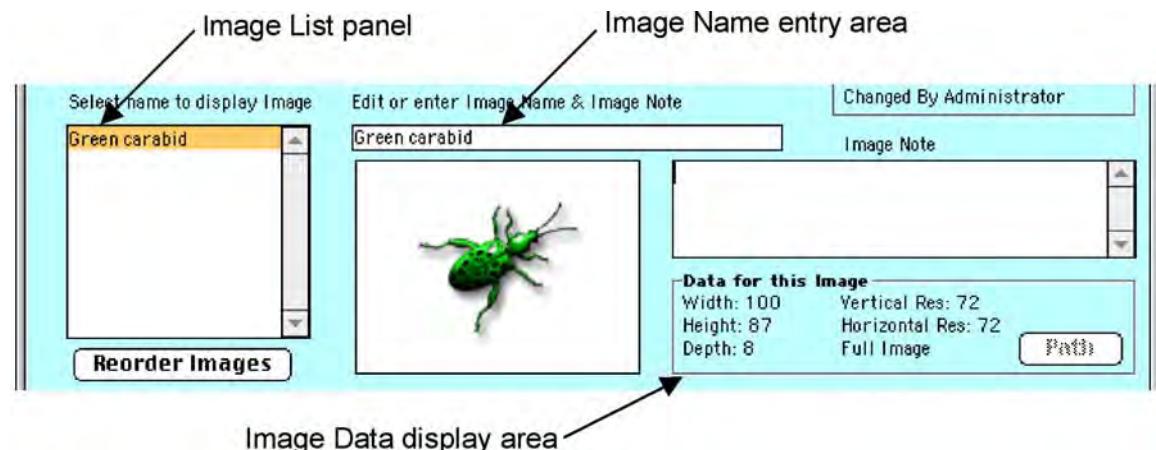


- b. Change the name of the Image record in Biota if you wish, then click the TAB key to enter the Image Name.

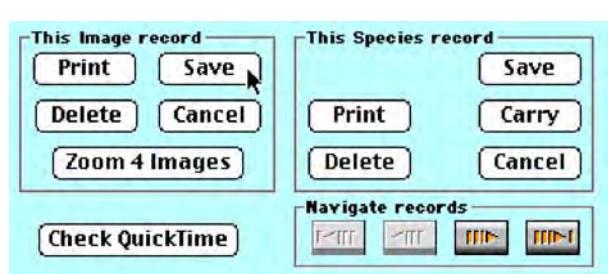
Note: The Image name that matches the file name is just a default suggestion. You may name the Image in the Biota Data File anything you want.

Size and resolution data for the saved *full* image appear in the Image Data display area on the right side of the Image Input screen, along with the designation “Full Image” to indicate that these data apply to the characteristics of the full-sized image stored in the Biota Data File.

The “Path” button in the Image Data display area is not enabled, since no link is maintained with the external image file that was the source of this image.



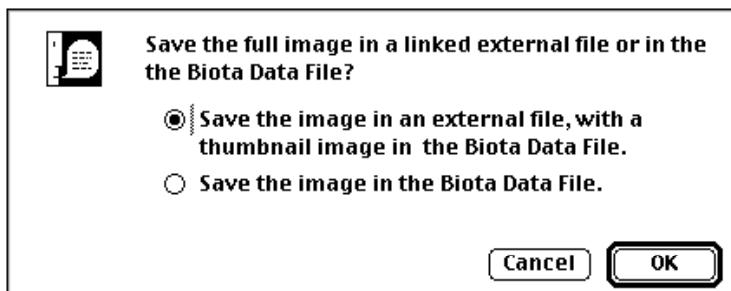
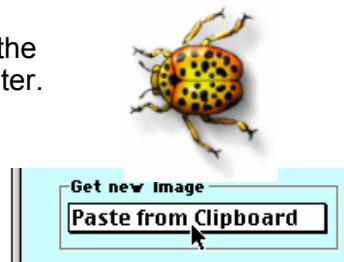
- c. Click the “Save” button in the pane titled “This Image record.” (Not the “Save” button for the parent record.)



Pasting an Image From the Clipboard

1. **Display an Image Input screen**, following the instructions in the section “[Displaying an Image Input screen](#)” earlier in this chapter.
2. **Copy an image to the Clipboard** from any application.
3. **From the “Get new Image” popup list** in the Image Input screen (illustrated on the right), choose “Paste from Clipboard.”

The Image Save Options window appears (below).



4. **Follow the instructions in the section “[Saving and Naming a New Image](#)” later in this chapter.**

Acquiring an Image From a TWAIN-compliant Digital Device

TWAIN is an image capture protocol (an industry standard that applies to both Windows and Mac OS) used to control digital scanners, cameras or other image acquisition devices from within an image-processing application, such as Biota or Adobe Photoshop. This means that, instead of having to capture the digital image in a separate program, save it and then re-open it in Biota, the TWAIN-compliant camera or scanner delivers the image directly to Biota. Using Biota’s onboard image editing tools (see “[Editing an Image](#)” later in this chapter), you can then correct color balance, size, cropping, orientation, and so on before saving the image in any of the ways described in the section “[Creating a New Image Record in Biota](#)” earlier in this chapter.

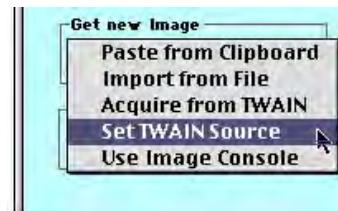
Although Biota supports TWAIN-compliant digital devices, it is up to you to install the latest TWAIN driver specific to your device. (Check the device manufacturer’s website for the latest driver.)

NOTE: According to www.twain.org, “The word TWAIN is from Kipling’s ‘The Ballad of East and West’—‘...and never the twain shall meet....’ reflecting the difficulty, at the time [TWAIN was established], of connecting scanners and personal computers. It was up-cased to TWAIN to make it more distinctive. This led people to believe it was an acronym, and then to a contest to come up with an expansion. None were selected, but the entry ‘Technology Without An Interesting Name’ continues to haunt the standard.”

1. **Display an Image Input screen**, following the instructions in the section “[Displaying an Image Input screen](#)” earlier in this chapter.

2. **Set up the connection to the digital device.**

- ***Either:* From the “Get new Image” popup list in the Image Input screen, choose “Set TWAIN Source.”**



- ***Or:* From the “Get new Image” popup list in the Image Input screen (illustrated on the right), choose “Use Image Console.”**

The Image Console appears. From the File menu in the Image Console, choose “Twain source....”



If one or more TWAIN-compliant devices are connected to your computer or local network, and the proper TWAIN driver has been installed, a list of devices appears. If no devices are connected, or the drivers are not installed, Biota informs you.



Note: If you are using Mac OS 9, the first time you try to access a TWAIN device Biota will post a message explaining how to enable this feature, which you need do only once.

3. **Select the digital device from the popup list.** The list of devices disappears, but the device is now set as the default.

4. **Acquire the image.**

- ***Either:* From the “Get new Image” popup list in the Image Input screen, choose “Acquire from TWAIN.” The Image Save Options window appears.**



- ***Or:* From the File menu in the Image Console, choose “Acquire....”**

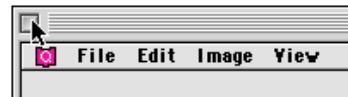
Depending on the device, either the captured image or an interface dialog window appears.



5. **Name, edit if necessary, and save the image.**

- ***Either:* In the Image Input screen, the Image Save Options window appears. Follow the instructions in the section “[Saving and Naming a New Image](#)” later in this chapter, for naming and saving the image and Biota Image record. If you want to edit the image, see the section “[Editing an Image](#),” later in this chapter.**

- **Or: From in the Image Console**, edit the image if you wish (see “[Editing an Image](#),” later in this chapter). Then click the Close Box in the Image Console.

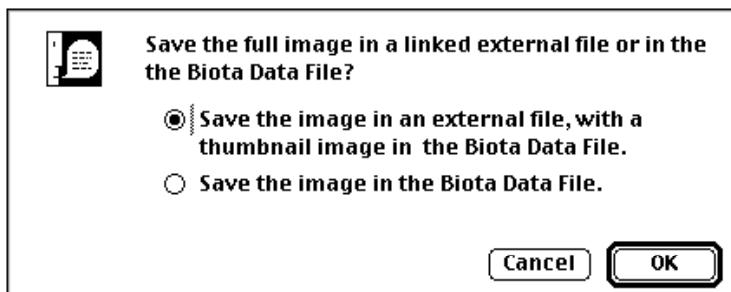


The Image Save Options window appears. Follow the instructions in the section “[Saving and Naming a New Image](#)” later in this chapter, for naming and saving the image and Biota Image record.

Saving and Naming a New Image

1. Follow the instructions in one of the following sections: “[Pasting an Image From the Clipboard](#)” or “[Acquiring an Image From a TWAIN-compliant Digital Device](#),” earlier in this chapter; or “[Editing an Image](#)” or “[Compressing an Image](#)” later in this chapter.

The Image Save Options window appears (below).



2. Choose an option for saving the Image:

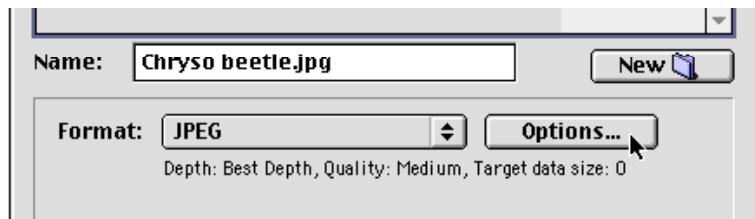
- **Either:** Save the image in an external file, with a thumbnail Image in the Biota Data File.

If you choose this option, Biota presents the Export Image screen. (The appearance of the screen depends on your operating system.)

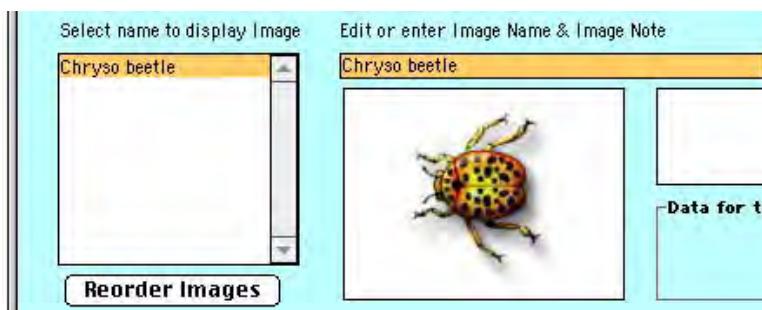
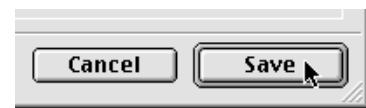
- a. Navigate to the folder that contains the Biota application (BiotaApp or Biota4d). If you have established a special sub-folder for image files, within the Biota application folder, open the image folder.

NOTE: To help ensure that linked image files remain where Biota expects them, ***you must place all linked image files somewhere inside the Biota application folder.*** You can create as many folders as you like to organize your images, at any number of levels, but all must be within the Biota Application folder.

- b. Enter a name for the file to be saved.
- c. Select an image format from the “Format” popup list. See “[Image File Formats](#)” earlier in this chapter. (Current Format settings are displayed in the Format pane in Mac OS.)



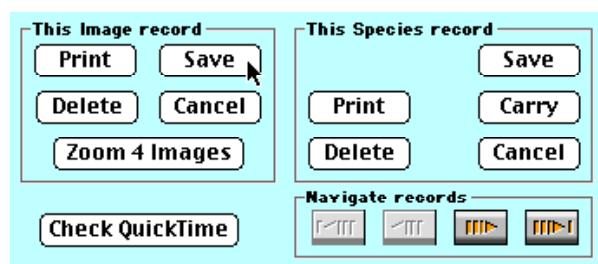
- d. If you need to change any options for the selected Format, click the “Options” button to the right of the popup list (illustrated above).
 - e. Click the “Save” button in the Export Image window.
- A thumbnail of the imported image appears in the Image display area, and the name you gave the external image file now appears automatically in the Image Name entry area in the middle of the Image Input screen. The name also appears in the Image List panel at the left side of the Image Input screen.



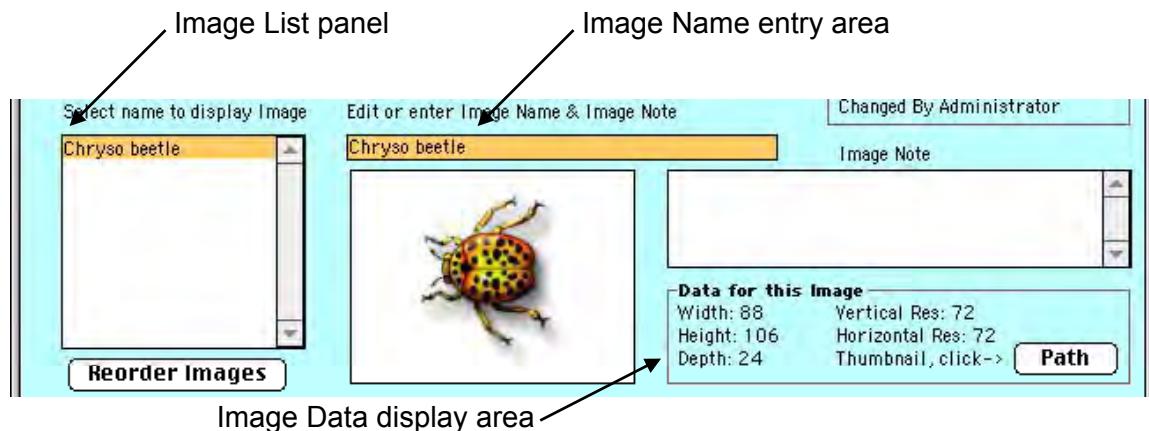
- f. Change the name of the Image record, if you wish.

NOTE: The Image name that matches the file name is just a default suggestion. You may name the Image in the Biota Data File anything you want. It does not have to be the same as the corresponding external file to maintain the linkage between the two.

- g. Click the “Save” button in the pane titled “This Image record.” (Not the “Save” button for the parent record, although this action will also allow you to save the Image.)



Size and resolution data for the saved thumbnail image appear in the Image Data display area on the right side of the Image Input screen, along with the designation “Thumbnail” to indicate that these data apply to the thumbnail image stored in the Biota Data File, not the image in the external file. The “Path” button in the Image Data display area is enabled.

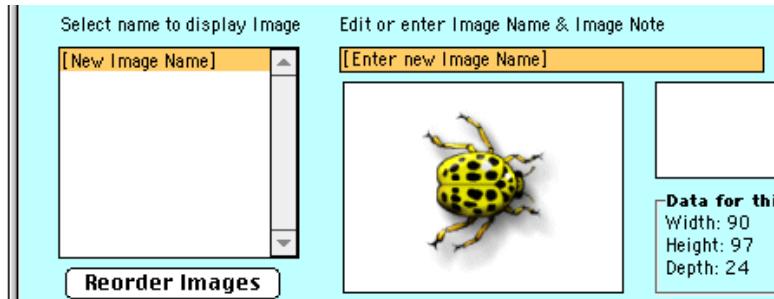


- h. To display the path to the saved Image file,** click the “Path” button in the Image Data display area (above). The path information is displayed in a separate window. (You might need this information to find the external file if you want to work with it in another application.)



- Or: Save the Image in the Biota Data File.**

If you choose this option, a thumbnail of the imported image appears in the Image display area, with the reminder “[Enter new Image Name]” in the Image Name entry area and in the Image List panel at the left side of the Image Input screen.

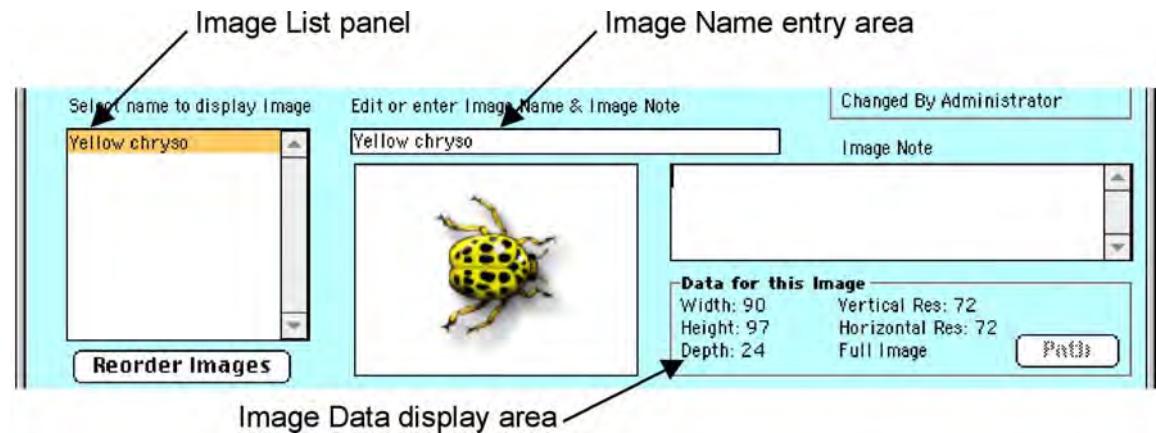
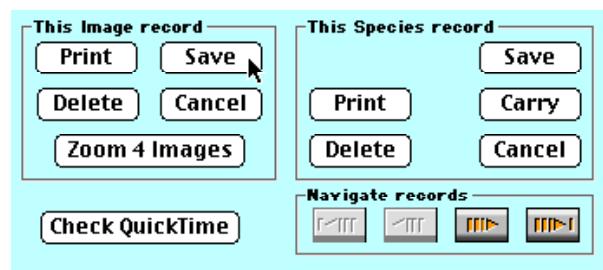


- a. Enter a name for the Image record.**

- b. Click the “Save” button in the pane titled “This Image record.” (Not the “Save” button for the parent record, although this action will also allow you to save the Image.)

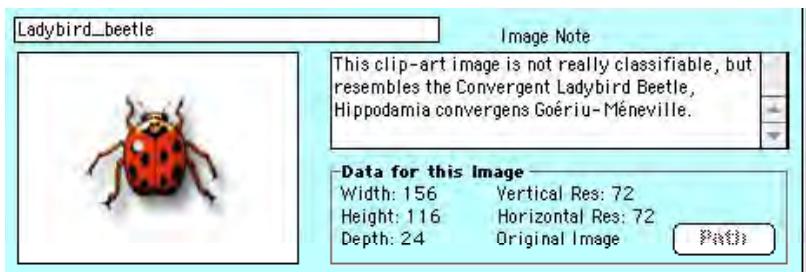
Size and resolution data for the saved *full* image appear in the Image Data display area on the right side of the Image Input screen, along with the designation “Full Image” to indicate that these data apply to the characteristics of the full-sized image stored in the Biota Data File.

The “Path” button in the Image Data display area is not enabled, since no link is maintained with the external image file that was the source of this image.

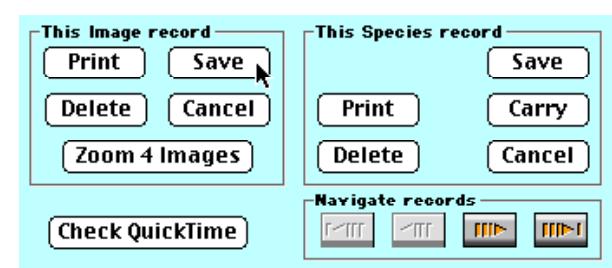


Adding an Image Note

Each Image record may have an associated Image Note, up to 32K characters in length (although short notes are expected, given the small size of the Note area).



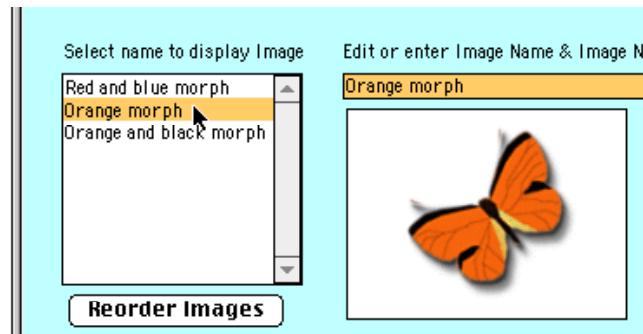
1. Enter the note in the Image Note area in the Image Input screen.
2. Click the “Save” button in the pane titled “This Image record.” (Not the “Save” button for the parent record, although this action will also allow you to save the Image.)



Exporting and Importing Images

Exporting Individual Images

1. **Display an Image Input screen**, following the instructions in the section “[Displaying an Image Input screen](#)” earlier in this chapter.
2. **Select an Image record from the Image List panel** on the left side of the Image Input screen. The Image is displayed in the adjacent thumbnail area.



3. **To place a copy of the image on the Clipboard**, select “Copy to Clipboard” from the “Send this image” popup list in the Image Input screen.

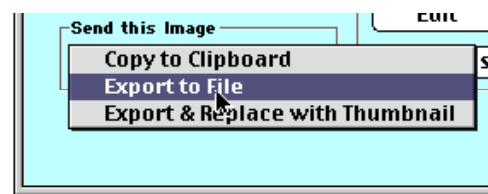
The image on the Clipboard can be pasted into any application that accepts images.



Note: The original image, not the thumbnail, is copied to the clipboard from the linked external image file or from the Biota Data File, depending upon where you have saved it. The original image format is maintained.

4. **To export the image to a new external file:**

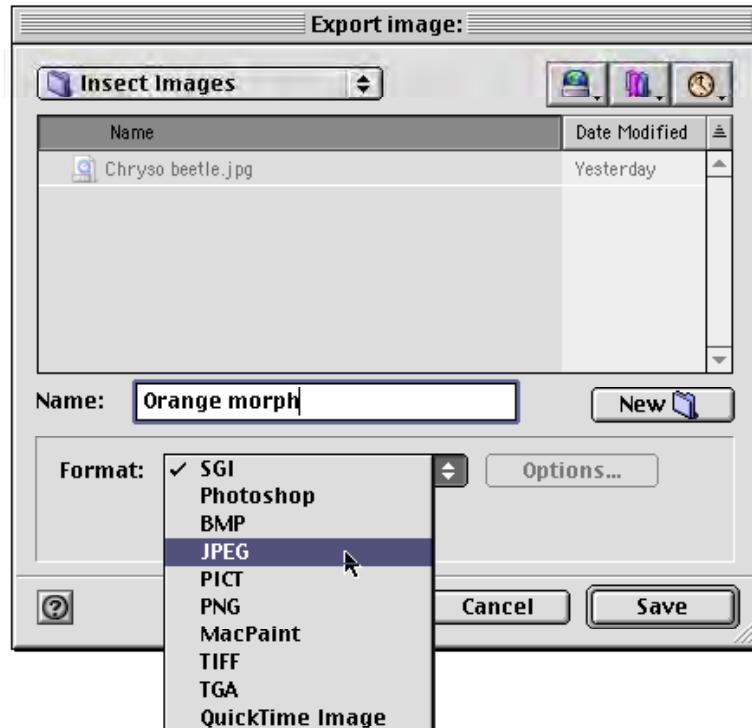
- **Either:** Select “Export to File” from the “Send this image” popup list in the Image Input screen.
- **Or:** Select “Export and Replace with Thumbnail” from the “Send this image” popup list in the Image Input screen. This option is intended to allow you to clear large images out of the Biota Data File, replacing them with thumbnails linked to newly exported external image files.



Biota presents the Export Image screen. (The appearance of the screen depends on your operating system.)

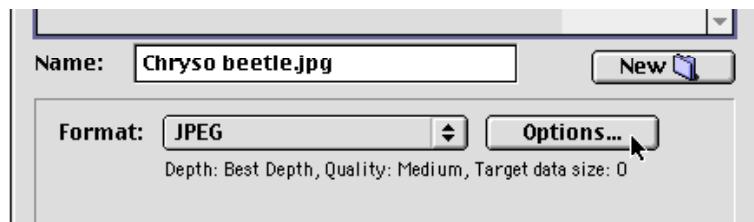
- a. Navigate to the folder where you wish to save the new image file.
- **Either:** If you do not intend to link the new image file to the Biota Data File, you may place it in any folder.
 - **Or:** If you are replacing a full image with a linked thumbnail, or you intend to link the new data file to the Biota Data File, you must place the new image file in the folder that contains the Biota application (BiotaApp or Biota4d). If you have established a special sub-folder for image files, within the Biota application folder, open that image folder.

NOTE: To help ensure that linked image files remain where Biota expects them, ***you must place all linked image files somewhere inside the Biota application folder.*** You can create as many folders as you like to organize your images, at any number of levels, but all must be within the Biota Application folder.



- b. Enter a name for the file to be saved.
- c. Select an image format from the “Format” popup list. See “[Image File Formats](#)” earlier in this chapter. (Current Format settings are displayed in the Format pane in Mac OS.)

- d. If you need to change any options for the selected Format, click the “Options” button to the right of the popup list.



- e. Click the “Save” button in the Export Image window.



Exporting Groups of Images

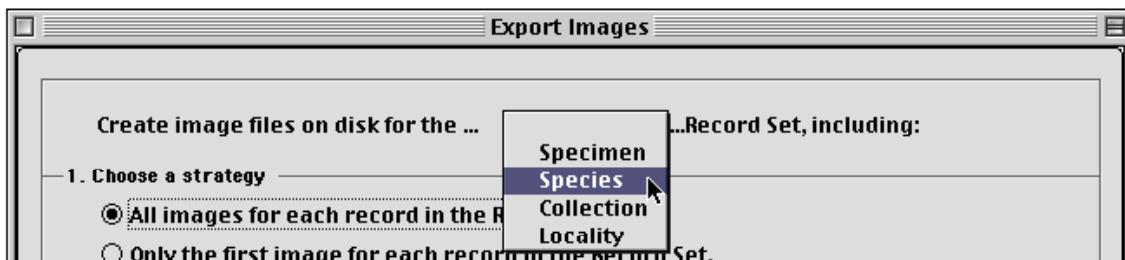
Biota has a special Export Images utility (in the Im/Export menu) for exporting groups of images to individual, external image files. Biota names the files automatically and creates a special log of the exports that can be used to import the same group of images into another Biota Data File. (For full instructions for importing, see “[Importing Groups of Images](#)” later in this chapter).

1. Using Biota search tools (Chapter 12, “[Finding and Updating Records](#)”), create a Record Set representing the Species, Specimen, Collection or Locality records for which you wish to export Image files.
2. From the Im/Export menu, choose “Export Image Files.”

Biota presents the Export Images screen.



3. Select the Parent table name (Species, Specimen, Collection, or Locality) from the popup list at the top of the options screen.



4. Choose an export strategy.



- **Either:** All Images for each [Species] record in the [Species] Record Set. (The name of the table depends on which Parent table you chose in [Step 3](#).)
- **Or:** Only the first Image for each [Species] record in the [Species] Record Set. (The name of the table depends on which Parent table you chose in [Step 3](#).)

5. Specify which images to export.



- **Either:** Export full images and thumbnails. With this option, an external image file is created for each Image record indicated in Step 4, including not only full images stored in the Biota Data File, but also thumbnail images linked to external image files.

NOTE: For full images from the Data File, the full image is exported. For thumbnails linked to external image files, the thumbnails themselves are exported, not the linked images.

- **Or:** Export full images only; skip thumbnails. With this option, an external image file is created for each Image record indicated in Step 4 for which the full image is stored in the Biota Data File. The full image is exported.

6. Choose an image format for the exported image files from the popup list. See “[Image File Formats](#)” earlier in this chapter.



7. Click the “Set Folder” button.

A folder selection window appears.



NOTE: The window’s appearance depends on your operating system. The Mac OS window, shown above, includes a “New Folder” button, should you wish to create a new folder to hold the exported images. In Windows, there is no such button, so if you need a new folder in Windows you will have to create it manually before exporting the images.

8. Choose the folder that will hold the exported image files. Be sure you have plenty of space on the drive you choose to hold the exported image files.
9. Click the “OK” button in the Export Images window to launch the image file export.

A progress indicator appears. When the export process is complete, Biota confirms it.



What Biota Exports. File names for the exported image files are assigned automatically, in the form RecordCode_ImageName.Extension, where the Extension identifies the image format that you specify in the popup list in [Step 6](#), above. If the total length of the file name, including the extension, exceeds 31 characters, it is truncated to 31 characters. If a proposed file name would duplicate an existing one in the Image Folder, a numerical suffix is automatically added after the Image Name component of the file name.

Two log document files are automatically created and placed in the Image Folder: an Error Log and an Image File List. Both are plain text documents, which can be read with any text editor. The initial exclamation point, which is part of the file name, forces the Error Log and Image File List documents to appear first in the image folder.

1. **!ImageExportErrors.txt, the Error Log**, lists any Image records that could not be exported to image files, with an error code for each failure. If you get errors, try to figure out why by looking at the offending Image record in the Biota Data File. (The most common errors involve corrupted image records.) If you cannot figure out the problem, try manually exporting the image following the instructions in the section “[Exporting Individual Images](#)” (earlier in this chapter), a tool that provides additional diagnostics.
2. **!ImageFileList.txt, the Image File List**, records all images exported and the file names assigned. If you want to import the image files into a different Data File, as detailed in the section “[Importing Groups of Images](#)” later in this chapter, Biota will use this list to link the external image files with corresponding thumbnail images that it creates in the recipient Biota Data File. (You may choose, instead, to import the full images into the recipient Biota Data File.)

The format for the Image File List (!ImageFileList.txt) is as follows:

- **Column 1: The name of the parent table** in Biota (Species, Specimen, Collection, or Locality).
- **Column 2: The Record Code** (Species Code, Specimen Code, Collection Code, or Locality Code) for the parent record.
- **Column 3: The Image Name** for this image.
- **Column 4: The full name (including extension) of the external image file** created.

Importing Individual Images

Please see the section “[Importing an Image From an External File](#)” earlier in this chapter.

Importing Groups of Images

Biota offers a special Import Images utility (in the Im/Export menu) for importing groups of images from individual, external image files in “batch mode.” To do this automatically, Biota needs to know where to look for the image files to import, what to name the Image records in the recipient Biota Data File, and where to link the new Image records in the recipient Biota Data File. For all this information, Biota looks for a special Image File List, which by convention is named “!ImageFileList.txt.”

1. Set up the Image File List to guide the import.

NOTE: If you are importing images that you exported automatically following the directions in the section “[Exporting Groups of Images](#)” earlier in this chapter, the Image File List, named “!ImageFileList.txt,” has already been created in the proper format. Proceed directly to [Step 3](#), below.

- **The name of the Image File List** may be any name you wish, but the convention is: **!ImageFileList.txt** (including the exclamation mark at the beginning, which causes the file to sort at the top of its folder).
- **The Image File List must be a tab-delimited, plain text file.** (To create such a file in Microsoft Excel, save the file as file type “Tab-Delimited Text.”)
- **The Image File List may be placed anywhere**, but it is conventional to place it inside the Image Folder (see [Step 2](#), below).
- **The format for the Image File List** must be exactly as follows, with a row for each image file to be imported:
 - ◊ **Column 1: The name of the parent table** in Biota (Species, Specimen, Collection, or Locality).
 - ◊ **Column 2: The Record Code** (Species Code, Specimen Code, Collection Code, or Locality Code) for the parent record.

NOTE: All parent records referenced in the Image File List must already exist in the recipient Biota Data File. If not, Biota displays an error message.

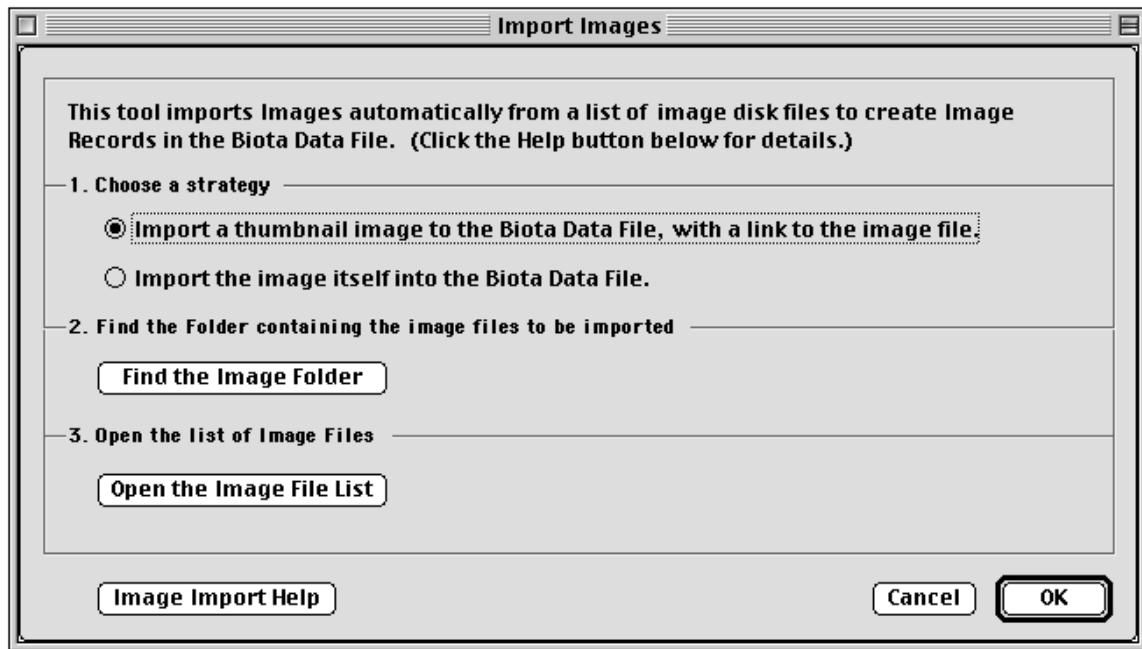
- ◊ **Column 3: The Image Name** for this image.
- ◊ **Column 4: The full name (including extension) of the external image file** to be used as a source for import.

NOTE: All external image source files must be placed in the same folder as the Image File List.

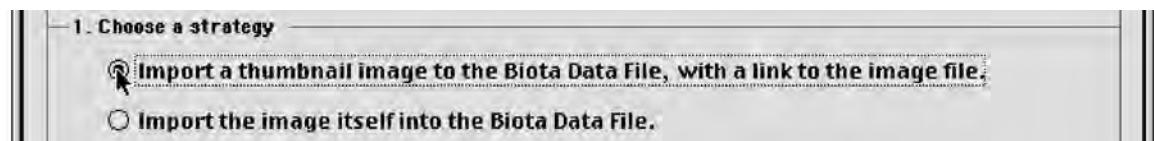
2. Set up the Image Folder. Each image to be imported must be in a separate image file on your hard disk.

- The image files can be in any image format supported by QuickTime. See “[Image File Formats](#)” earlier in this chapter.
- All image files to be imported must be contained in a single folder, called the Image Folder.
- **If you intend to import thumbnail versions** of each image (linked to the original image files), the Image Folder must be inside the same folder (call it the Data Folder) that contains the Biota Data File. Furthermore, in this case, the Image Folder must remain within the Data Folder. This requirement allows the Data Folder itself (containing both the Biota Data File and the Image Folder) to be moved to any location without losing the links, since Biota addresses the Image Files relative to the location of the Data File.

- If you will be importing the full images, instead of thumbnails, the Image Folder can be in any location, because no links are recorded in this case.
3. From the Im/Export menu, choose Import Images. The Import Images setup screen appears.



4. Choose an import strategy.

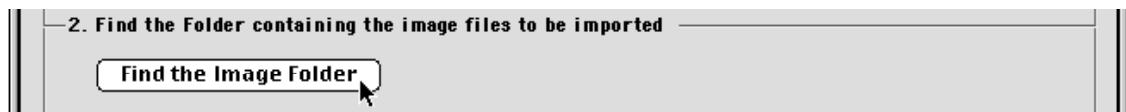


- **Either: Import a thumbnail image to the Biota Data File, with a link to the image file.** This option creates a thumbnail image in your Biota Data File for each external image file in the Image File List, with a persistent link to the external image file. The external image file remains unchanged.

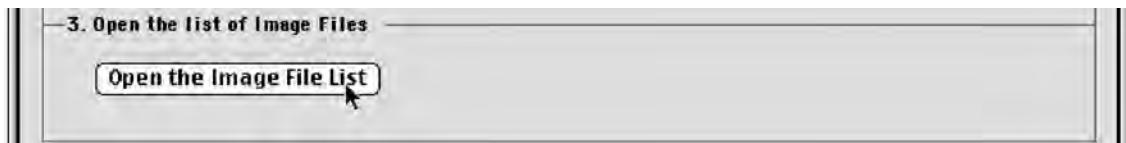
NOTE: This option is highly recommended for any Biota Data File that has more than a few images or any large images.

- **Or: Import the image itself into the Biota Data File.** In this case, a full copy of the image is imported to the Biota Data File for each image file in the Image File List. The external image file remains unchanged.

5. **Find the Image Folder** containing the image files to be imported. Click the “Find the Image Folder” button and locate the folder.



6. **Find and open the Image File List.** Click the “Open the Image File List” button and locate file.



7. **Click OK to launch the import.** While displaying a progress indicator, Biota automatically reads the file names, Image Names, and Record Codes from the Image File List.



If you chose the thumbnail option, Biota creates and saves a thumbnail image in the Biota Data File, for each external image file. The path to the external image file is also saved in the Biota Data File, allowing the full image from the external file to be transparently displayed in zoomed views or edited within Biota.

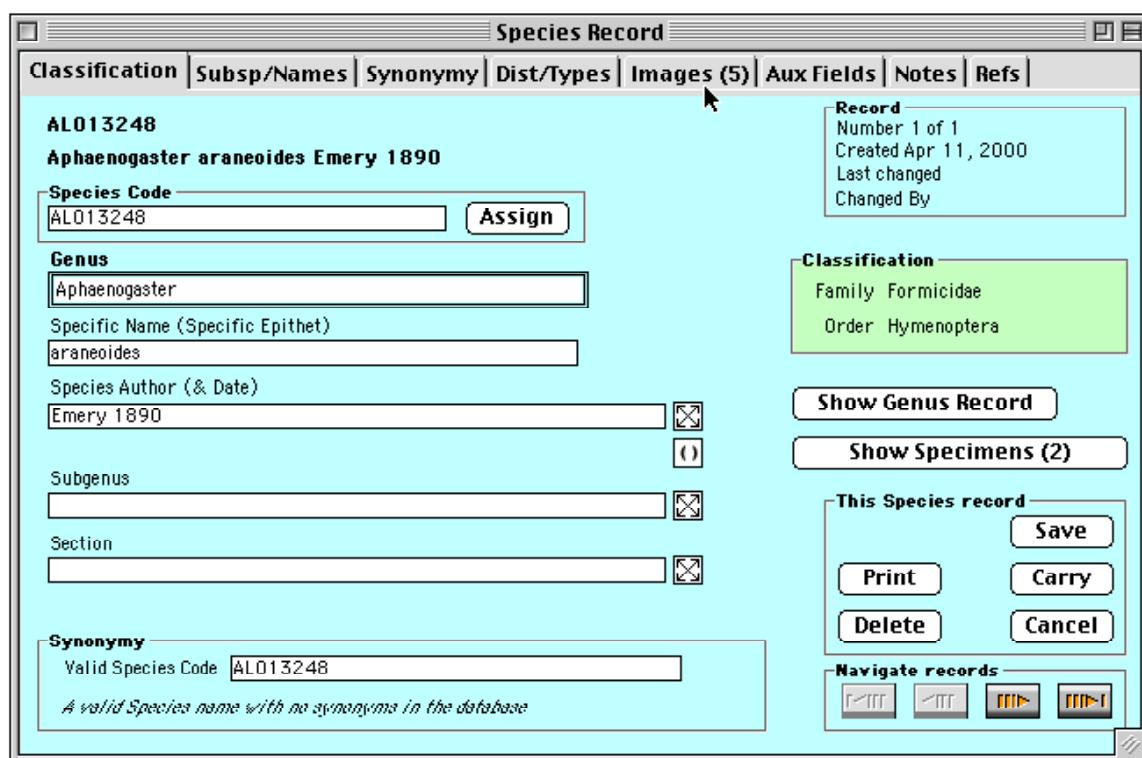
8. **Test the images in Biota** when the import process is complete.

Displaying, Zooming, Reordering, or Deleting Images in the Image Input screen

Displaying an Image in the Input Screen

1. Display a Specimen, Collection, Locality, or Species record in the Input screen. The Species Input screen is illustrated here.

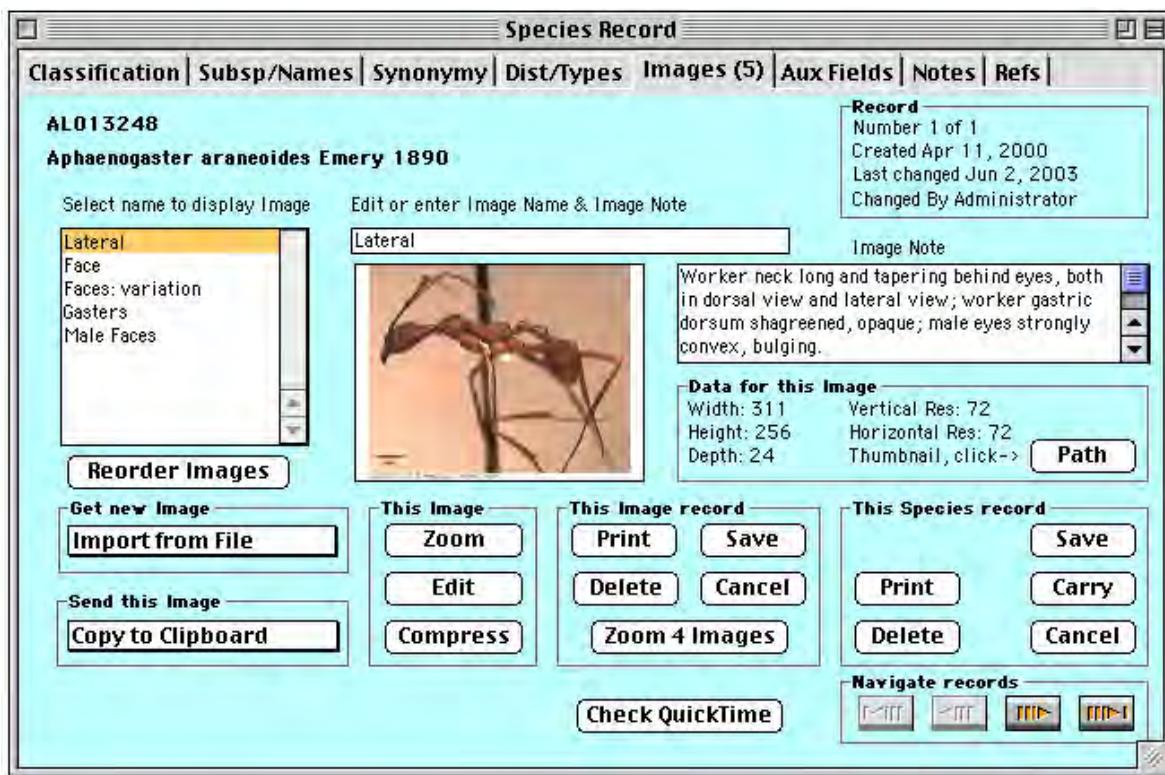
The number of linked images is displayed in the parenthesis on the Image tab (there are 5 in the example below).



2. Click the **Images tab** to display the Images Input screen for the table. The keyboard shortcuts for the Image tab are CTRL-I for Windows or COMMAND-I (⌘-I) for Mac OS.



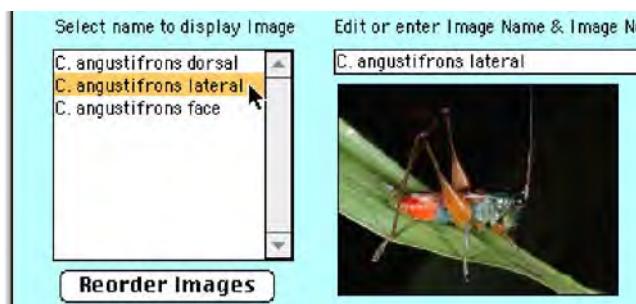
The Images Input screen for the record appears, with the first Image displayed in the central panel. A scrollable list of all linked Images for this parent record appears on the left, an Image Note (if any) for the displayed Image appears in the upper panel on the right, with data for the displayed image shown in the lower panel ("Data for this image") on the right.



Note: If you want to change the order of the Image records in the scrolling display (which controls the order in other contexts as well), see “[Changing the Order of Linked Image Records in the Input Screen](#)” later in this chapter.

Zooming Images in the Input Screen

1. **Display an Image** in the Image Input screen. (See “[Displaying an Image in the Input Screen](#)” earlier in this chapter.)
2. **Select an Image to zoom** by clicking the Image Name in the scrolling list of Image Names. An Image linked to a Species record is illustrated here.

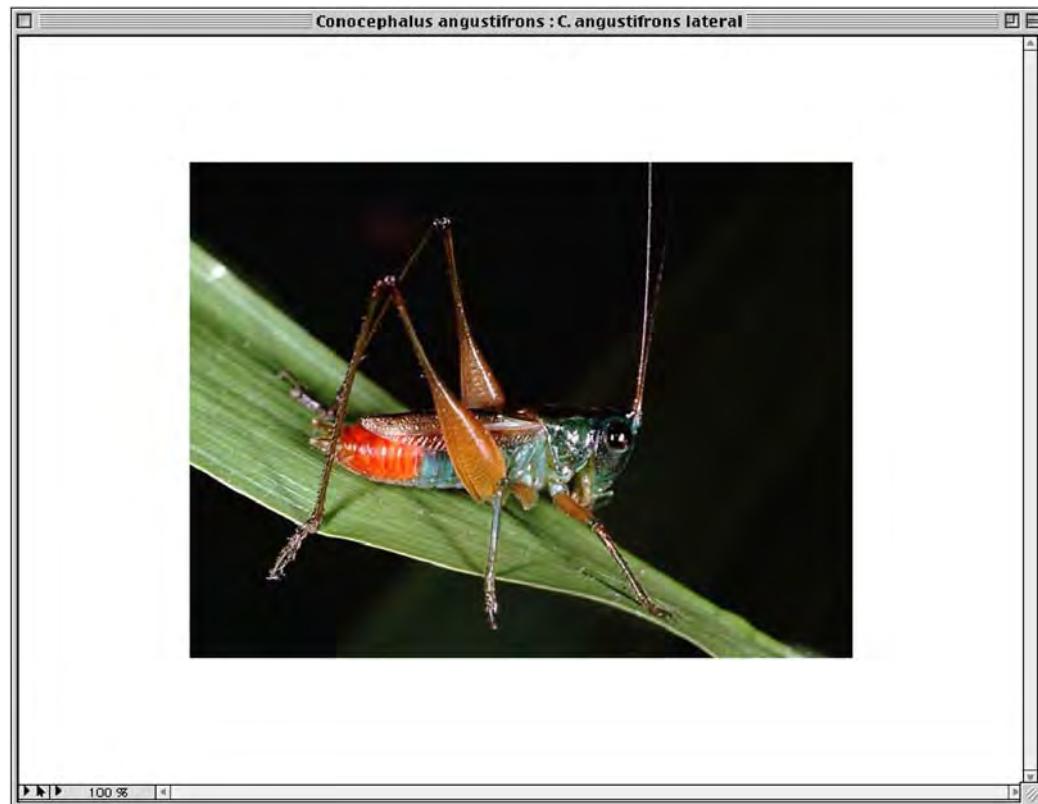
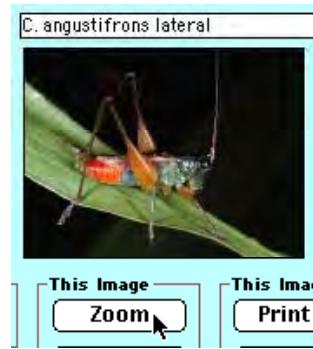


3. To zoom the image, click the “Zoom” button on the screen, located in the panel labeled “This Image.”

The image is displayed at full size in a new window.

NOTES:

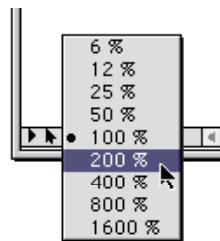
- a. The original image is always displayed when you zoom, not the thumbnail. If the original image is in an external file, that file is accessed and the image displayed.
 - b. If the original image is smaller than 576 x 768 pixels, the full Image is displayed, but is not initially enlarged (example below).
 - c. If the original image is larger than 576 x 768 pixels, the Image is displayed at full resolution, even if it is larger than the 576 x 768 pixel area.
-



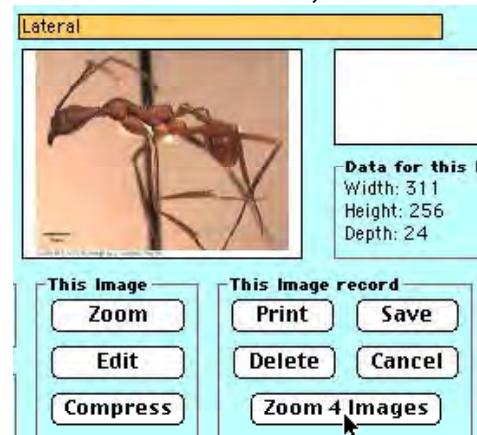
4. To zoom in further or zoom out from the Image, select a zoom percentage from the popup at the bottom left of the image display window.



If the image is larger than the display area, select a percentage less than 100. You can also use the “Hand” tool, activated from a popup menu just to the left of the zoom menu, to move the Image around in the viewing area.

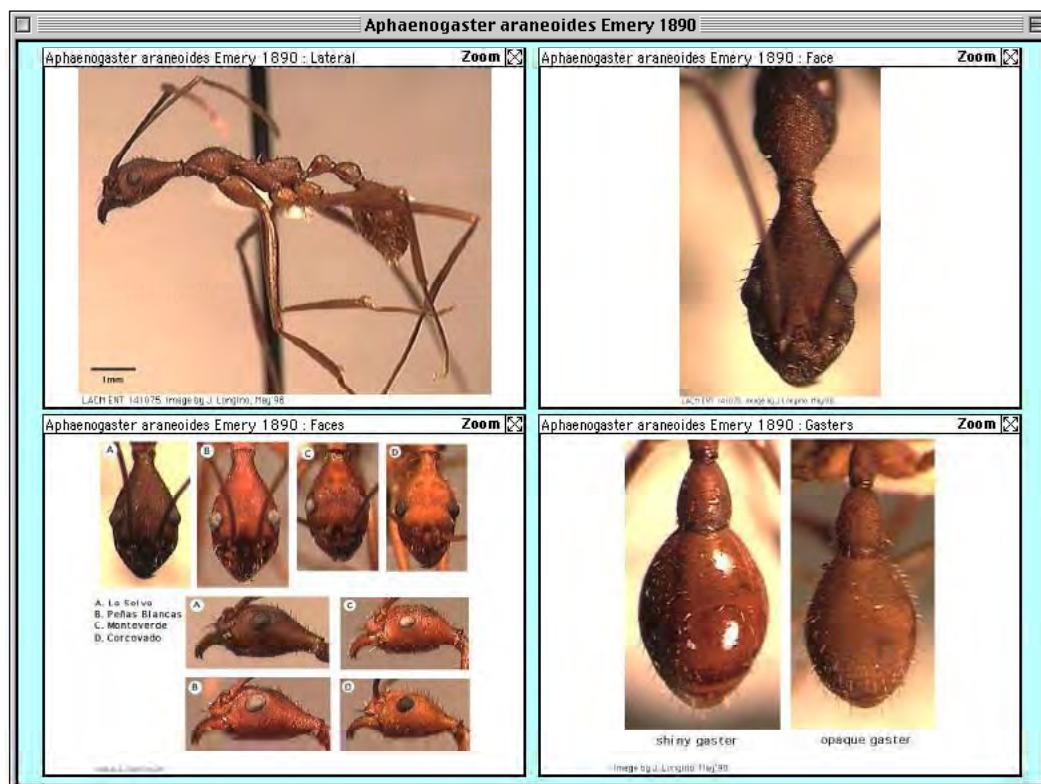


5. To display the first 4 Images for a parent record in the Zoom 4 Screen, click the “Zoom 4 Images” button on the screen. The button is located in the panel labeled “This Image record.”



NOTES:

- Original images are always displayed when you use the Zoom 4 tool, not thumbnails. If an original image is in an external file, that file is accessed and the image displayed.
- If an original image is smaller than 340 x 240 pixels (Windows) or 359 x 255 pixels (Mac OS), the full Image is displayed, but is not enlarged.
- If an original image is larger than 340 x 240 pixels (Windows) or 359 x 255 pixels (Mac OS), the Image is displayed, without distortion, at the largest magnification that will fit in the display area.



6. To zoom a single image from the Zoom 4 Screen, click the “Zoom” button in the upper right corner of one of the four image panels.



Changing the Order of Linked Image Records in the Input Screen

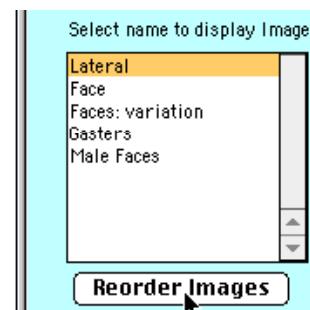
When you create a new Image record for a Species, Specimen, Collection, or Locality (see “[Creating a New Image Record in Biota](#)” earlier in this chapter), the Image Name is added to the end of the scrolling list of Image records for that parent record. This section explains how to change the order of the Images in the scrolling list for an individual parent record.

The order of the Image Names in the scrolling Image list of the Image Input screen for a parent record is important in three contexts in Biota.

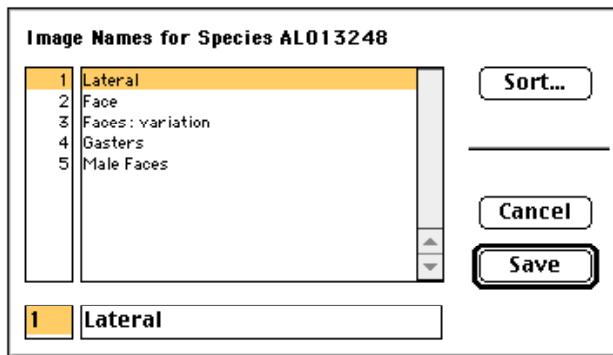
- **The thumbnail image Record Listing screens** use this order to display the first four images for each parent record (see “[Displaying Thumbnail Images in the Record Listing Screens](#),” later in this chapter). To allow easy comparison of analogous views of related species by scanning “columns” of the thumbnail image screen, it is best to order images by view (and thus by Image Name) identically for related species. The images for four ant species in the section “[Displaying Thumbnail Images in Record Listing Screens](#)” later in this chapter are a good example of this technique.
- **The Export Image Files tool** can export either the first image for each selected parent record, as ordered in the scrolling Image Name list in the Image Input screen, or all images in the list for each selected parent record. See “[Exporting Groups of Images](#)” earlier in this chapter.
- **The Create Web Pages tool** exports the first image for each Species, as ordered in the scrolling list in the Species input screen, and creates a hyperlink to the image from the Species record in a Species Web page. See Chapter 33, “[Exporting Static Web Pages](#).”

If you want to change the order of the Images in the scrolling list for a parent record, follow these steps.

1. **Display the Image tab of a Specimen, Collection, Locality, or Species record** in the Input screen, following directions in the section “[Displaying an Image in the Input Screen](#)” earlier in this chapter.
2. **Click the “Reorder Images” button** in the Image Input screen. (If there are no Image records linked to this parent record, the “Reorder Images” button is disabled.)



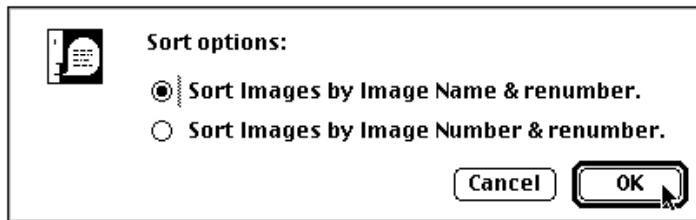
The Image Order Editor appears (below), displaying the Image Names for the parent record. The Image Names are ordered by Image Number, which is displayed in the left column. The first Image Name is displayed at the bottom of the window, with its Image Number highlighted in the Image Number editing area.



3. To sort Images alphabetically by Image Name:

- Click the “Sort” button in the Image Order Editor window.

A Sort option window appears.

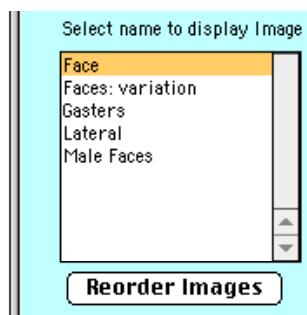
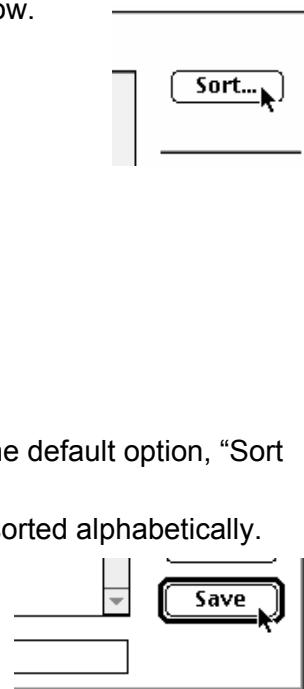


- Click the “OK” button in the option window to accept the default option, “Sort Images by Image Name and renumber.”

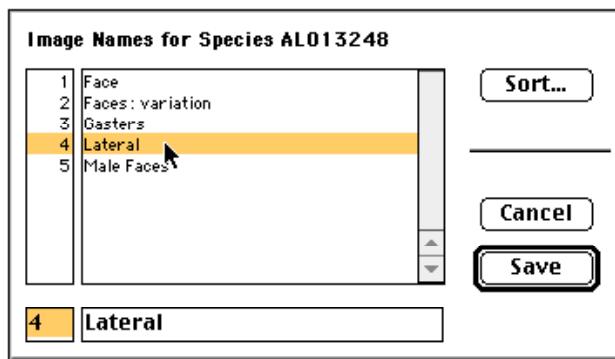
The Image Names reappear in the Image Order Editor, sorted alphabetically.

- Click the “Save” button in the Image Order Editor.

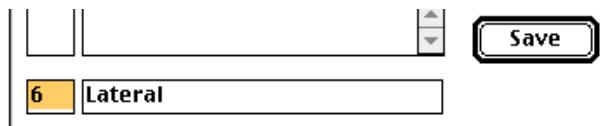
The list reappears in alphabetical order in the Species input screen.



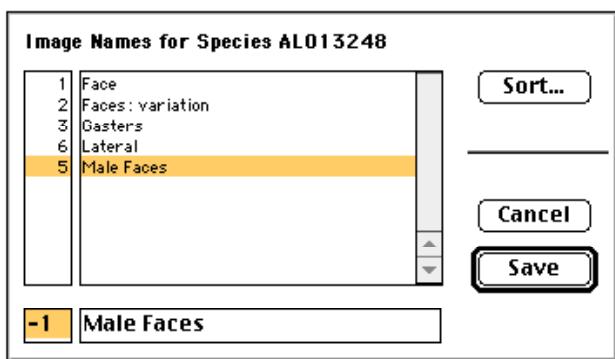
4. To reorder Images as you wish (non-alphabetically), you edit the Image Numbers in the Image Order Editor to reflect the order you wish. You can skip numbers and use decimal or negative numbers if you wish.
- Click the Image Name of the Image you want to reorder. “Lateral” is clicked, below. The Image Name you clicked appears at the bottom of the editor.



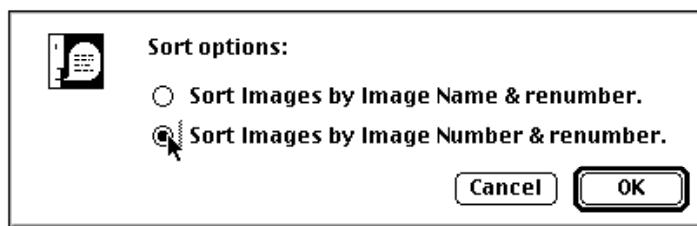
- Change the Image Number (in the Image Number editing area at the lower left) to place the Image in the desired position among the remaining Images in the list. In this example, the Image Number for “Lateral” has been changed to 6, so this Image will sort numerically at the end of the list.



- To move an Image to the beginning of the list, enter a fractional or negative Image number. The Image called “Male Faces” will be moved to the beginning of the list in the example below.



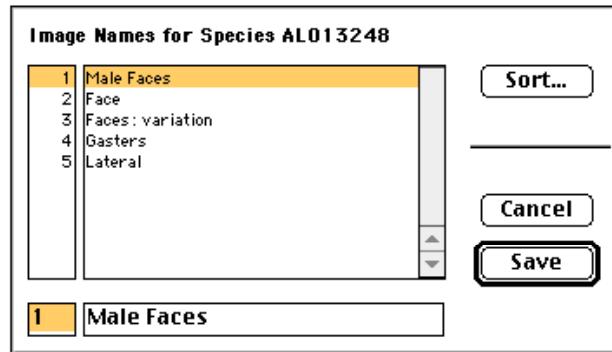
- d. Click the “Sort” button in the Image Order Editor window. A Sort option window appears.



- e. Choose the second option, “Sort Images by Image Number and renumber.”
f. Click the “OK” button in the option window.

The Image Names reappear in the Image Order Editor, sorted numerically according to the edited Image Numbers, but renumbered sequentially by integers.

- g. Click the “Save” button in the Image Order Editor. The list reappears in the new order in the Species input screen.

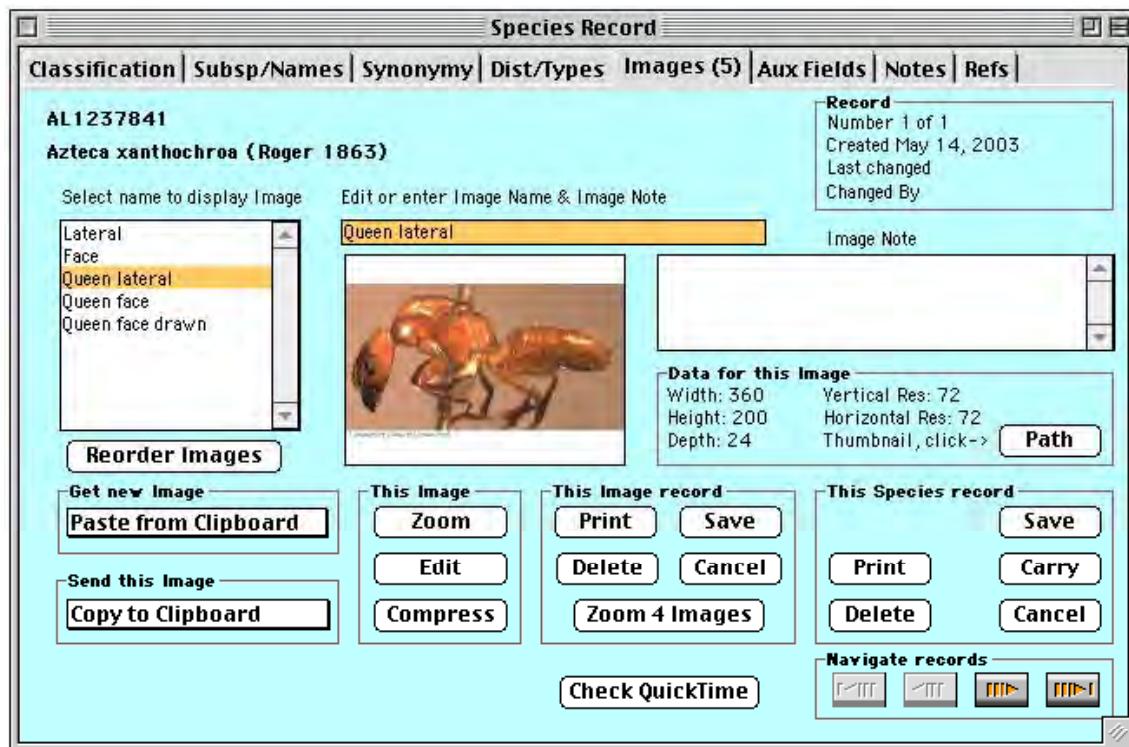


NOTES:

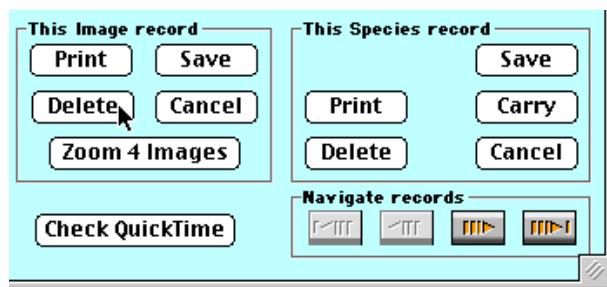
- a. When you click the “Save” button in the Image Order Editor, Biota automatically reassigned Image Numbers in sequential, integer order, based on the Image Numbers you have assigned. So if you want, you can skip the last steps, above, and just click the “Save” button.
- b. If you delete an Image record, Biota automatically reassigned Image Numbers in sequential, integer order to the remaining Image records linked to the parent record, without changing their order, to account for the deleted Image record.
-

Deleting an Image Record From the Input Screen

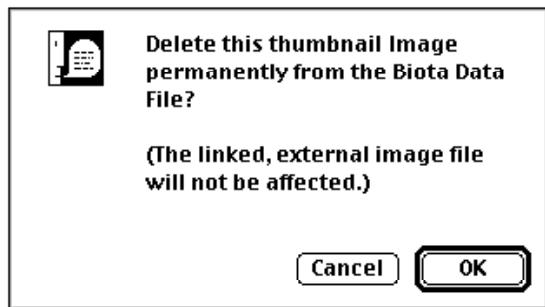
1. **Display an Image** in the Image Input screen. (See “[Displaying an Image in the Input Screen](#)” earlier in this chapter.) An Image linked to a Species record is illustrated here.



2. Click the “Delete” button in the panel labeled “This Image record.” Do not click the “Delete” button for the parent record (in the panel labeled “This Species record,” in the example below).



- If the Image record is a linked thumbnail, only the thumbnail is deleted. The external image file is not touched. Biota posts the following confirmation message.



- If the Image record is a full image in the Biota Data File, the image itself is permanently deleted. Biota posts this message.



Editing or Compressing Images Displayed in the Image Input screen

Once an Image is displayed in the Image tab of the parent (Species, Specimen, Collection, or Locality) Input screen, you can edit it in the Image Console using a variety of image editing tools, and/or compress the image.

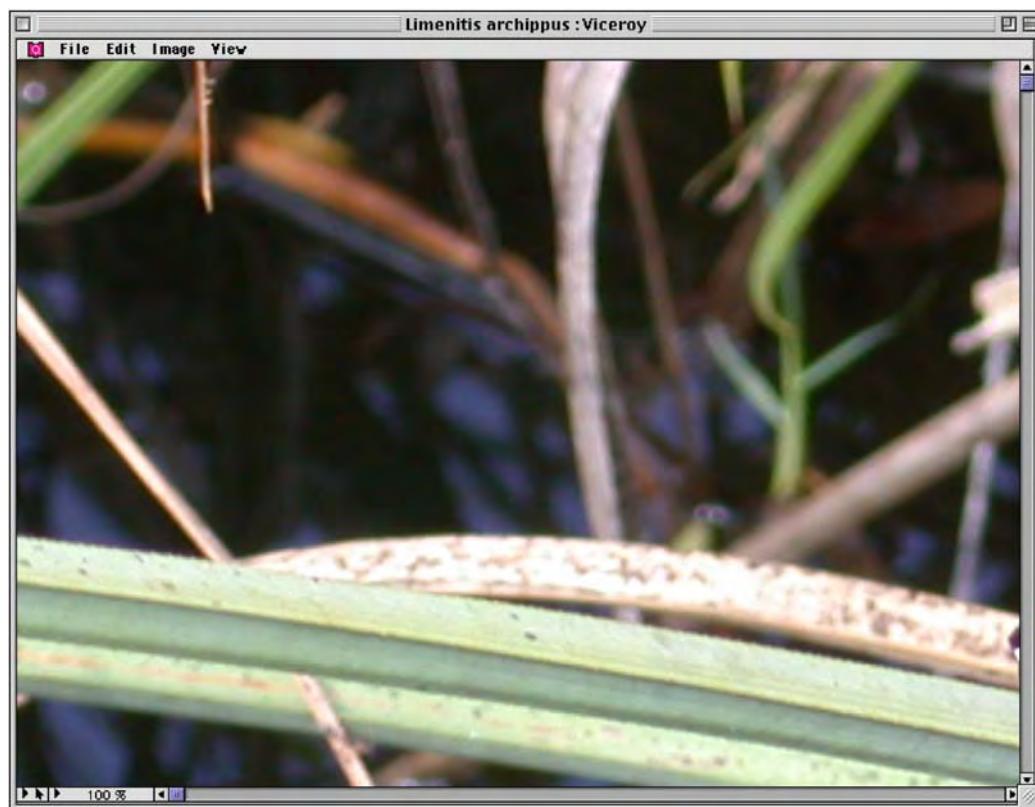
Editing an Image

- Display a Specimen, Collection, Locality, or Species record in the Image Input screen (see “[Displaying an Image in the Input Screen](#)” earlier in this chapter.) or import a new Image (see “[Creating a New Image Record in Biota](#)” earlier in this chapter).**
- Click the “Edit” button in the panel labeled “This Image.”**

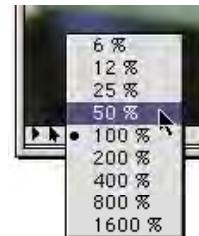
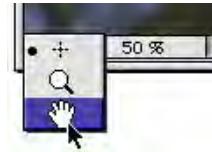
The Image is displayed in the Image Editing Console, at its full, original resolution, regardless of whether it is smaller or larger than the display area of the Console.

- Moving or changing the displayed size of the Image in the display window.**

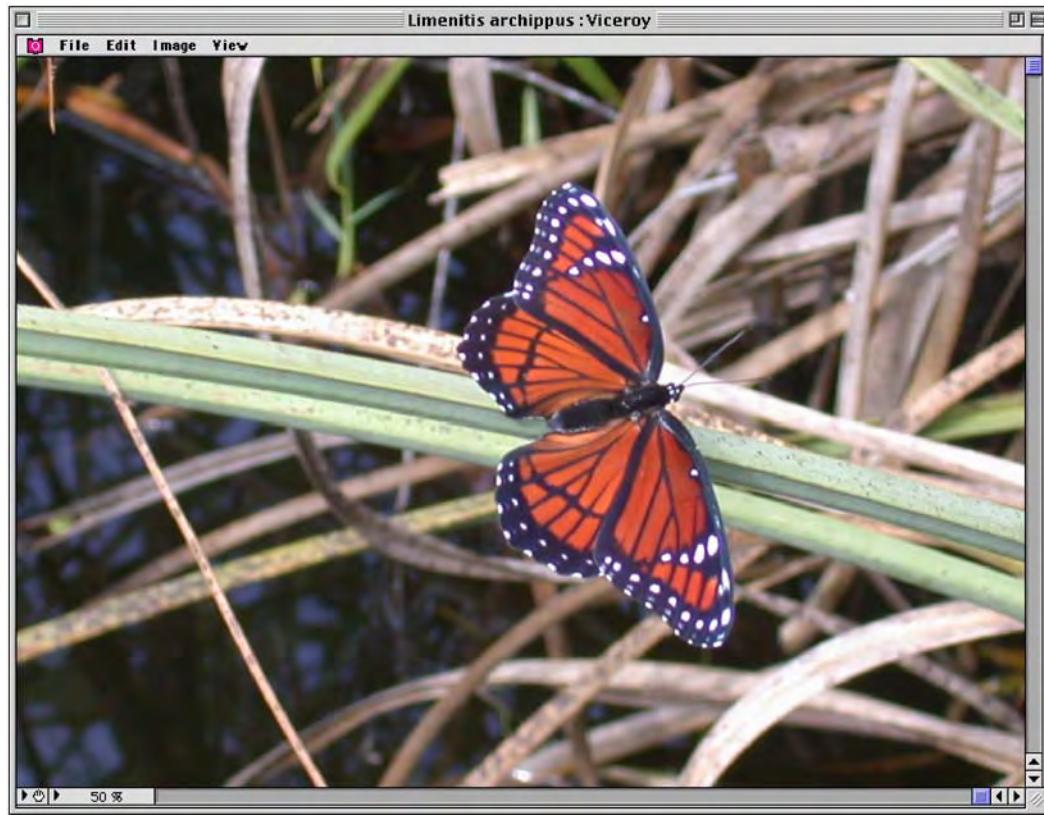
For example, the Image shown below (the viceroy butterfly shown in the Image Input screen, above) is much larger than the display area, which by default shows the upper left corner of the original Image. The butterfly is not visible.



- To view a different part of the image (e.g., to center the view on the butterfly, in the example above), you can:
 - ◊ Use the scroll bars in the display area of the Console.
 - ◊ Select the “Hand” tool from the tool popup at the lower left corner of the Console, then use it to move the image.
- To change the displayed size of the image, you can:
 - ◊ Select the Zoom Out (or Zoom In) item from the View menu in the Image Editing Console.



- ◊ Zoom out (or in), using the zoom selection popup at the lower left corner of the Console (illustrated on the right).
- ◊ Select the “Zoom” (magnifying glass icon) tool from the tool popup at the lower left corner of the Console, then depress the SHIFT key and Click to zoom out (Click to zoom in).

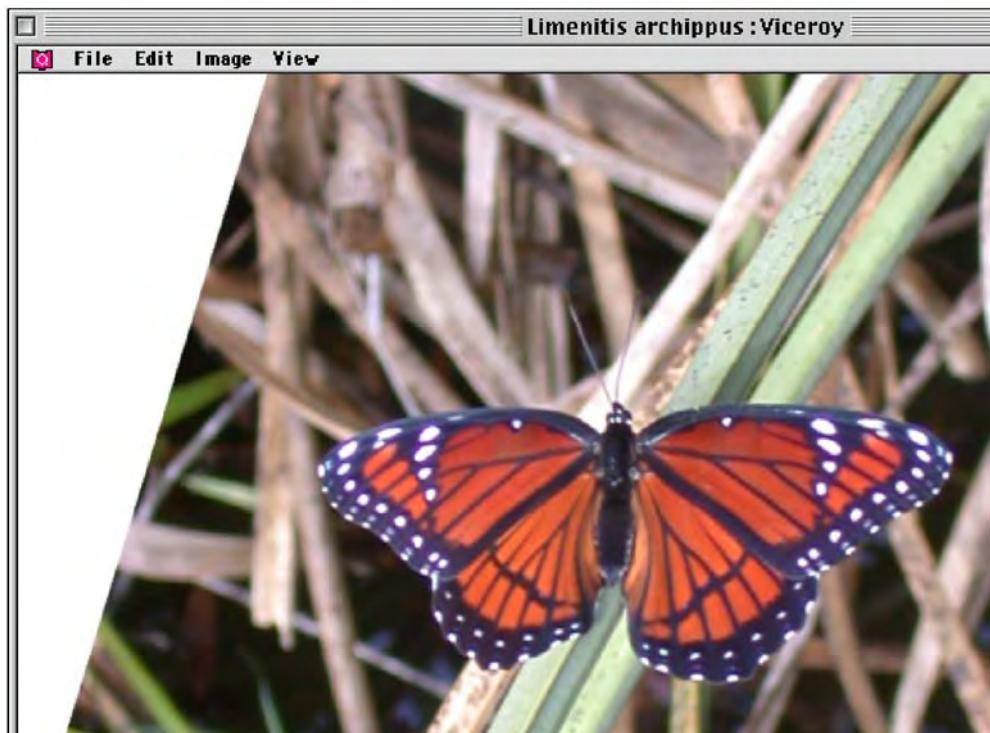


The image of the butterfly, above, is now displayed at 50% of its actual size (the original image file is unchanged), and has been centered using the Hand tool.

4. To Flip or Rotate an Image in the display window, select “Flip” or “Rotate” from the Edit menu in the Image Editing Console.



Below, the “Image...Rotate...Arbitrary” tool has been used to rotate the butterfly image.



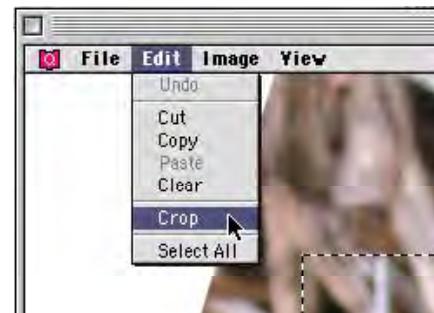
5. To Crop an Image in the display window:
 - a. Select the Crop (“cross-hairs”) tool from the tool popup at the lower left corner of the Console.
 - b. Using the cursor, select the area you wish to keep after cropping the image.

The butterfly is being selected below.

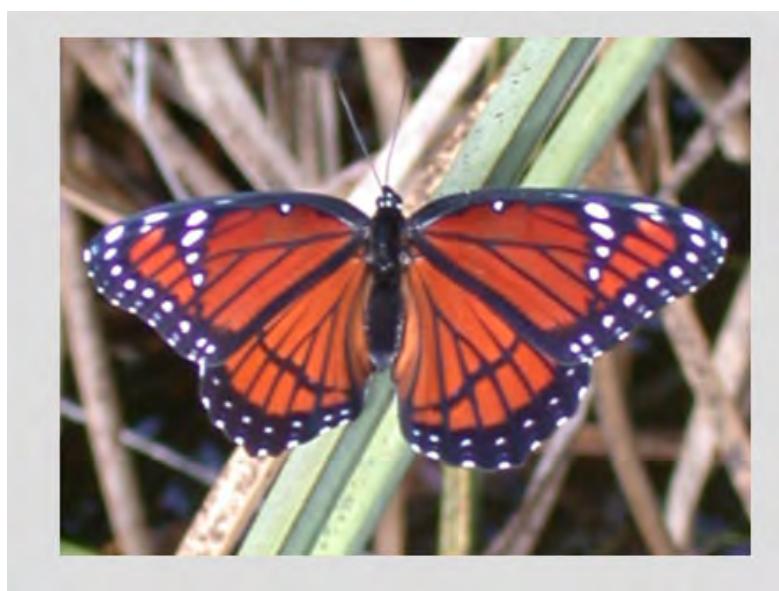




- c. Select “Crop” from the Edit menu in the Image Editing Console window.

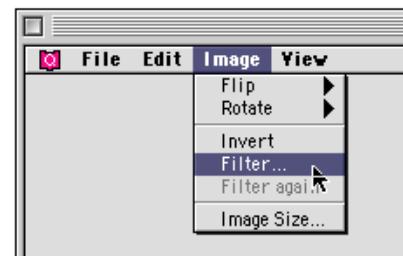


The cropped image remains.

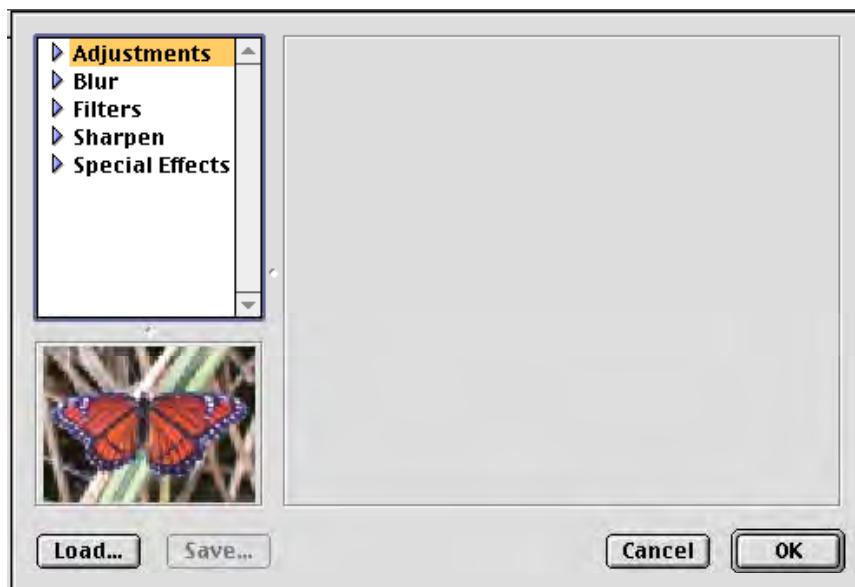


6. To use QuickTime's Adobe Photoshop-style tools to modify an Image:

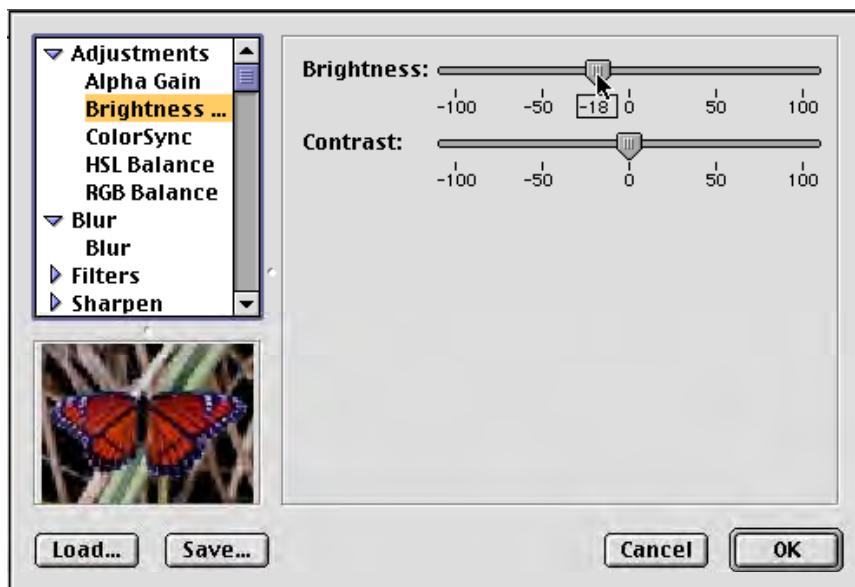
- a. Select “Filter” from the Image menu in the Image Editing Console.



The Filter setup window appears, including a preview image for effects.



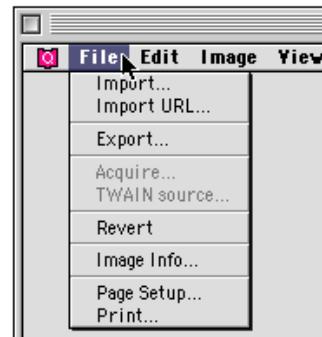
- b. Expand a category, select a tool, and adjust the settings, if appropriate. In the example below, Brightness has been reduced to intensify the colors in the butterfly image.



NOTE: Instructions for using the many QuickTime effects tools in the Filters window are beyond the scope of this Manual.

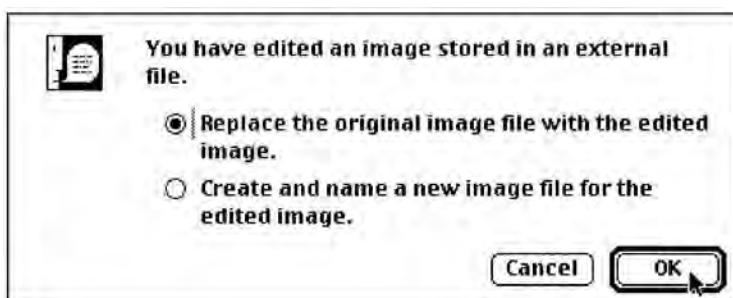
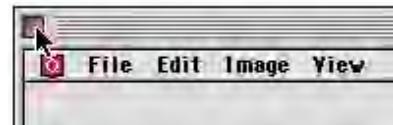
7. **The File menu** includes tools for importing, exporting, printing, reverting to the original image, or displaying format information about the image.

NOTE: The Import and Export tools in the Image Console File menu are identical to those in Biota's Image Input screen. See "[Creating a New Image Record in Biota](#)" and "[Exporting Individual Images](#)" earlier in this chapter. You can use the Image Editing Console to carry out virtually all image processing, if you wish. (The TWAIN tools are not enabled in the Image Console.)



8. **To save an edited Image**, click the close box in the Image Console window. (The Mac OS close box is shown here.)

A save option window appears.



- **Either:** Replace the original Image file with the edited Image.
- **Or:** Create and name a new Image file for the edited Image. If you choose this option, Biota presents the Save dialogue screen so you can name and place the Image file. The save Image window appears. Follow the instructions for saving and naming the Image file in the section "[Saving and Naming a New Image](#)" earlier in this chapter.

NOTE: Be sure to place the edited Image in a folder positioned next to the active Biota Data File. If you try to place it outside the folder that contains the Data File, Biota warns you, and you may then place the edited Image correctly.

Compressing an Image

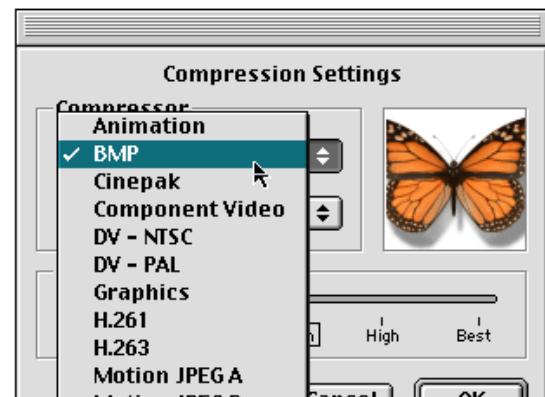
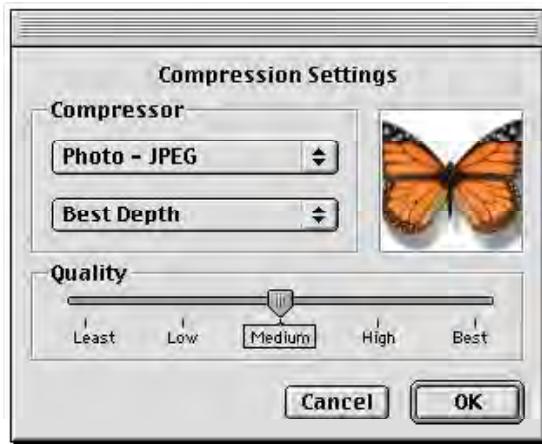
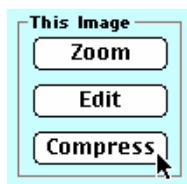
For general information on Image compression, see the section “[Image Compression](#)” earlier in this chapter.

By default, when Biota saves a new or edited Image, it compresses the Image using the “Photo-JPEG” compression codec (with “normal” resolution), whether the Image is stored in the Biota Data File or placed in external files. Images are transparently decompressed before they are displayed on the screen. JPEG compression is both efficient and ubiquitous in the world of computer imaging. But in some circumstances (e.g., no compression for print publication of TIFF’s) you may wish to use other compression codecs or image formats.

NOTE: Photo-JPEG compression is not the same as the JPEG *image format* (also the default in Biota). Theoretically, an image in any format (e.g., TIFF, Photoshop, BMP, as well as JPEG) can be compressed using any codec (Photo-jpeg and others). In practice, certain combinations of codec and image file format are best used together: Photo-JPEG compression with JPEG file format, BNP compression with BMP format.

1. **Display a Specimen, Collection, Locality, or Species record in the Image Input screen (see “[Displaying an Image in the Input Screen](#)” earlier in this chapter.) or import a new Image (see “[Creating a New Image Record in Biota](#)” earlier in this chapter).**
2. **Click the “Compress” button in the panel labeled “This Image.”**

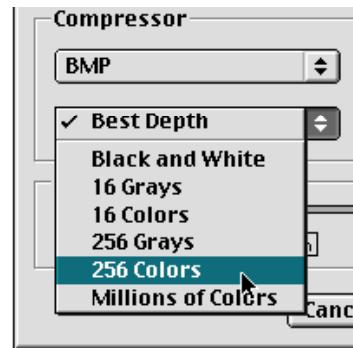
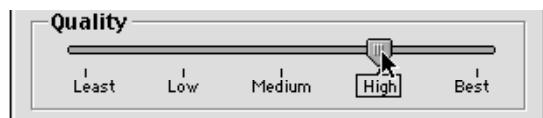
The compression options screen appears.



3. **Choose a compression codec from the upper popup list in the Compressor panel. (Photo-JPEG is the default. Note that not all codecs listed by QuickTime are useful for still images.)**

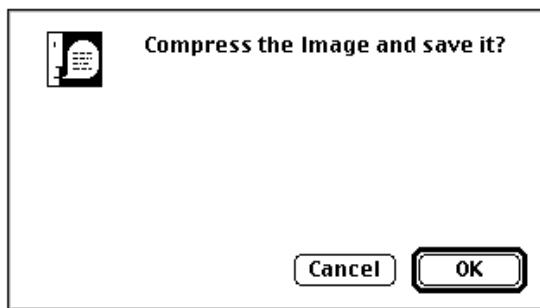


4. Choose a color depth from the lower popup list in the Compressor panel. (“Best Depth,” is the default.) Different codecs offer different option lists for color depth.
5. Choose a Quality setting using the slider in the lower panel of the option screen.



6. Click the “OK” button in the option screen to save the settings, or the “Cancel” button to cancel them.

A confirmation screen appears, offering you one more chance to change your mind.



7. Click the “OK” button in the confirmation screen to compress the Image.
 - If the full Image you intend to compress is stored in the Biota Data File, the Image is compressed and saved to the Data File.
 - If the full Image you intend to compress is stored in an external file, Biota presents the standard save Image dialog. Follow the instructions for saving and naming the Image file in the section “[Saving and Naming a New Image](#)” earlier in this chapter.

NOTE: If the original Image is in an external file, you can either replace that file with the compressed one, by assigning the compressed file the same name and placing it in the same folder as the original, or you can save the compressed image as a new file. In either case, a new thumbnail is created based on the compressed image and a new link is established to the external file.

Displaying Thumbnail Images in Record Listing Screens

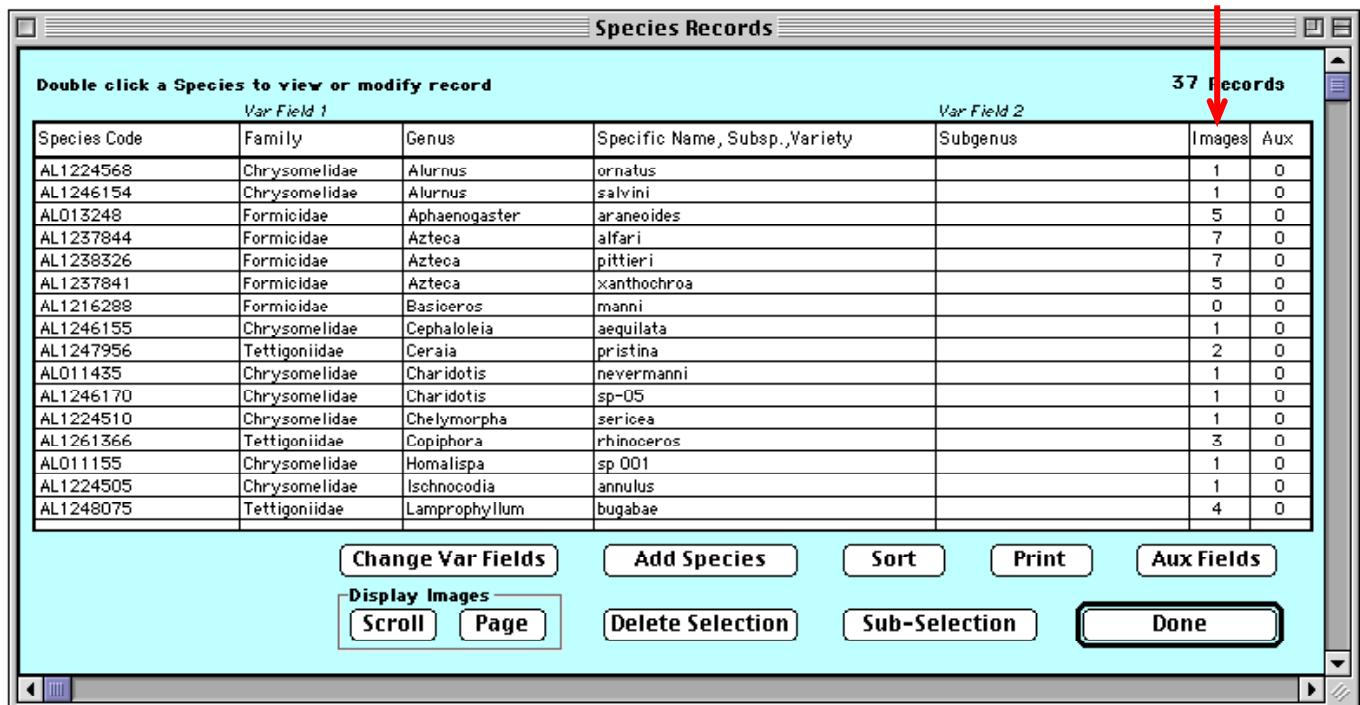
If you want to compare images for several Species, Specimen, Collection, or Locality records at once, you have three options:

- You can launch separate processes and open the images simultaneously in separate windows, using tools in the Image Input screen as described in the section “[Displaying, Zooming, Reordering, or Deleting Images in the Image Input screen](#)” earlier in this chapter.
- You can use the Scroll option for displaying images in a Record Listing screen for Species, Specimen, Collection, or Locality records.
- You can use the Page option for displaying images in a Record Listing screen.

Using the Scroll Images Record Listing Screen

1. Find the Species, Specimen, Collection, or Locality records for which you want to display and compare images. To find the records, you can use any of the tools described in Chapter 12, “[Finding and Updating Records](#).”

The standard Species Record Listing screen is illustrated below as an example. Notice that the Images column in the Species Record Listing screen shows the number of linked Image records for each Species.



A screenshot of a computer window titled "Species Records". The window contains a table of data with the following columns: Species Code, Family, Genus, Specific Name, Subsp., Variety, Subgenus, Images, and Aux. A red arrow points from the text "37 Records" in the top right corner down to the "Images" column header. The table data is as follows:

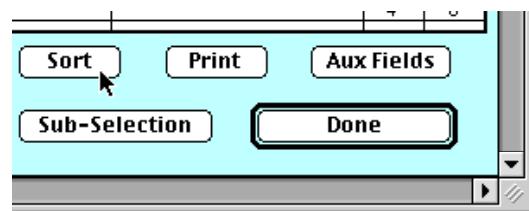
Species Code	Family	Genus	Specific Name, Subsp., Variety	Subgenus	Images	Aux
AL1224568	Chrysomelidae	Alurnus	ornatus		1	0
AL1246154	Chrysomelidae	Alurnus	salvini		1	0
AL013248	Formicidae	Aphaenogaster	araneoides		5	0
AL1237844	Formicidae	Azteca	alfari		7	0
AL1238326	Formicidae	Azteca	pittieri		7	0
AL1237841	Formicidae	Azteca	xanthochroa		5	0
AL1216288	Formicidae	Basioeros	manni		0	0
AL1246155	Chrysomelidae	Cephaloleia	aequilata		1	0
AL1247956	Tettigoniidae	Ceraia	pristina		2	0
AL011435	Chrysomelidae	Charidotis	nevermanni		1	0
AL1246170	Chrysomelidae	Charidotis	sp-05		1	0
AL1224510	Chrysomelidae	Chelymorpha	sericea		1	0
AL1261366	Tettigoniidae	Copiphora	rhinoceros		3	0
AL011155	Chrysomelidae	Homalispia	sp 001		1	0
AL1224505	Chrysomelidae	Ischnocodia	annulus		1	0
AL1248075	Tettigoniidae	Lamprophyllum	bugabae		4	0

At the bottom of the window are several buttons: Change Var Fields, Add Species, Sort, Print, Aux Fields, Display Images (with sub-options Scroll and Page), Delete Selection, Sub-Selection, and Done.

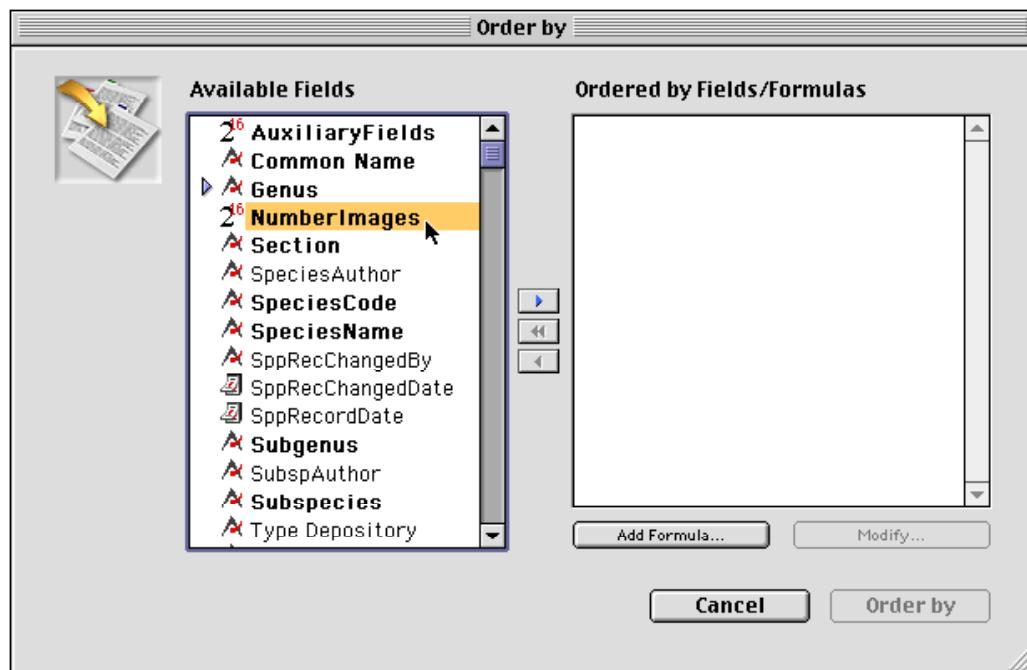
2. If you wish, sort the parent table (Species, Specimen, Collection, or Locality) records by decreasing the number of linked images. (Of course, you can sort by other criteria instead or in addition to number of images.)

To sort the Species records by number of images, follow these steps.

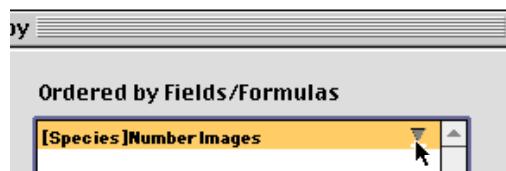
- Click the “Sort” button at the bottom of the parent table Record Listing screen.



The “Order by” window appears.



- Click the “Number Images” field name in the “Available Fields” panel on the left.
- Click the “add field” button (blue horizontal triangle) in the middle of the Order By window to add “Number Images” to the sort criteria panel on the right (labeled “Ordered by Fields/Formulas”).
- Click the sort order indicator (triangle) at the upper right to point it downwards, for descending order.



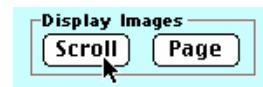
- e. Click the “Order by” button at the bottom of the Sort Species window (above).



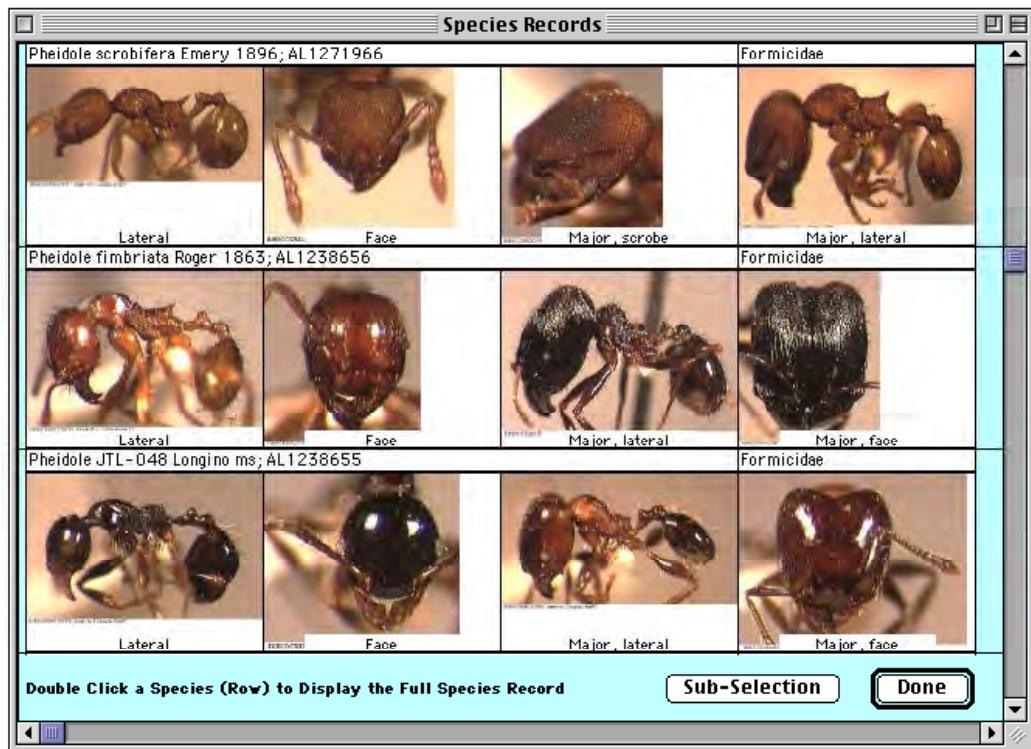
37 Records	
Images	Aux
7	0
7	0
7	0
6	0
6	0
6	0
5	0
5	0

The parent table records reappear, sorted by *decreasing* number of linked images.

3. Click the “Scroll” button in the “Display Images” button at the bottom of the Record Listing screen.



The first four Image records for each record in the current parent table selection (Species, in the example below) appear as a row of thumbnail images, one parent record per row.



- For each parent record, identifying information appropriate to the parent table appears in a text bar above the horizontal group of images for that record. For the Species table illustrated above, for example, Genus, specific name (Species Name), Species Author, Species Code, and Family appear in the text band.

- **The Image Name** for each Image appears in a small inset at the base of each image.
- **The order of the images, within rows**, follows the order you have set for the Image records in the parent table input screen. See “[Changing the Order of Linked Image Records in the Input Screen](#)” earlier in this chapter.
- **To display a parent record** in the parent table Input screen from the thumbnail Record Listing display, double-click the row of images for the parent record. You can then go to the Images tab to work with the images for that record.
- **To view Images for other parent records**, use the vertical scroll bars, just as you would for a text Record Listing screen.
- **To create a Sub-Selection of parent records (thumbnail image rows)**, select the rows you want to keep in the Sub-Selection, then click the “Sub-Selection” button at the bottom of the screen.
- **To return to the standard (text) Record Listing screen**, click the “Done” button in the thumbnail display.

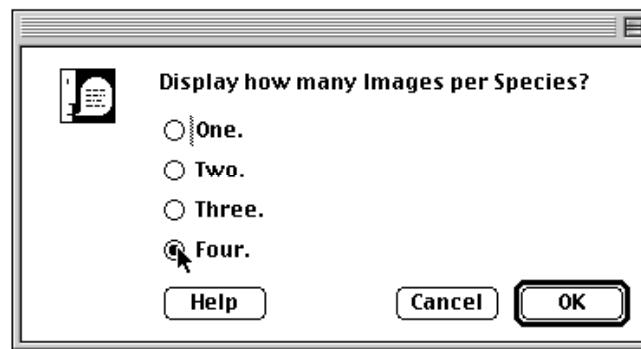


Using the Page Images Record Listing Screen

1. **Find the Species, Specimen, Collection, or Locality records** for which you want to display and compare images. To find the records, you can use any of the tools described in Chapter 12, “[Finding and Updating Records](#).”
2. **If you wish, sort the parent table (Species, Specimen, Collection, or Locality) records by decreasing the number of linked images.** For instructions, see [Step 2](#) in the section “[Using the Scroll Images Record Listing Screen](#)” earlier in this chapter. (Of course, you can sort by other criteria instead or in addition to the number of images.)
3. **Click the “Page” button** in the “Display Images” panel at the bottom of the Record Listing screen.



An option screen appears for setting the number of images per parent record to be displayed.



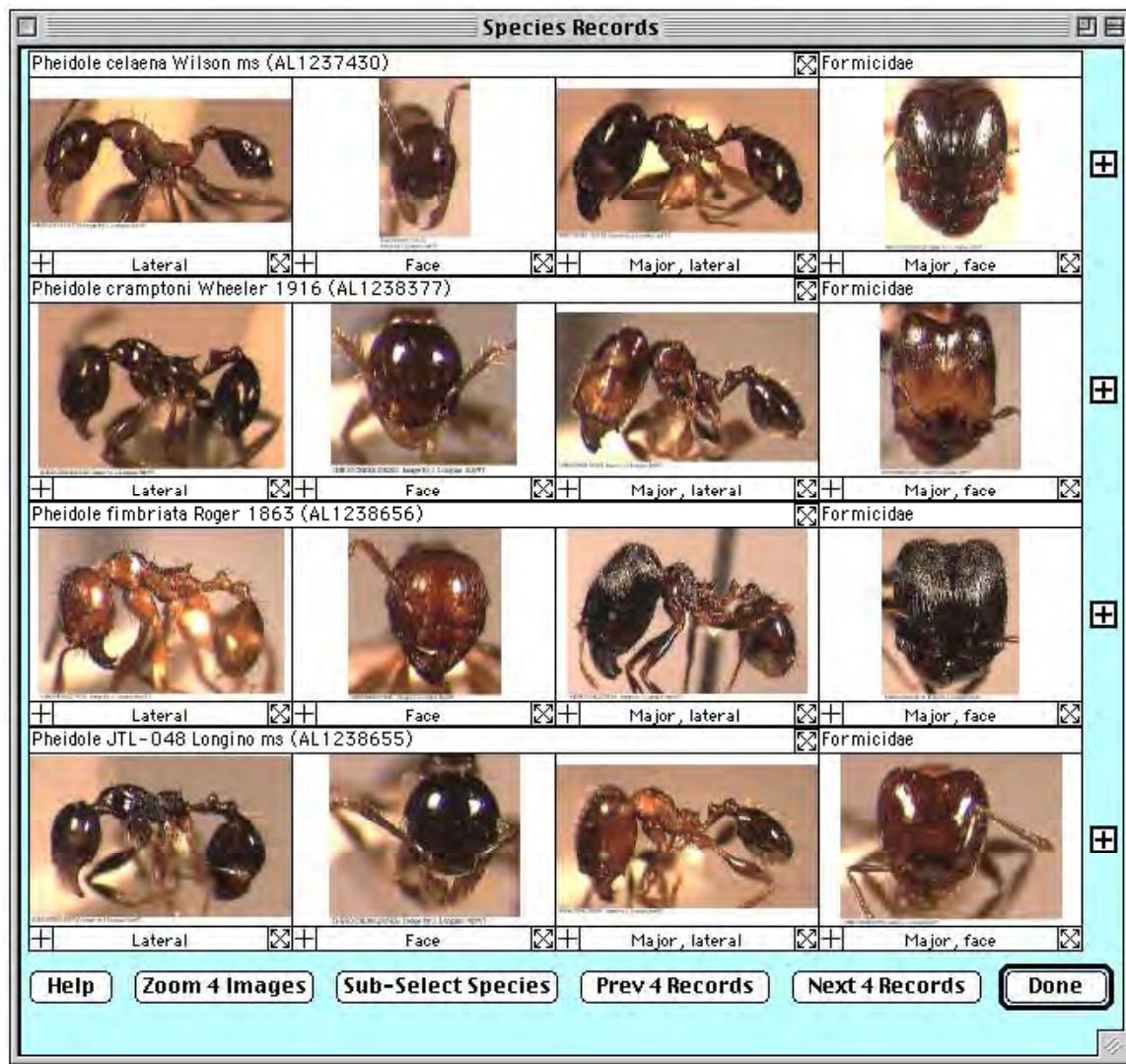
4. **Select the number of images per parent record** that you want to display and click the “OK” button.

On slower computers, a full page of images can take a few seconds to display, but a smaller number per parent record displays faster. Once you set the number, Biota remembers it until you change it or end the work session and quit Biota. Because

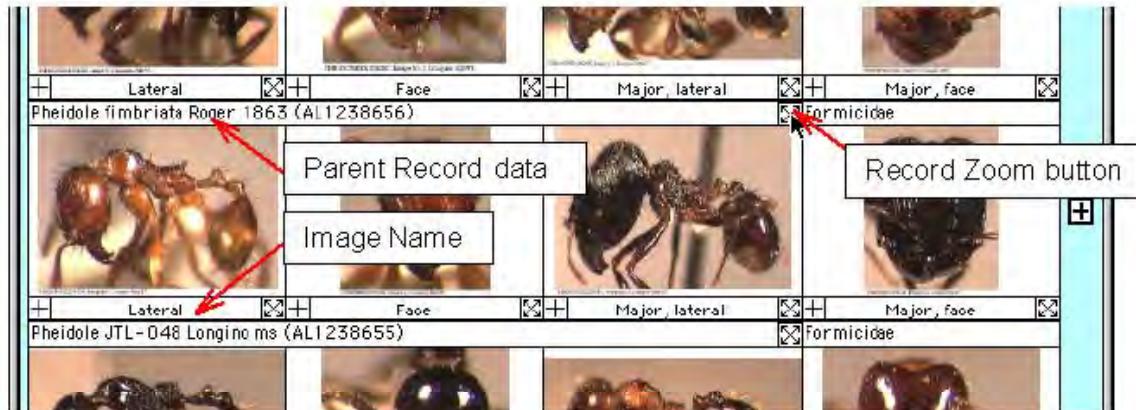
the “OK” button in this screen is a default button, you can just “key past” this screen with the ENTER key (Windows) or the RETURN key (Mac OS) once you have set it.

The first n (1, 2, 3, or 4) Image records for each record in the current parent table selection (Species, in the example below) appear as a row of thumbnail images, one parent record per row, for the first four parent records in the selection. (In other words, if you asked for four images per parent record, Biota posts 16 images.)

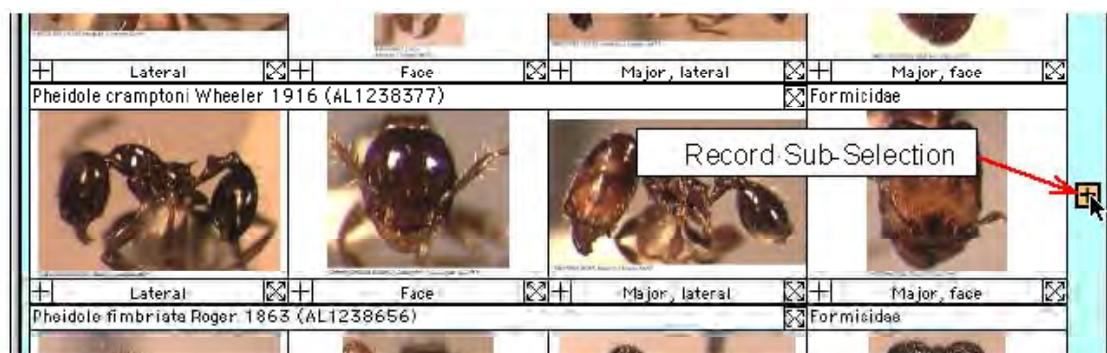
The example below is for four species in the ant genus *Pheidole*, considered a very “difficult” genus, with many very similar species. Notice that the images for each Species records are ordered identically, to easily allow visual comparison of analogous images among the species.



- For each parent record, identifying information appropriate to the parent table appears in a text bar above the horizontal group of images for that record. For the Species table illustrated above, for example, Genus, specific name (Species Name), Species Author, Species Code, and Family appear in the text band.



- **To display a parent record** in the parent table Input screen directly from the Page Image display, click the “Record Zoom” button at the right end of the main text bar for the parent record. You can then go to the Images tab to work with the images for that record.
- **The Image Name** for each Image appears in a text band at the base of each image.
- **The order of the images, within rows**, follows the order you have set for the Image records in the parent table input screen. See “[Changing the Order of Linked Image Records in the Input Screen](#)” earlier in this chapter.
- **To view Images for other parent records**, four records at time, click the “Next 4 Records” button or the “Prev 4 Records” button.
- **To create a Sub-Selection of parent records (thumbnail image rows)**, select the rows you want to keep in the Sub-Selection by clicking the “Add Record to Sub-Selection” box (the “+” boxes in the right margin of the screen, for a parent record).

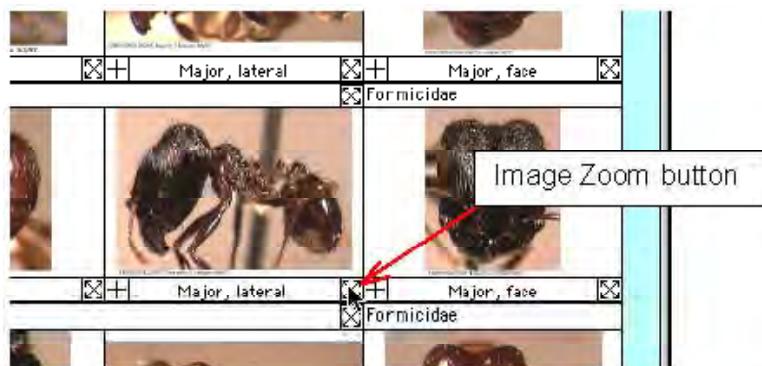


Then click the “Sub-Select [Records]” button at the bottom of the screen. (The button reads “Sub-Select Species,” in this example.)



NOTE: The Sub-Selection carries over between screens of Images. You can click as many “Add Record to Sub-Selection” boxes (the “+” boxes in the right margin of the screen) as you wish, on any number of screens within a selection of parent records, before clicking the “Sub-Select [Records]” button.

- To zoom an individual Image, click the “Image Zoom” button at the lower right corner of any individual thumbnail image.



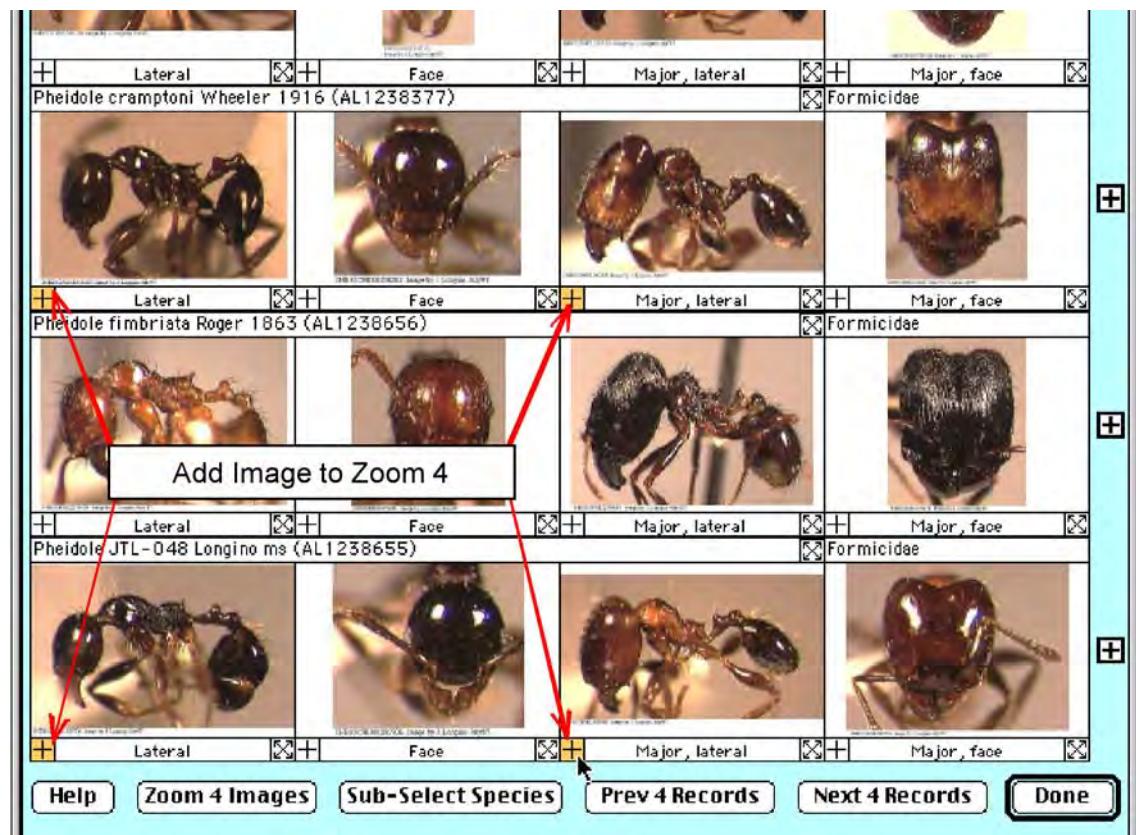
The zoomed Image (not an enlarged thumbnail) appears at full original size, unless it is larger than the zoom viewing area. See “[Zooming Images in the Input Screen](#)” earlier in this chapter for notes and instructions on further use of this screen.



- To display any four images, from any combination of parent records in the Zoom 4 Screen, take these steps:

- a. Click the “Add Image to Zoom 4” box (the “+” box at the left lower corner of an individual Image pane) for up to four Images, on any record on any page of Images.

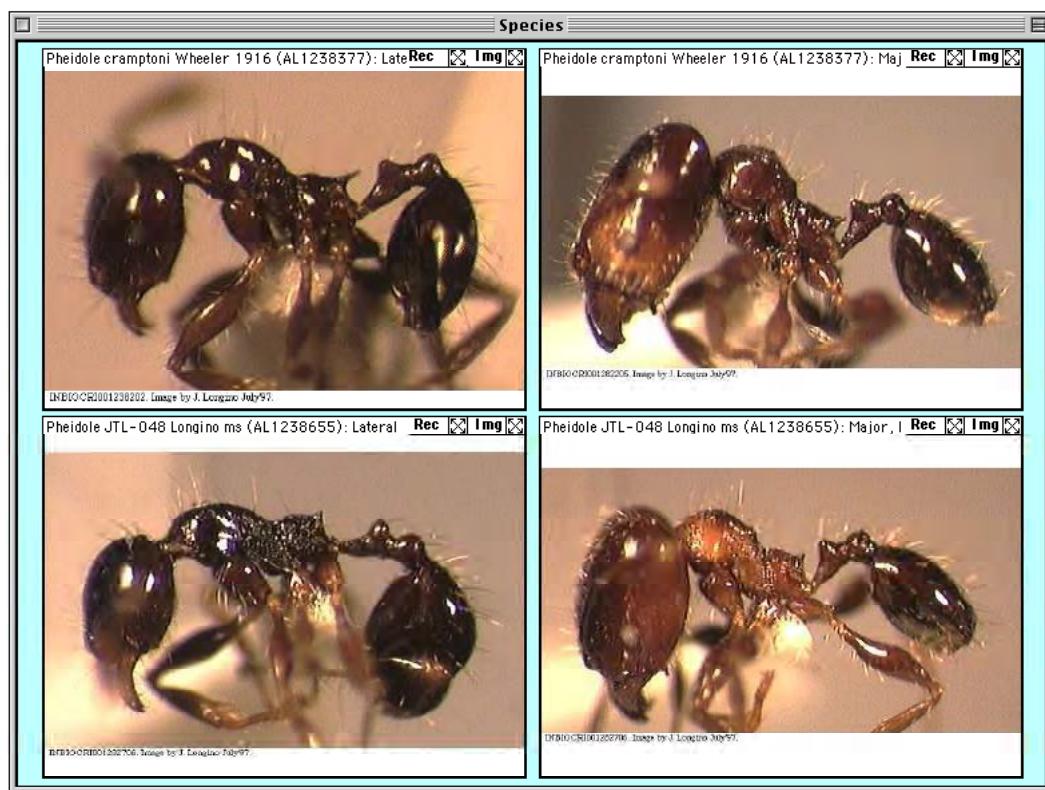
To simplify the illustration, four images from a single page have been selected (the selected boxes are in yellow), below.



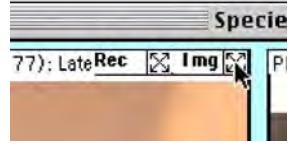
- b. To display the selected Images in the Zoom 4 Screen, click the “Zoom 4 Images” button at the bottom of the Page Image window.

The selected images appear in a new window in the Zoom 4 Screen.





- c. **To further zoom a single image from the Zoom 4 Screen**, click the “Img” zoom button in the upper right corner of one of the four image panels. (See “[Zooming Images in the Input Screen](#)” earlier in this chapter for notes and instructions on further use of this screen.)
- d. **To display the parent record for an Image in the Zoom 4 Screen**, click the “Rec” zoom button in the upper right corner of one of the four image panels.
- **To return to the standard (text) Record Listing screen**, click the “Done” button in the thumbnail display.



Deleting Images for a Species, Specimen, Collection, or Locality Record Set

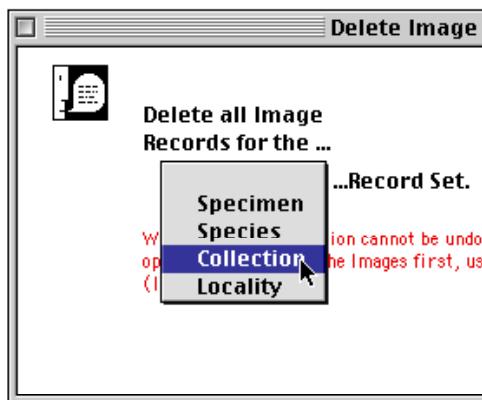
Occasionally, you might need to delete all the Image records linked to particular group of parent records in the Species, Specimen, Collection, or Locality table.

NOTES:

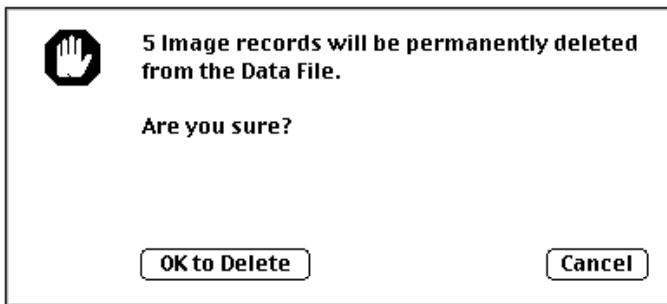
- a. This operation deletes records in Biota's ImageArchive table only. It does not affect parent (Species, Specimen, Collection, or Locality) records, nor any external image files in disk, even if they are linked to Biota.
 - b. This operation cannot be undone, so if you have any doubts, make a fresh backup of your Biota Data File first.
1. **Find the Species, Specimen, Collection, or Locality (parent) records** for which you want to delete all linked Image records. To find the parent records, you can use any of the tools described in Chapter 12, "[Finding and Updating Records](#)."
 2. **From the Special menu, choose "Delete Images by Record Set."** A warning and table selection screen appears.



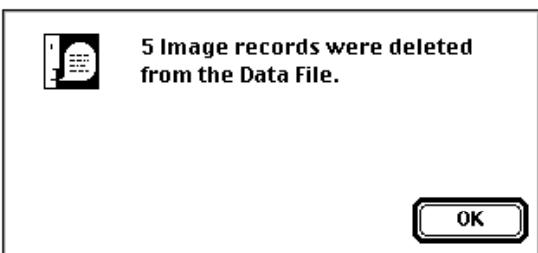
3. **From the table popup, select the parent table** for which you want to delete linked Image records.



4. Click the “OK” button. Yet another warning and confirmation screen appears.



5. Click the “OK to Delete” button. Biota confirms the deletions.



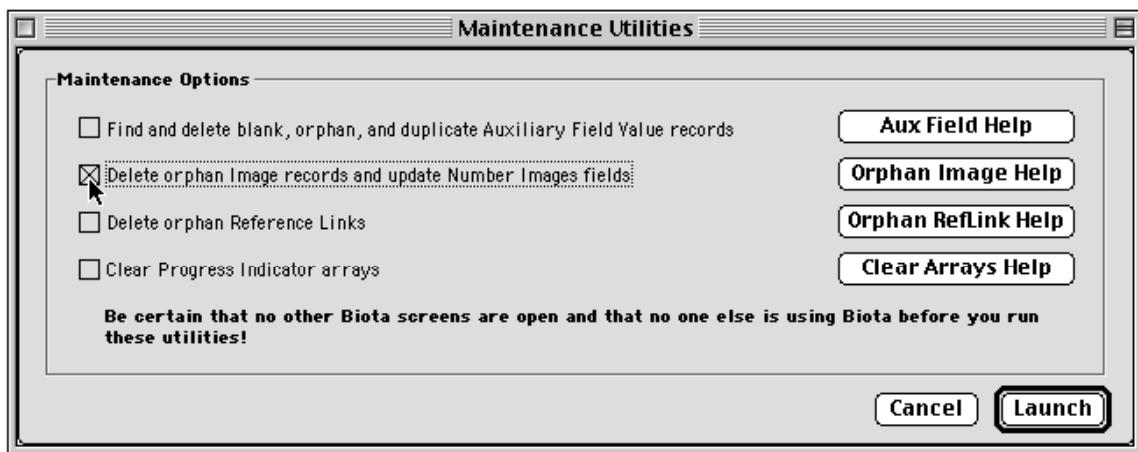
Maintaining and Repairing Image Links

Under normal operations, Biota correctly maintains links between parent records in the Specimen, Species, Collection, and Locality tables and Image records (records in the Image Archive table).

Power failures, system crashes, and incorrectly imported data, however, can produce orphan Image records, or the NumberImages field of a parent record (a Specimen, Species, Collection, or Locality record) may indicate the wrong number of linked Images.

You can correct these problems, without in any way affecting legitimate records, by running the Image Maintenance Utility. Whereas neither of these problems is very serious, it is recommended that you run this utility from time to time if you work with Images in Biota, especially if you suspect problems.

1. **To run the Image Maintenance Utility**, choose “Maintenance Utilities” from the Special menu. The option screen appears.



2. Activate the option “Delete orphan Image records and update Number Image fields.”
3. Click the “Launch” button. The utility presents a series of reports on its activities.

Chapter 20

References

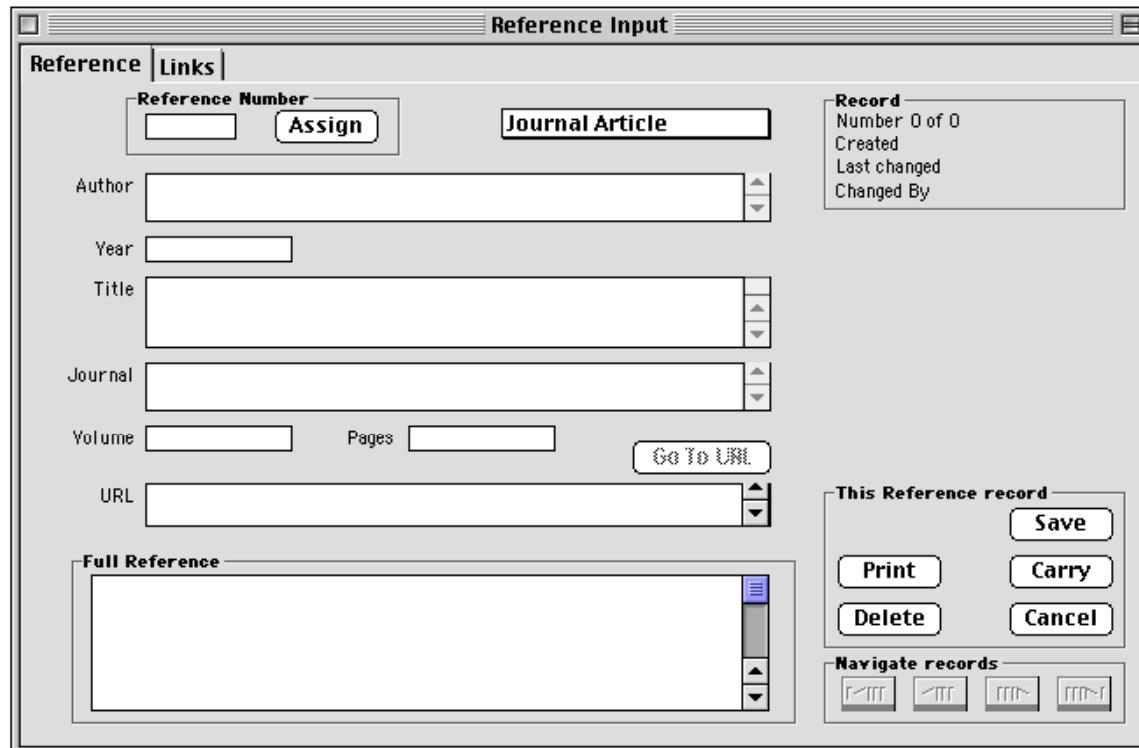
This chapter explains how to use Biota's literature reference tools. Reference records are stored in their own table (called References). Each Reference record can be linked to any number of Species, Specimen, Collection, or Locality records. Likewise, each Species, Specimen, Collection, or Locality record can be linked to any number of Reference records. (This is called a "many-to-many" relationship.)

A separate table, called ReferenceLinks, keeps track of which Reference records are linked to which Species, Specimen, Collection, or Locality records. There is one record in the ReferenceLinks table for each link. You do not normally need to pay any attention to the ReferenceLinks table, since its records are maintained transparently by Biota. (The only reason you would ever need to deal with it would be to merge two Biota Data Files.)

Reference Input

You can create a new record in the Reference Input screen by selecting "Reference" from the Input menu, by clicking the "Add Reference" button on the Reference Record Listing screen, or by clicking the "New Ref" button on the "Refs" tab of the Species, Specimen, Collection, or Locality Input screen.

The Reference Input screen has two tabs. Once you have entered a Reference Code or accepted the default, you can move to either tab. See "[Keyboard Shortcuts for Input Screen Tabs](#)" in Chapter 7 for information on using keyboard shortcuts to move between the tabs.



Entering Reference Data: The “Reference” Tab

Biota handles four types of references: Journal Article, Book, Book Section, and Online Source.

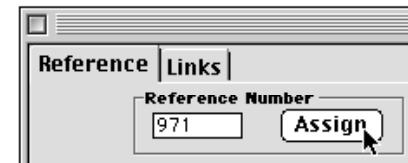
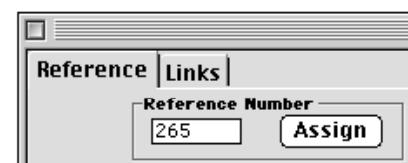
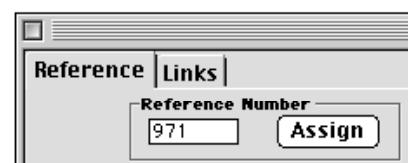
- Except for Online Source, the fields, their attributes, and their use in Biota are identical to the EndNote 4 format for the same information. (EndNote does not have an Online reference type).
- All four Reference Types have a URL Field and a “Go to URL” button that launches your default Web browser and brings up the URL. The button is activated when the URL Field is not blank.
- Three fields (Author, Title, Editor, and JournalOrEditedBook) allow very long entries. These fields are 4D Text fields, allowing entries up to 32K in length. Since Text fields cannot be indexed or sorted, matching Index fields (80 characters, maximum), maintained behind the scenes, allow rapid sorts and searches based on the first 80 characters of each entry. The full Text fields are always displayed.

To create a new Reference record, take the following steps:

1. Create a new record in the Reference Input screen by one of the following methods:
 - Select “Reference” from the Input menu.
 - Or: Click the “Add Reference” button on the Reference Record Listing screen.
 - Or: Click the “New Ref” button on the “Ref” tab of the Species, Specimen, Collection, or Locality Input screen.
2. Enter a Reference Number or accept the default Reference Number offered by Biota.

NOTE: Unlike all other Record Codes in Biota, Reference Numbers (the Record Code for the Reference table) are integer numbers, for compatibility with stand-alone reference management software, such as EndNote.

- Biota automatically generates a suggested Reference Number: the next integer after the highest numbered existing Reference Number in your Biota Data File.
- You can enter a different Reference Number manually, if you prefer, by typing it in the Reference Number entry area. (Biota ensures that whatever number you enter is unique.)
- To restore the suggested Reference Number, click the “Assign” button in the Reference Number panel.



3. Click the Reference Type popup list (which by default has “Journal Article” selected.)



4. Select a Reference Type from the popup List.



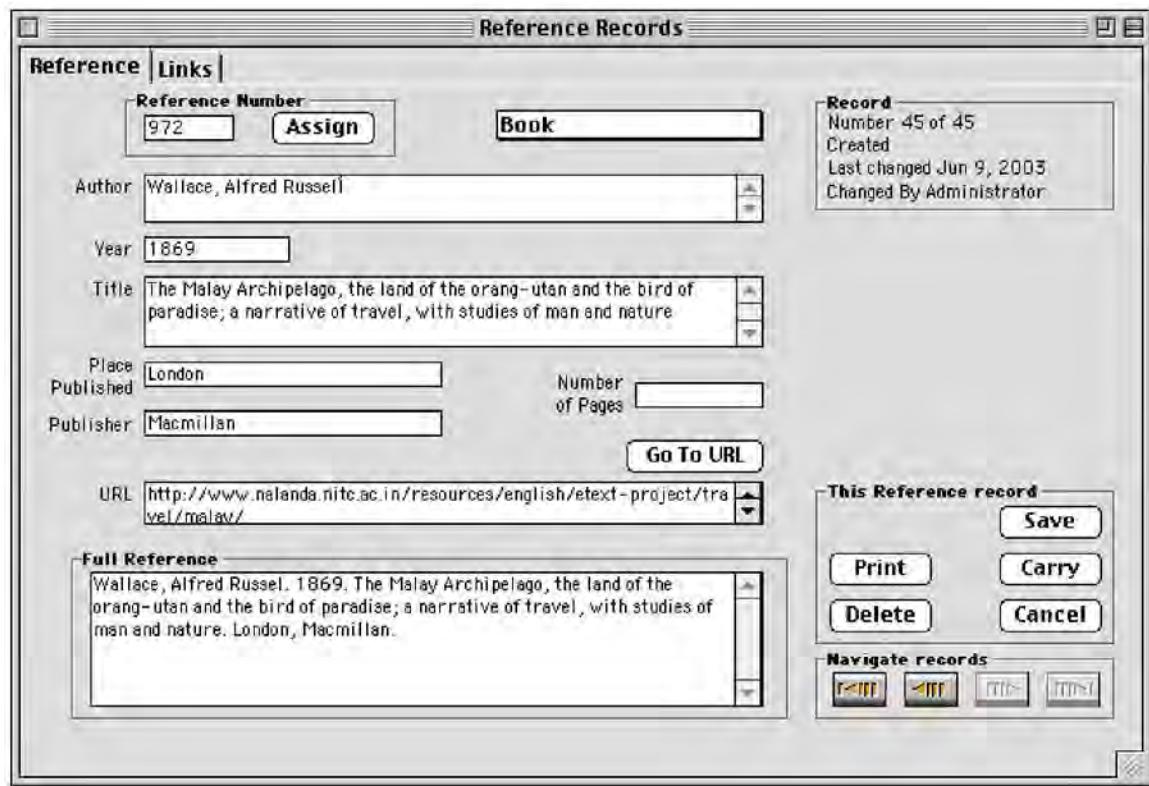
Each Reference Type presents a different version of the Reference Input screen (see the next step for illustrations).

5. Fill in the input fields on the Reference screen. As you fill in the fields, the “Full Reference” panel shows the reference in a typical (although of course not universal) format.

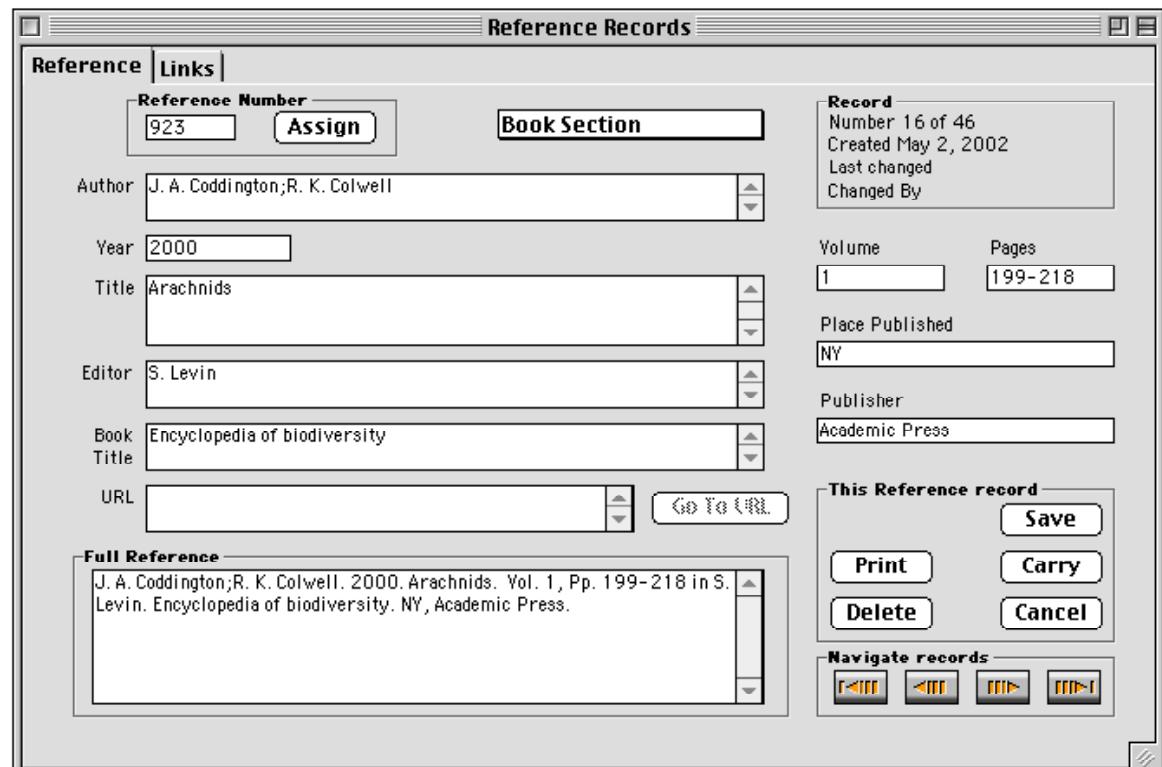
Here are examples for all four Reference Types.

- Journal Article (note URL at www.jstor.org).

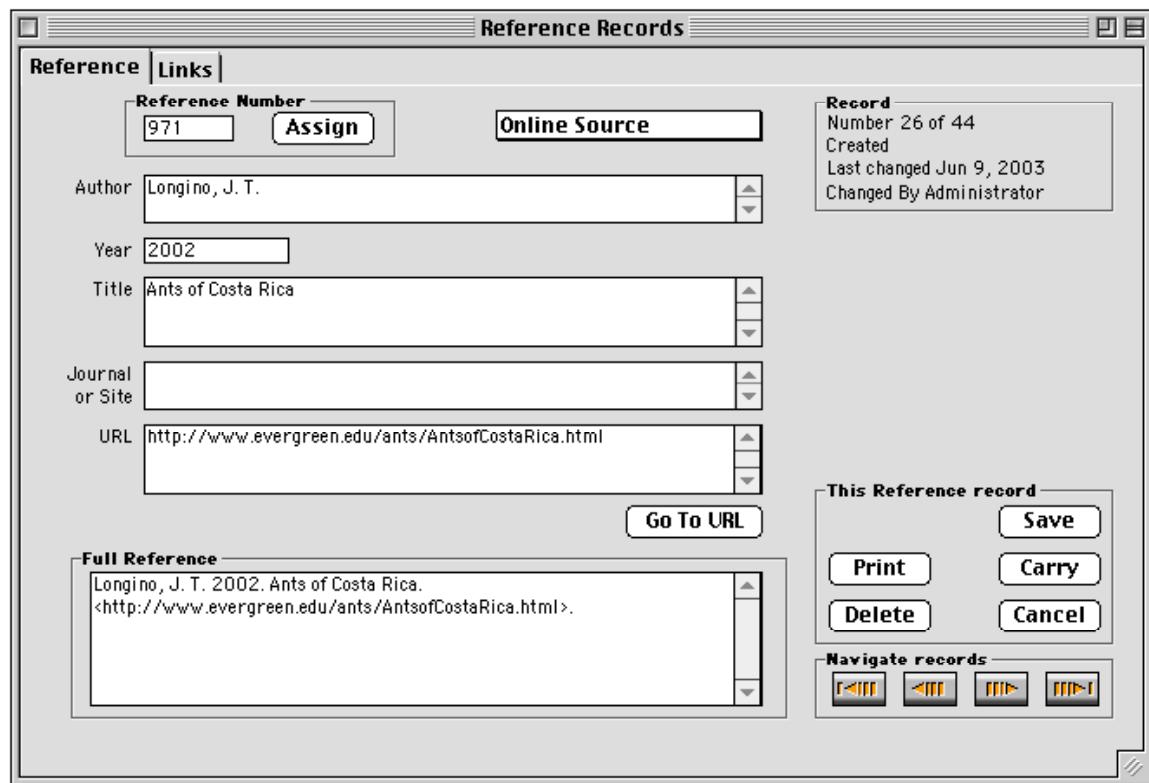
- **Book** (with a URL for the text of this classic book).



- **Book Section** (note that the “Go to URL” button is disabled when the URL field is blank).



- **Online Source.**



NOTE: You can select text from the “Full Reference” pane and copy it to the Clipboard. But changes made in this pane are not saved. To edit the Reference, you must edit the fields themselves in the upper part of the screen.

6. Save the Reference record.

Examining or Deleting Reference Links: The “Links” Tab

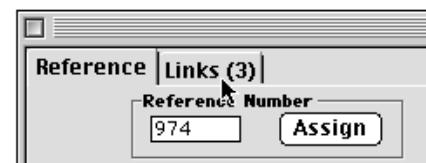
The Links tab of the References Input screen displays a scrolling list of all Species, Specimen, Collection, and Locality records that are currently linked to the Reference displayed in the Input screen. For a new References record, therefore, the list of links will be empty.

Reference Links are created from the Refs tab of individual Species, Specimen, Collection, and Locality records. For instruction on creating Reference Links see “[Linking a Reference to Species, Specimen, Collection or Locality Record](#)” later in this chapter.

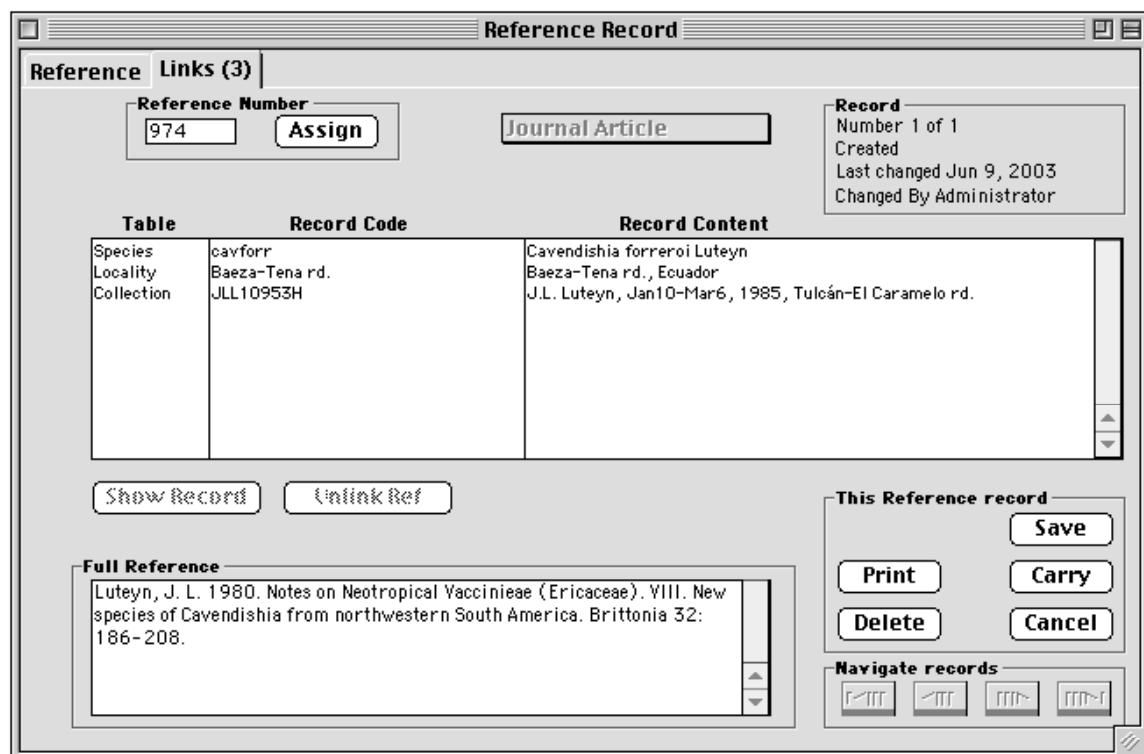
When a Reference record that has been linked in this way is displayed in the Record Input screen, the Links tab shows these links.

- Display a Reference record in the Reference Input screen** (see Chapter 12, “[Finding and Updating Records](#)”).
- Click the “Links” tab** in the Reference Input screen.

Note that the number of links between this Reference record and Species, Specimen, Collection, and Locality records appears on the tab.



The Links tab screen for this Reference record appears.



The scrolling list in the middle of the screen lists each Link for this Reference record, showing the table (Species, Specimen, Collection, or Locality), Record Code, and a brief identifying content summary for each Link.

3. To display a Species, Specimen, Collection, or Locality record linked to this Reference record:

- a. Click the Link in the scrolling list of Links to select it.

Table	Record Code	Record Content
Species	cavforr	Cavendishia forneroi Luteyn
Locality	Baeza-Tena rd.	Baeza-Tena rd., Ecuador
Collection	JLL10953H	J.L. Luteyn, Jan10-Mar6, 1985, Tulcán-El Caramelo rd.

Buttons at the bottom: Show Record, Unlink Ref, This Reference record, Save.

- b. Click the “Show Record” button below the scrolling list of Links.



The linked record appears in a new window.

Locality Record

General | Georeference | Images | Aux Fields | Notes | Refs (1)

Locality Code: Baeza-Tena rd. Assign

Locality Name: Baeza-Tena rd.

District: [empty]

State/Province: Napo - Pastaza

Country: Ecuador

Elevation (m): 2030-2175 Convert ft to m

Record
Number 1 of 1
Created Jan 16, 2003
Last changed
Changed By

Show Collections (3)

This Locality record
Save
Print
Carry
Delete
Cancel

Navigate records

4. To Unlink a Species, Specimen, Collection, or Locality record linked to this Reference record:
- Click the Link in the scrolling list of Links to select it.

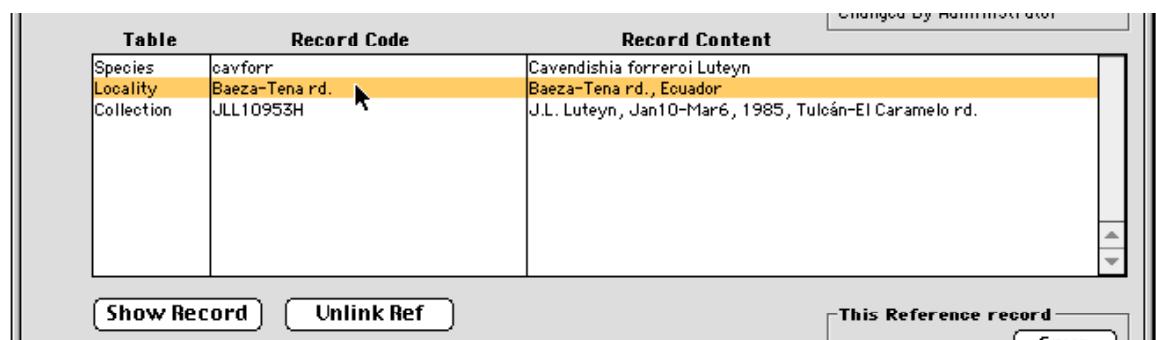


Table	Record Code	Record Content
Species	cavforr	Cavendishia forreroi Luteyn
Locality	Baeza-Tena rd.	Baeza-Tena rd., Ecuador
Collection	JLL10953H	J.L. Luteyn, Jan10-Mar6, 1985, Tulcán-El Caramelo rd.

Buttons at the bottom: Show Record, Unlink Ref, This Reference record, Unlink Ref (highlighted).

- Click the “Unlink Record” button below the scrolling list of Links.

The Link is deleted and the linked record disappears from the list of Links.

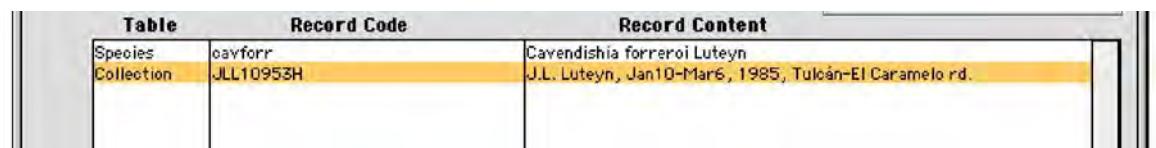


Table	Record Code	Record Content
Species	cavforr	Cavendishia forreroi Luteyn
Collection	JLL10953H	J.L. Luteyn, Jan10-Mar6, 1985, Tulcán-El Caramelo rd.

Linking or Unlinking a Reference to a Species, Specimen, Collection, or Locality Record

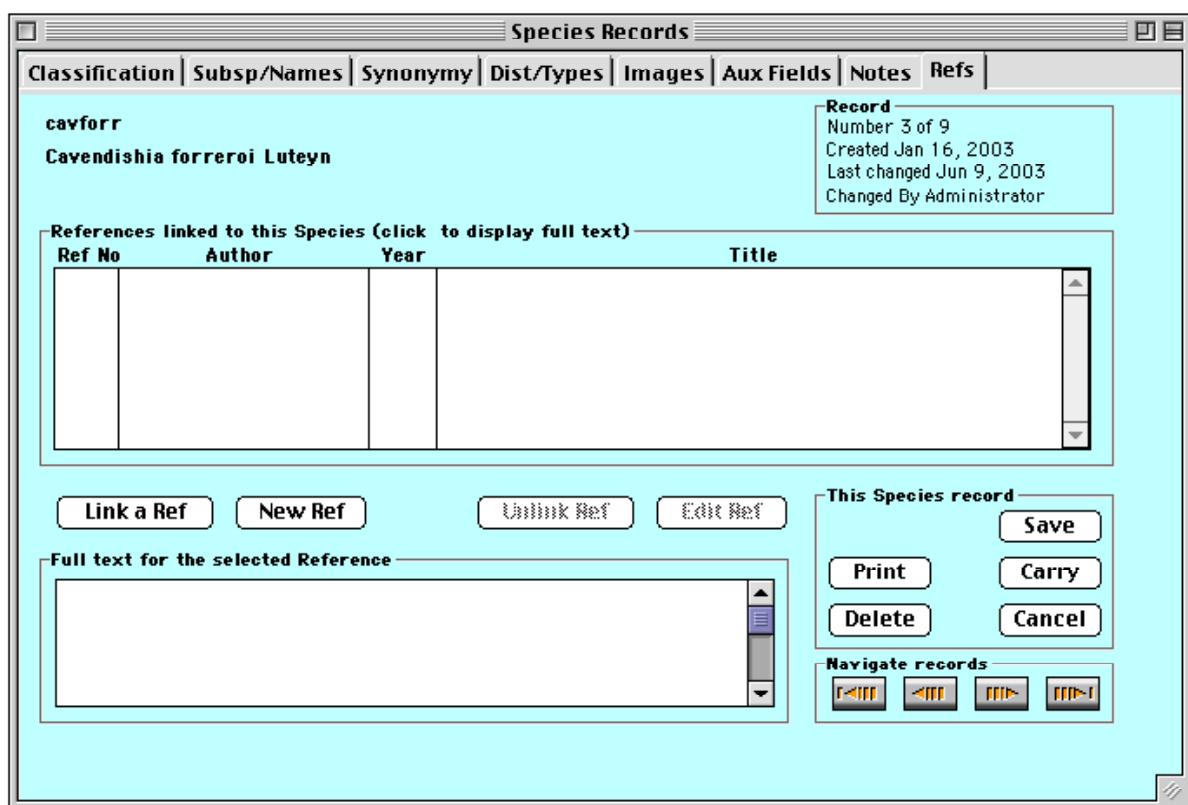
References are linked or unlinked from the Refs tab of individual Species, Specimen, Collection, and Locality records. When a Reference record that has been linked in this way is displayed in the Record Input screen, the Links tab of the Reference record shows the link (see “[Examining or Deleting Reference Links: The ‘Links’ Tab](#)” earlier in this chapter for details).

Linking a Reference to a Species, Specimen, Collection, or Locality Record

1. **Display a new or existing Species, Specimen, Collection or Locality record.** (See Chapter 11, “[Input](#),” or Chapter 12, “[Finding and Updating Records](#).”)
2. **Click the “Refs” tab in the Input screen.**



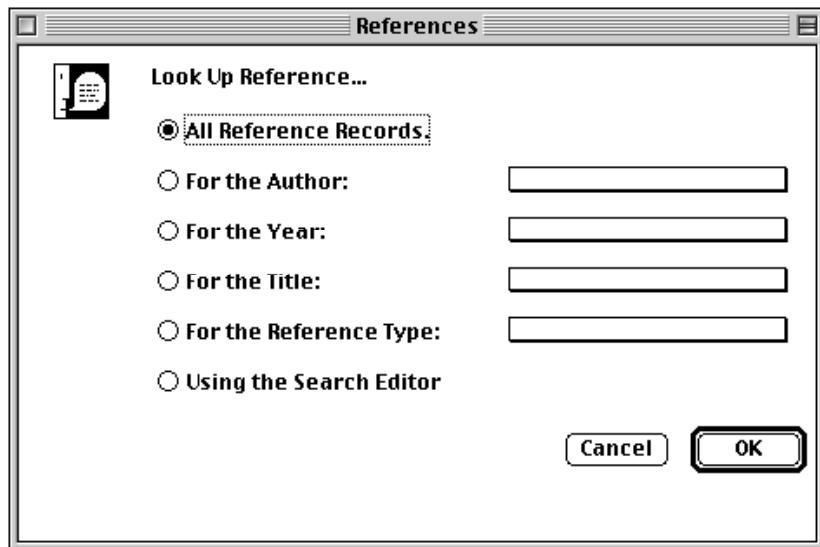
The References tab screen for the record appears.



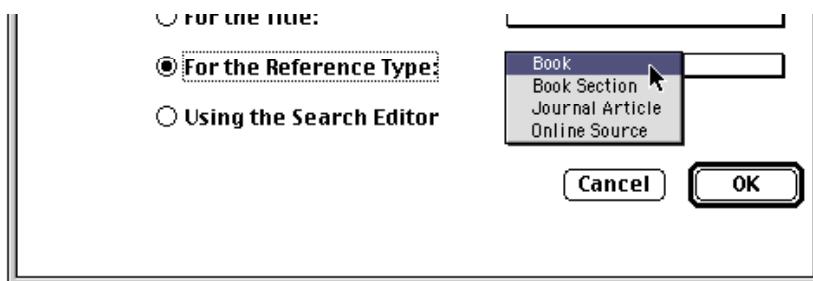
3. Click the “Link a Ref” button in the middle of the Refs screen.



The References lookup options window appears.



- Select a display option by clicking a button in the References lookup options window. You can display All Reference Records (not the best approach if there are hundreds of records) or restrict the choices displayed to a certain value for Author, Year, Title, or Reference Type. Or, you can launch the Query Editor (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12) to find a Reference record using ad hoc criteria.
- If you select the Author, Year, Title, or Reference Type option, Biota creates a list of all unique values for the selected field.
 - If there are only a few values, Biota displays the list in a popup list to the right of the selected button. Click and hold the popup to display the list of values, as shown below.

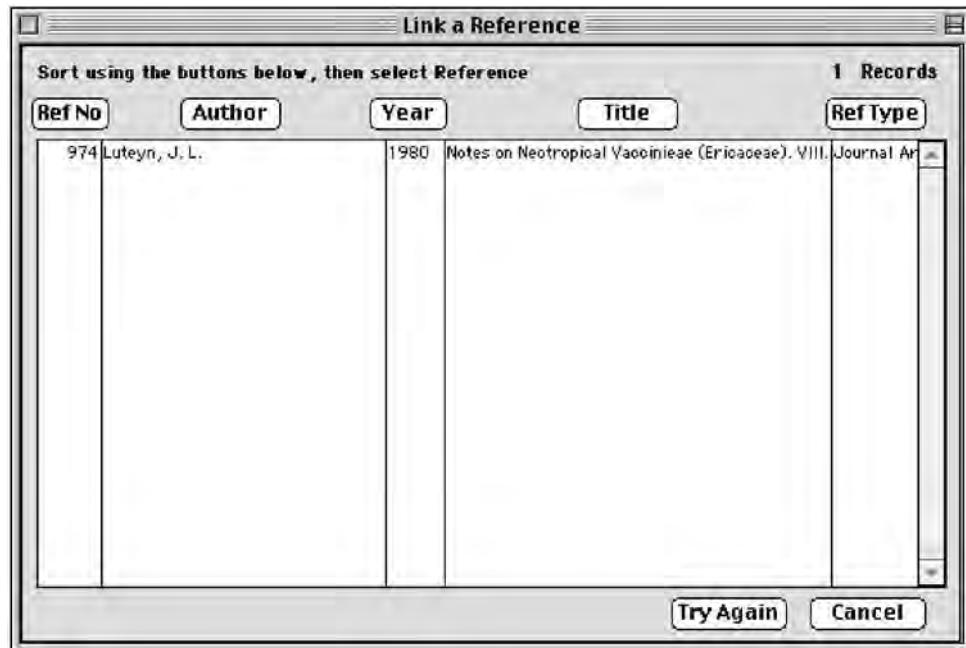
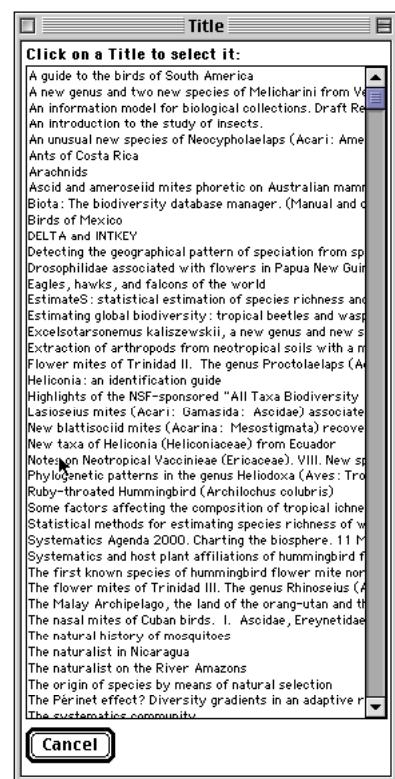


- ◊ If there are many values, Biota displays the list in a separate window with a scrollbar, as shown on the right.
- c. Select the value you want from the popup list or the scrolling list. Biota then shows the selected value in the popup area.



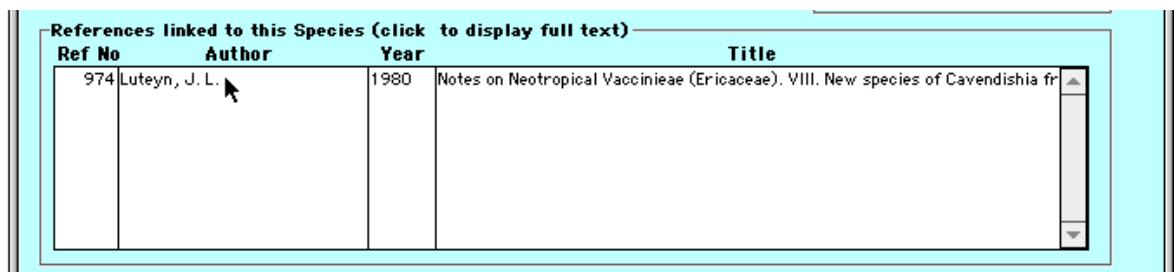
- d. Click the “OK” button in the References lookup options window. The “Link a Reference” display screen appears, listing all Reference records that match the option and criteria you selected in steps a. and b. above (see below).

 - ◊ If there are many records in the display screen (there is only one match in the example below, but you might have many for “Author” or “Year”) you may first want to use the sort buttons at the top of each column to sort the records displayed by the values for that column.
 - ◊ If you want to try a different selection option or field value to display records, click the “Try Again” button at the bottom of the “Link a Reference” selection screen.



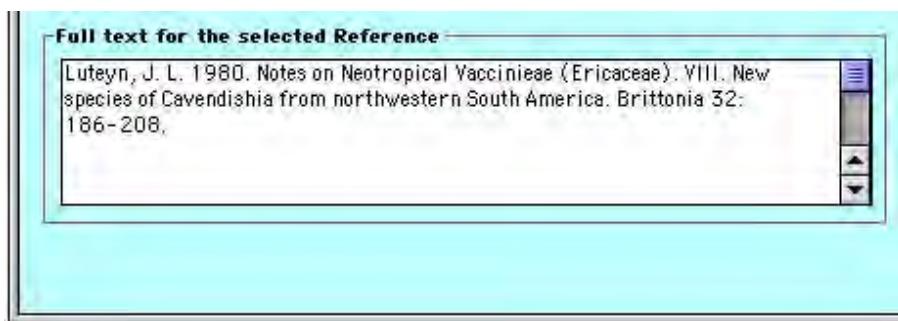
- e. When you find the record you want in the “Link a Reference” display screen, click it to create the link to the Species, Specimen, Collection, or Locality record.

The linked Reference record now appears in the scrolling list of links in the middle of the Refs tab window.



References linked to this Species (click to display full text)			
Ref No	Author	Year	Title
974	Luteyn, J. L.	1980	Notes on Neotropical Vaccinieae (Ericaceae). VIII. New species of Cavendishia from northwestern South America. Brittonia 32: 186–208.

- f. **To see the full, formatted Reference**, click the Reference entry in any panel of the scrolling list. The full reference appears in the “Full text for the selected Reference” pane at the bottom of the screen.



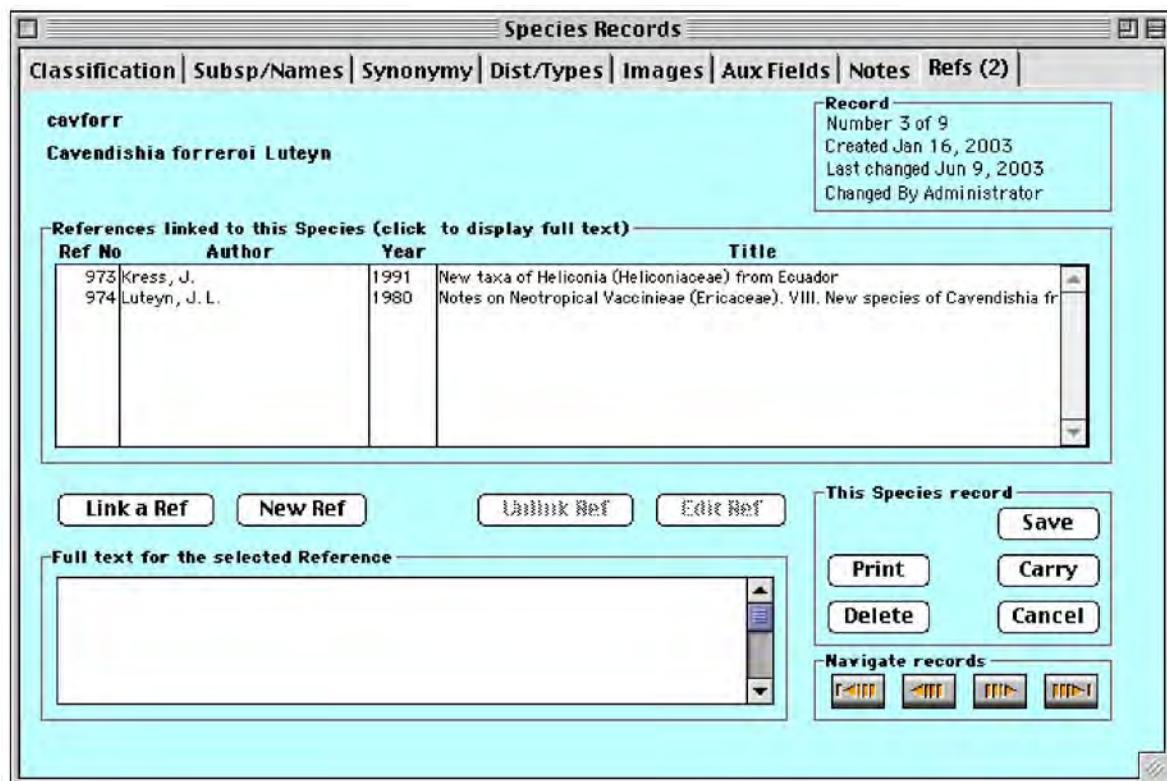
NOTE: You can select text from the “Full text for the selected Reference” pane to the Clipboard. But changes made in this pane are not saved. To edit the Reference, click the “Edit Ref” button and follow the instructions in the section [“Editing a Reference Record On the Fly From a Species, Specimen, Collection or Locality Record”](#) later in this chapter.

Unlinking a Reference from a Species, Specimen, Collection or Locality Record

1. **Display the Species, Specimen, Collection or Locality record.** (See Chapter 12, “[Finding and Updating Records](#).”)
2. **Click the “Refs” tab** in the Input screen. Note that the number of linked References is indicated on the tab.



The References tab screen for the record appears.



3. Select the Reference to be unlinked, from the scrolling list of links in the middle of the Refs tab window. The full Reference appears in the “Full text for the selected Reference” pane at the bottom of the screen.

References linked to this Species (click to display full text)			
Ref No	Author	Year	Title
973	Kress, J.	1991	New taxa of Heliconia (Heliconiaceae) from Ecuador
974	Luteyn, J. L.	1980	Notes on Neotropical Vaccinieae (Ericaceae). VIII. New species of Cavendishia from

Buttons: Link a Ref, New Ref, Unlink Ref, Edit Ref

Full text for the selected Reference:

Kress, J. . 1991. New taxa of Heliconia (Heliconiaceae) from Ecuador. Brittonia 43: 253–260.

4. Click the “Unlink Ref” button in the middle of the screen.

The selected Reference link is removed.



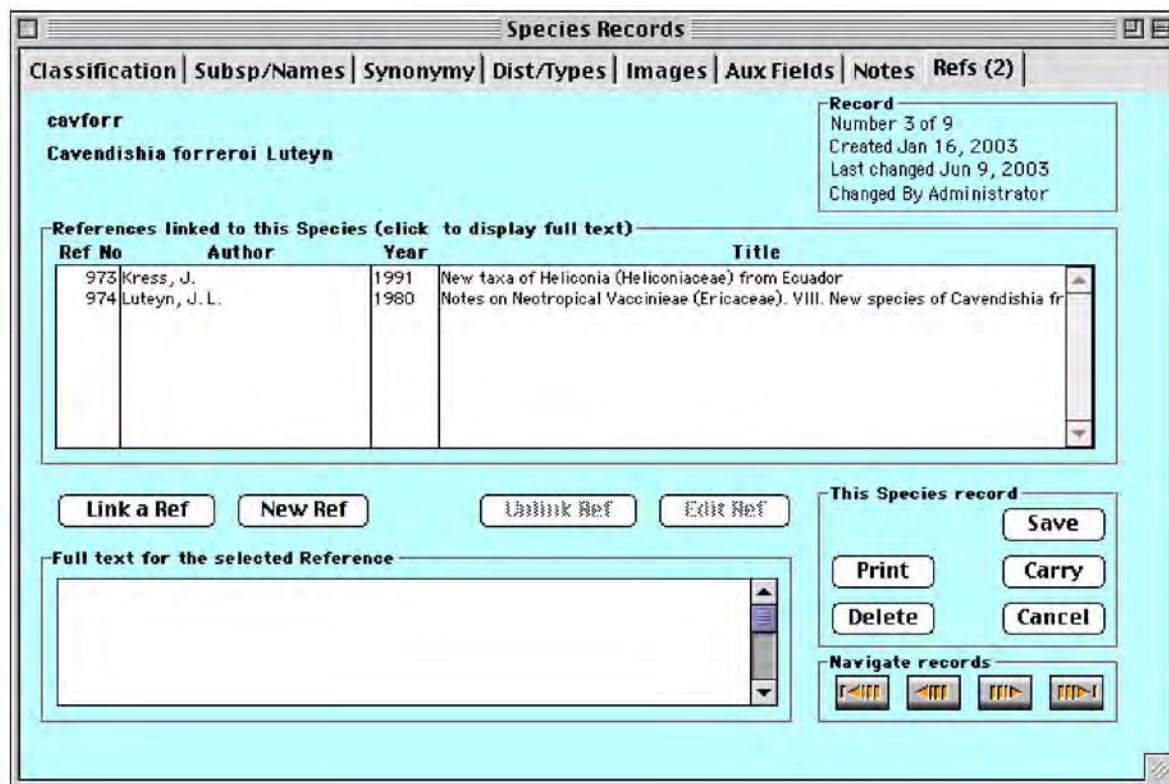
References linked to this Species (click to display full text)			
Ref No	Author	Year	Title
974	Luteyn, J. L.	1980	Notes on Neotropical Vaccinieae (Ericaceae). VIII. New species of Cavendishia from

Editing a Reference Record “On the Fly” From a Species, Specimen, Collection, or Locality Record

1. Display the Species, Specimen, Collection or Locality record. (See Chapter 12, [“Finding and Updating Records.”](#))
2. Click the “Refs” tab in the Input screen. Note that the number of linked References is indicated on the tab.

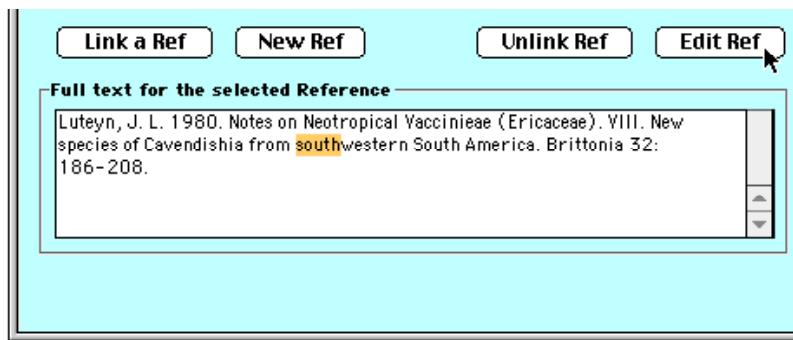


The References tab screen for the record appears.



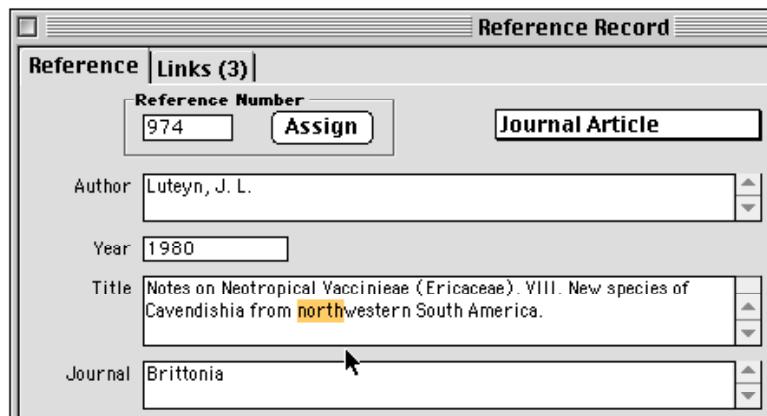
3. Select the Reference to be edited, from the scrolling list of links in the middle of the Refs tab window. The full Reference appears in the “Full text for the selected Reference” pane at the bottom of the screen.

In the example below, the word “southwestern” should be “northwestern.” Rather than searching for the Reference record in the References table and correcting the error there, you can simply edit the linked Reference record “on the fly” from (in this example) the Species record.



4. Click the “Edit Ref” button in the middle of the screen (see above).

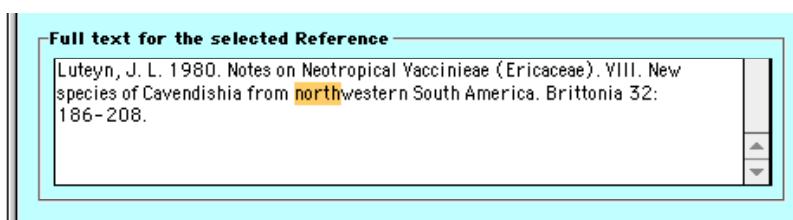
The linked Reference record appears in a new window.



5. Edit the Reference record as needed (see above).

6. Click the “Save” button in the Reference Input screen.

The Reference Input screen closes and returns control to the “Refs” tab of the Species, Specimen, Collection or Locality screen, with the edited Reference data displayed.



Importing and Exporting References

Importing References

It is likely that you already have many references in specialized reference management software (e.g., EndNote, ProCite, etc.). Rather than start all over, entering them manually into Biota, you can export them from your reference management application and import them directly into Biota.

Note: Because EndNote is the most widely used reference management application, on both Windows and Mac OS, and has a straightforward design, Biota's Reference management system was designed around EndNote fields and document types. Other reference management applications (e.g., ProCite) can also be made to export citations in a form that can be imported into Biota, with some modifications, but instructions for applications other than EndNote are beyond the scope of this manual.

1. **In your application management software**, select the references you want to export to Biota.
2. **Set up the export tools in your application management software** to export a tab-delimited, plain text file, with the following fields (or their equivalents), with comments on each field:

NOTE: You must know the order of these fields in the exported file, but they may be in any order in the exported file.

- **Reference Number** (*ReferenceNo* in Biota). This must be an integer; no alphabetic characters are allowed.
- **Reference Type** (*ReferenceType* in Biota). Biota accepts only four Reference Types:
 - ◊ **Journal Article**
 - ◊ **Book**
 - ◊ **Book Section**
 - ◊ **Online Source**

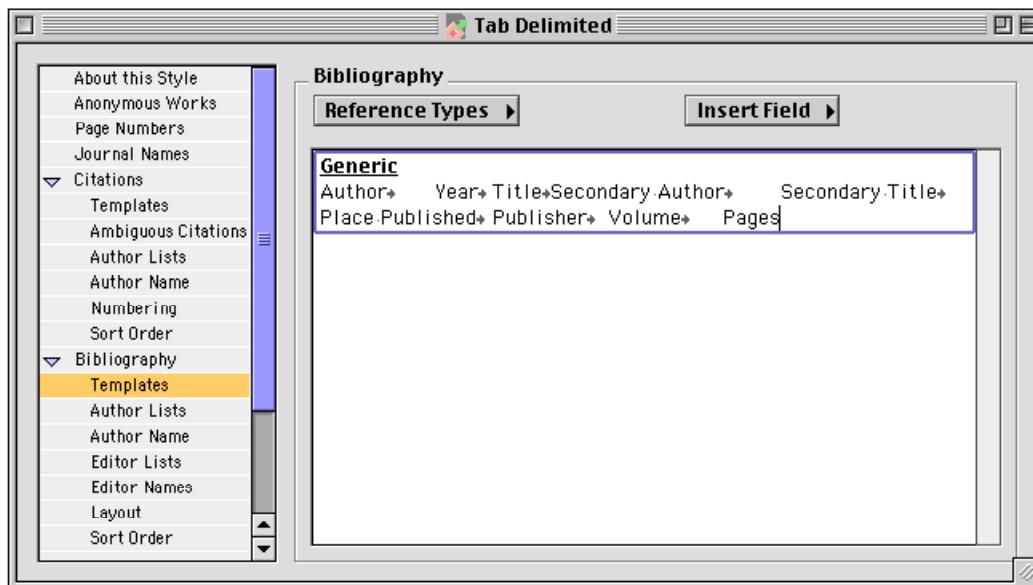
NOTE: The text of *ReferenceType* field must *exactly* match one of these four entries, including spaces. Biota flags any other entry in this field during import, and offers to import the reference in "Book" format.

- **Author(s)** (*Author* in Biota; *Author* in EndNote). Biota has only one field for Author, but it may contain as long a list of authors as necessary (up to 32K).
- **Year of Publication** (*Year* in Biota; *Year* in EndNote). This is an alphabetic field (up to 20 characters), so you can use date ranges (e.g., "1996-1999") or brief text notations (e.g., "Unknown" or "Late 18th Century").

- **Article or Book Title** (*Title* in Biota; *Title* in EndNote). The title may be of virtually any length (up to 32K characters).
- **Editor** (*Editor* in Biota; *Secondary Author* in EndNote). This field may be of virtually any length (up to 32K characters).
- **Title of Journal or Edited Book** (*JournalOrEditedBook* in Biota; *Secondary Title* in EndNote). This field may be of virtually any length (up to 32K characters).
- **Place of Publication** (*PlacePublished* in Biota; *PlacePublished* in EndNote). This field may contain up to 60 characters.
- **Publisher** (*Publisher* in Biota; *Publisher* in EndNote). This field may contain up to 80 characters.
- **Journal Volume** (*Volume* in Biota; *Volume* in EndNote). This text field may contain up to 10 characters.
- **Pages or Article or Book Section** (*Pages* in Biota; *Pages* in EndNote). This text field may contain up to 20 characters.
- **URL for Online Source** (*URL* in Biota; no corresponding field in EndNote). This text field may contain up to 32K characters.

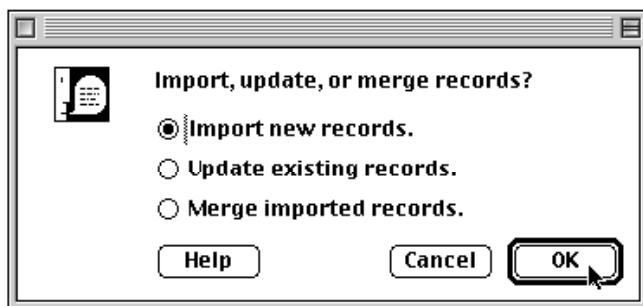
Notes for EndNote Users:

- a. **Set up the export file format by choosing “Tab Delimited” from the Style Manager** (choose “Output Styles” from the File menu to get to the Style Manager).
- b. **Edit the Tab Delimited style to export only the above fields** (except for “Record Number” and “Reference Type”). In the EndNote Style Editor, go to the “Bibliography” theme, then click “Templates” and modify the “Generic” Reference Type template to include the above fields, as shown below. Do not specify anything for any other Reference Types.



- c. **Click the “Layout” tab** (still in the Bibliography theme) and confirm that “Record Number” and “Reference Type” will be included in the export.

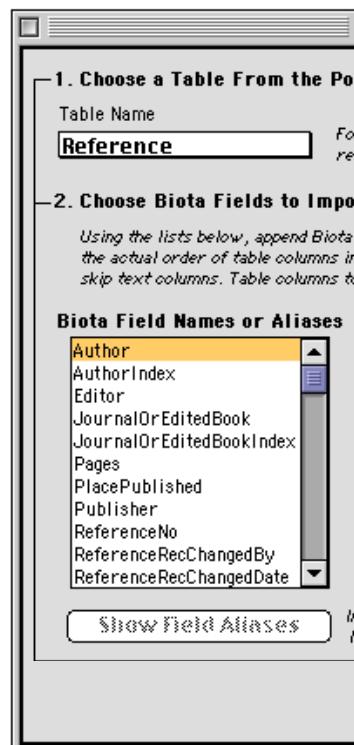
3. **Export the text file** from your application management software.
4. **Open the exported file (e.g., in Excel) to verify** that: (a) the file begins with the first record (there are no header rows), and (b) only the four Reference Types that Biota supports are specified. (Change the Reference Type field to one of these four, if any Reference Types appear in the exported file. For files exported by applications other than EndNote, you will need to enter the appropriate Biota/EndNote Reference Type.)
5. **Close the exported file**, taking care to ensure that it saved as filetype “Text” (or “Tab-delimited Text”).
6. **From the Im/Export menu in Biota, choose Import by Table and Fields.** The Import Options screen appears.



Note: For help with the Import Editor, refer to Chapter 28, “[Importing Data](#).”

7. **Choose the default, “Import new records,”** and click the “OK” button. The Import Editor appears.
8. **Choose “Reference” from the “Table Name” popup.**
9. **Select and Append fields from the left panel** (Biota Field Name or Aliases) to create a list in the right panel (Text File Fields) that precisely matches the order of fields in the text file to be imported. (Use the “Skip” button if necessary.)

Note: Do not select any of the “Index” fields: *AuthorIndex*, *TitleIndex*, or *JournalOrEditedBookIndex*. These fields are automatically filled by Biota, with the first 80 characters of the corresponding Text fields: *Author*, *Title*, and *JournalOrEditedBook*.



10. Click the “Save Import Setup” box, in case you need to come back and modify the setup or import additional References.
11. Click the “Import” button. If error messages appear, consult Chapter 28, “[Importing Data by Tables and Fields](#).”



Exporting References

You can export Reference records from Biota, for the current Reference Record Set (see “[Record Sets](#)” in Chapter 3) in either two ways:

- **Using the Export Editor.** You can export any or all fields from the Reference table, for the Reference Record Set for all Reference records, using the Export Editor, just as you can for any other Core table in Biota. See “[Exporting Data by Tables and Fields](#)” in Chapter 27.
- **Using the “Export References” tool from the Im/Export menu.** This tool exports all records for the current Reference Record Set, in *American Naturalist* format, to a text file. This format was chosen as approximately representative of many journals in ecology, evolutionary biology, and systematics, and because this leading journal publishes papers in all these areas.

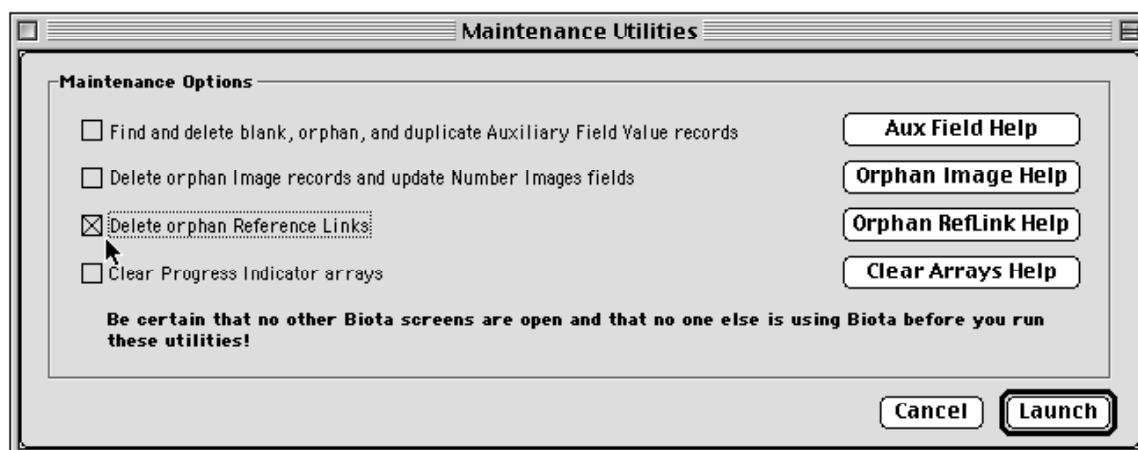
Maintaining and Repairing Reference Links

Under normal operations, Biota correctly maintains links between parent records in the Specimen, Species, Collection, and Locality tables and Reference records, by means of records in the ReferenceLinks table.

Power failures, system crashes, and incorrectly imported data, however, can produce orphan ReferenceLinks records.

You can correct this problem, without in any way affecting legitimate records, by running the Reference Links Maintenance Utility. Whereas this problem is not serious (orphan ReferenceLink records simply take up space), it is recommended that you run this utility from time to time if you work with References in Biota, especially if you suspect problems.

1. To run the Reference Link Maintenance Utility, choose “Maintenance Utilities” from the Special menu. The option screen appears.



- 2. Activate the option “Delete orphan Reference Links.”**
- 3. Click the “Launch” button.** The utility reports on its activities.

Chapter 21

The Specimen Loan System

The Loans menu contains the primary tools for managing Specimen Loans. Using these tools, you can keep track of loans you make to others as well as specimens you borrow from others. You can review existing Loan records and print or reprint Loan forms and lists of Specimens loaned.

How Biota Keeps Track of Specimen Loans

To use the Loan system, it is essential to understand how Biota keeps track of Loans. Each Specimen record in your Data File has a field called "Deposited." Biota uses this field to identify each group of Specimen records that constitute a Loan. You can view the "Deposited" field in the standard Specimen Record Listing screen, as well as in the individual Specimen records in the Specimen Input screen.

- **When you create new Specimen records** for your own specimens, you should enter a name or code in the Deposited field (up to 20 alphanumeric characters), indicating that the physical specimens are presently in your custody. (You may wish to set up this code as the default entry for the Deposited field, by using the Field Value Defaults utility from the Special menu. See "[Setting Default Entries: Field Value Defaults](#)" in Chapter 17.)
- **When you lend a group of specimens** from your collection to another institution or individual, you create a new record in the Loans table to record the loan, with a unique Loan Code to identify the Loan. Once you have indicated which Specimen records will be included in the Loan, Biota changes the Deposited field of each Specimen record in the Loan, replacing the existing value with the Loan Code.
- **When loaned specimens are returned** to your collection, you use the Record Returns tool to change the Deposited field of the corresponding Specimen records back to your institutional or personal collection name or to some other meaningful code.

NOTE: Since there is, as yet, no loan history capability in Biota to keep track of previous (as opposed to current) loan status of Specimens, you could devise a system of codes to indicate which returned specimens have been previously lent and to whom, although there are obviously serious limitations to this approach if you repeatedly lend the same specimens.

- **When you borrow a group of specimens** from another institution or individual, you can create a Loan Code for the group and use the New Loan screen to record the specimens as a loan to your own institution or to your own collection.
- **When you return borrowed specimens**, you can use the Record Returns tool to change the Deposited field in the corresponding Specimen records of your Data File to a new code, indicating that the physical specimens have been returned.

Recording a New Loan

To create a Loan record for a new loan from your collection, or to record a loan you have received from another collection, take the following steps:

1. **From the Loans menu, choose “New Loan.”** The New Loan Input screen appears.

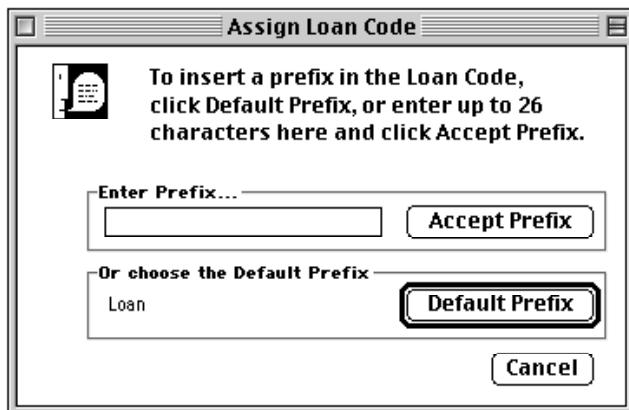
2. **Enter a Loan Code.** You can enter the Code either by typing it in the Loan Code entry area or by using the adjacent “Assign” button (see [“Assigning New Record Codes Using an ‘Assign’ button: Step by Step”](#) in Chapter 8).

Loan Codes may be up to 80 characters in length.

Loan Code, the Key field for the Loan table, is an obligatory entry, which must be made first. All remaining entry areas are optional. The Loan Code you enter must not duplicate the Loan Code of any existing Loan Record, or you will receive an error message.

See [“How Biota Keeps Track of Specimen Loans,”](#) earlier in this chapter, for ideas on how to set up a system of Loan Codes.

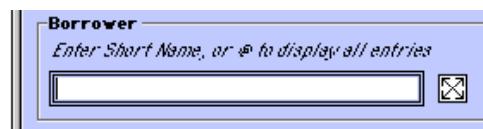
If you use the “Assign” button, the Assign Loan Code window offers two options.



- You can enter a prefix of your own choice, then click the “Accept Prefix” button.
- You can click the “Default Prefix” button to use the prefix “Loan.” (This default is fixed and cannot be altered in the Record Code Prefix screen, unlike other Record Code prefixes.)

In either case, Biota will format the Loan Code with the prefix (up to 14 characters in the case of an ad hoc prefix) plus a four-digit integer counter derived from the Loans table sequence number.

3. Enter the Borrower’s “Short Name” in the Borrower entry area. Because this field is linked to the Short Name field of the Personnel table, the entry area has a double border. You can use any of the techniques for entering data in linking fields described in Chapter 7, “[Overview of Record Input Screens](#).”

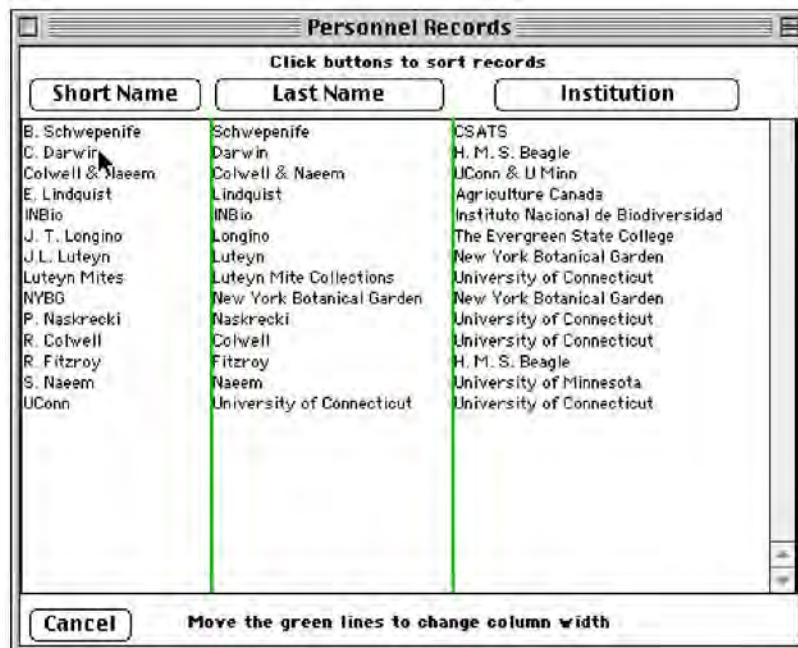


- If you know that the Borrower has no existing record in the Personnel table, enter a Short Name for the determiner in the “Borrower” entry area (e.g., Albert B. Smith or A. B. Smith) and press the TAB key. If the entry you make does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Loan record without creating a link to the Personnel table (a “Personnel-orphan” Loan record) (see “[Entering Data in Linking Fields](#)” in Chapter 7).

NOTE: On Pin, Slide, Vial, and Herbarium labels, Biota uses the Short Name field for the collector’s name (see Chapter 15, “[Printing Labels](#)”). Although the Short Name may have up to 80 characters, it is best to make it substantially shorter (20-30 characters is a good guideline) if you intend to use Biota to produce specimen labels. Since Borrowers are often also collectors, be sure to choose a version of the Borrower’s name that is appropriate for collector’s names on labels—e.g., initials and last name, or first name and last name. You can also use a “Group Name” in the “Determined By” field, e.g., A. B. Smith & C. D. Jones

(for help with Group Names, see “[Entering Personnel Data: The ‘Group’ Tab](#)” in Chapter 11).

- If you think the Borrower may already have a Personnel record, but you are not sure what Short Name the record carries, enter the @ character and press the TAB key. A scrollable list of all existing Personnel records appears (below), from which you can choose the correct record by clicking it. You can sort the records by Short Name, Last Name, or Institution by clicking the buttons above the columns.



The screenshot shows a dialog box titled "Personnel Records" with the instruction "Click buttons to sort records" at the top. Below are three buttons: "Short Name" (highlighted with a red box), "Last Name", and "Institution". The main area contains a table with three columns. The first column lists "Short Name" entries, the second "Last Name", and the third "Institution". The table has 15 rows of data. The "Short Name" column includes entries like "B. Schwenepenife", "C. Darwin", "Colwell & Naeem", etc. The "Last Name" column includes "Schwenepenife", "Darwin", "Colwell & Naeem", etc. The "Institution" column includes "CSATS", "H. M. S. Beagle", "UConn & U Minn", etc. At the bottom of the dialog box are "Cancel" and "Move the green lines to change column width" buttons.

Click buttons to sort records		
Short Name	Last Name	Institution
B. Schwenepenife	Schwenepenife	CSATS
C. Darwin	Darwin	H. M. S. Beagle
Colwell & Naeem	Colwell & Naeem	UConn & U Minn
E. Lindquist	Lindquist	Agriculture Canada
INBio	INBio	Instituto Nacional de Biodiversidad
J. T. Longino	Longino	The Evergreen State College
J. L. Luteyn	Luteyn	New York Botanical Garden
Luteyn Mites	Luteyn Mite Collections	University of Connecticut
NYBG	New York Botanical Garden	New York Botanical Garden
P. Naskrecki	Naskrecki	University of Connecticut
R. Colwell	Colwell	University of Connecticut
R. Fitzroy	Fitzroy	H. M. S. Beagle
S. Naeem	Naeem	University of Minnesota
UConn	University of Connecticut	University of Connecticut

- If you know the Short Name for the Borrower’s existing Personnel record, enter the first letter, the first few letters of the Short Name, or the full Short Name, and press the TAB key. If a single match is found, Biota completes the name and the cursor moves into the next field. If more than one match is found, a choice list like the one above appears, with all matches shown.

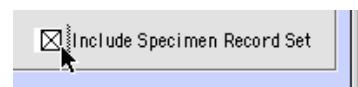
If the Borrower entry you make in the Loan record does not match the Short Name field of any existing Personnel record, Biota offers you a choice between creating a new Personnel record for that name, “on the fly,” or accepting the Loan record without creating a link to the Personnel table (a “Personnel-orphan” Specimen record) (see “[Entering Data in Linking Fields](#)” in Chapter 7).

NOTE: Creating a “Personnel-orphan” Loan record is not recommended. If you do so, none of the information on the Borrower’s institution or contact information can be entered in the loan forms.

4. **Enter the Date Loaned.** When the New Loan screen opens, today's date (the date in your computer's internal clock) is entered in the Date Loaned entry area. If you need to change it, enter a full date (see "[Dates](#)" in Chapter 9). If you want to keep today's date, just "TAB through" the date entry areas.
5. **Enter the Loan Period.** This alphanumeric entry can be up to 20 characters.
6. **Indicate the Specimens Loaned.** Although you can create a Loan record without linking it to any Specimen records (e.g., for unmounted material not in the Data File), normally a Loan record is linked to the Specimen records for the physical specimens loaned (see "[How Biota Keeps Track of Specimen Loans](#)" earlier in this chapter).

There are two, non-exclusive methods of indicating which Specimen Records are included in the Loan.

- **Click the Include Specimen Record Set checkbox** in the Specimens Loaned panel.



To use this option, you must first have defined a Specimen Record Set (see "[Record Sets](#)" in Chapter 3). You can find the Specimen records using any of the tools of the Find or Series menus (see Chapter 12, "[Finding and Updating Records](#)").

Once you click the checkbox, the Specimen Code for the last record in the Record Set appears in the Last Code Entered display area, showing the current value of the [Specimen] Deposited field for that record in the Previous Deposition display area (below).

 A screenshot of the "Specimens Loaned" panel. At the bottom right, there is a checkbox labeled "Include Specimen Record Set" which is checked. The rest of the panel shows fields for "Enter Specimen Code" (HMSB007), "Last Code Entered" (HMSB007), "Previous Deposition" (MNH), and "Number Specimens Loaned" (17).

The Number of Specimens display area (above) counts the number of Specimen Records you have entered so far—including the number in the Specimen Record Set plus any records entered using the "one by one" option described below.

- **Enter the Specimen Codes, one by one,** in the Enter Specimen Code entry area of the Specimens Loaned panel.

 A screenshot of the "Specimens Loaned" panel. At the bottom right, there is a checkbox labeled "Include Specimen Record Set" which is unchecked. The rest of the panel shows fields for "Enter Specimen Code" (HMSB010), "Last Code Entered" (HMSB007), "Previous Deposition" (MNH), and "Number Specimens Loaned" (3).

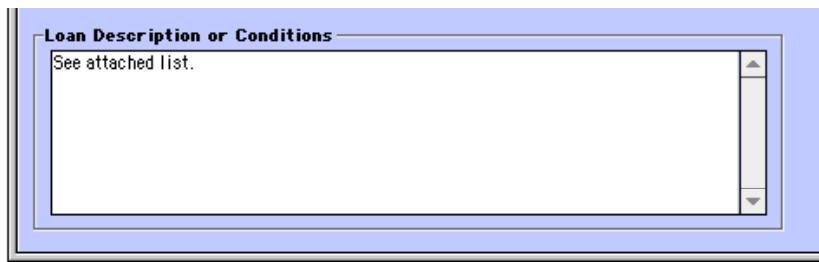
You can enter the Specimen Codes manually, pressing TAB after each entry, enter them with a barcode reader, or use both methods for the same Loan. If the

barcode reader is set to enter an end-of-line character after each read, you can enter all Specimen Codes without touching the keyboard or mouse.

Once entered, each Specimen Code appears in the Last Code Entered display area, showing the current value of the [Specimen] Deposited field for that record in the Previous Deposition display area.

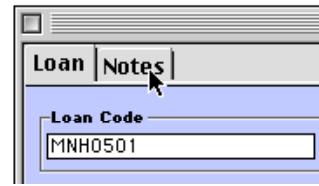
The “Number of Specimens” display area counts the number of Specimen Records you have entered so far—including any in the current Specimen Record Set if the Include Record Set checkbox has been checked.

7. **Make an entry in the “Loan Description or Conditions” text area.** This optional entry (up to 32,000 characters) will appear on the printed Loan Invoice (see [“Previewing, Printing, and Exporting Loan Records”](#) later in this chapter). If the Loan includes any specimens or other material not represented by Specimen records,



this is the place to describe that material. When you create a new Loan record, the “Loan Description or Conditions” text area displays the default entry “See attached list,” referring to the list of specimens that would usually be attached to the Loan Invoice. You are of course free to delete or change this entry.

8. **Click the Notes tab to add a Loan Note (or Notes),** if you wish. Loan Notes should be used for any comments on the loan that are *not* intended to appear on the Loan Invoice itself. Any number of additional Loan Notes can be added to the Loan record later, to document notices sent to the Borrower, condition of returned specimens, and so on. See [“Notes Input”](#) in Chapter 11 for detailed instructions.
9. **Click the “Save and Continue” or the “Save and Close” button to save the Loan record (or the “Cancel” button to cancel it).**
 - **The “Save and Continue” button** saves changes in the “Deposited” field of any Specimens so far included in the new Loan and saves the Loan record itself. It leaves the New Loan window open so you can include additional Specimens or make other changes. If you are entering a large number of specimens manually, or with a barcode reader, it is a good idea to click this button periodically.
 - **The “Save and Close” button** saves all changes in the “Deposited” field of any Specimens included in the new Loan, saves the Loan record itself, and closes the New Loan window. If you want to add Specimens or make other changes to the Loan later, you can do so by re-opening the Loan record. See [“Displaying and Editing an Existing Loan”](#) later in this chapter.



- 10. If you have clicked the “Save and Close” button, the next step depends on whether or not any Specimen records have been included in the Loan in [Step 6](#), above.**

- **If no Specimen Records are linked to the Loan record,** the message below appears.



If you click the “OK” button, the Loan form printing sequence begins. See [“Previewing, Printing, and Exporting Loan Records,”](#) later in this chapter. You might create a Loan record, for example, for a group of unsorted and unmounted specimens.

- **If one or more Specimen Records are linked to the Loan record,** the Specimen Records appear in a special version of the Specimen Record Listing screen entitled “Specimens in Loan.” Notice that the “Deposited” field of each record in the new Loan has been changed to the Loan Code (“MNH0501” in the example below).

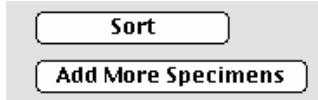
Specimens in Loan									
Loan Code MNH0501		17 Records							
Specimen Code	Genus	Species	Collection Code	Collector	Method	Stage/Sex	Host	Height	Deposited
HMSB001	Geospiza	fortis	CDO01	C. Darwin	Shotgun				MNH0501
HMSB002	Geospiza	fortis	RF001	R. Fitzroy	Shotgun				MNH0501
HMSB003	Geospiza	fuliginosa	RF001	R. Fitzroy	Shotgun				MNH0501
HMSB004	Geospiza	scandens	CDO01	C. Darwin	Shotgun				MNH0501
HMSB005	Geospiza	scandens	CDO02	C. Darwin	Shotgun				MNH0501
HMSB006	Camarhynchus	psittacula	CDO02	C. Darwin	Shotgun				MNH0501
HMSB007	Camarhynchus	pauper	CDO02	C. Darwin	Shotgun				MNH0501
HMSB008	Camarhynchus	parvulus	CDO02	C. Darwin	Shotgun	Female			MNH0501
HMSB009	Certhidea	olivacea	RF002	R. Fitzroy	Shotgun				MNH0501
HMSB010	Geospiza	magnirostris	CDO03	C. Darwin	Shotgun				MNH0501
HMSB011	Geospiza	fortis	CDO03	C. Darwin	Shotgun				MNH0501
HMSB012	Geospiza	difficilis	CDO03	C. Darwin	Shotgun				MNH0501
HMSB013	Cactospiza	heliobates	RF003	R. Fitzroy	Shotgun				MNH0501
HMSB014	Cactospiza	pallida	CDO04	C. Darwin	Shotgun				MNH0501
HMSB015	Certhidea	olivacea	CDO04	C. Darwin	Shotgun				MNH0501
HMSB016	Geospiza	difficilis	CDO04	C. Darwin	Shotgun				MNH0501
HMSB017	Camarhynchus	parvulus	CDO04	C. Darwin	Shotgun	Male			MNH0501

Double Click a Specimen to View or Modify Record
Resize Columns in the Header

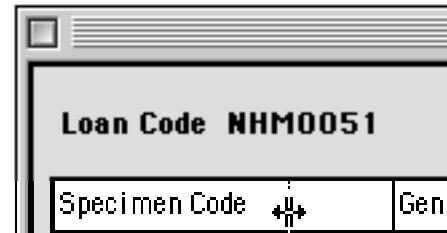
Sort Print Loan Forms
Add More Specimens Done

The purpose of this screen is to provide an opportunity to confirm that no errors have been made in specifying the content of the Loan.

- **To sort the records**, click the “Sort” button (see “[Sorting Records in Record Listing Screens](#)” in Chapter 10).
- **To incorporate additional Specimens in the Loan**, click the “Add More Specimens” button. The New Loan screen reappears.
- **To examine a full Specimen record** in the standard Specimen Input screen, double click the record in the Record Listing screen.



NOTE: If you wish, you can re-size the columns in the “Specimens in Loan” Record Listing screen (above) by dragging the column dividers in the header area. The cursor changes to a “splitter” icon.



11. If the Specimens have been displayed,

- **Either:** Click the “Print Loan Forms” button to print a Loan Invoice and, if you wish, print a list of the Specimen records in the Loan and/or export a text file with these records.
The “Print Setup” (Windows) or “Page Setup” (Mac OS) window appears. Please continue with the next section, “[Previewing, Printing, and Exporting Loan Records](#).”
- **Or:** Click the “Done” button to leave the New Loan procedure without printing or exporting. The Record Set Options screen appears to allow you to declare the Specimen records in the Loan to be the current Specimen Record Set, if you wish (see “[The Record Set Options Screen](#)” in Chapter 3). (It is not necessary to create a Specimen Record Set to complete the Loan process.)



NOTE: This is the place to stop if you are recording a loan made to you from another individual or institution (see “[How Biota Keeps Track of Specimen Loans](#),” earlier in this chapter).

Previewing, Printing, and Exporting Loan Records

This section describes the procedures and options for printing Loan invoices, printing a list of the Specimen records in a Loan, and exporting text files to disk for the Specimen records in a Loan.

1. **Follow the instructions** for “[Recording a New Loan](#)” (earlier in this chapter) or for “[Displaying and Editing an Existing Loan](#)” (later in this chapter) until instructed to proceed with this section.
2. **Check or adjust any settings** in the “Print Setup” (Windows) or “Page Setup” (Mac OS) window, **then click the “OK” button**. The “Print” window for your active printer appears. (Because “Print” windows vary greatly among printers and between operating systems, none is illustrated here.)

3. **Choose a Preview option.** Look for a “Print preview” (Windows) or “Preview on screen” (Mac OS) checkbox in the lower-left corner of the Print window. If you don’t see the checkbox, look for a popup menu of print options and select “4D x.x.x” (where “x.x.x” is the version number of 4th Dimension used to compile the current version of Biota), then locate the checkbox.



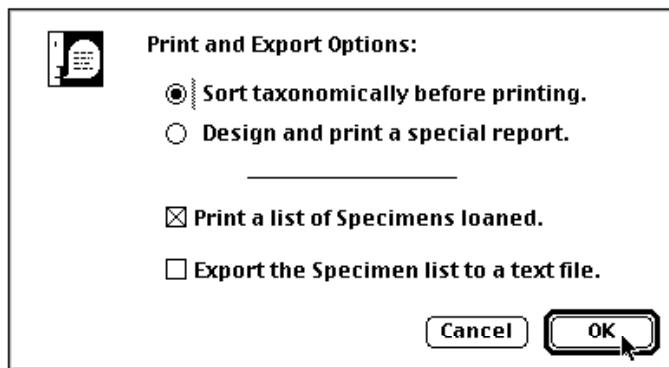
- **If you leave the Preview checkbox unchecked,** the Loan invoice goes directly to your printer.
 - **If you click the Preview checkbox,** you can check the Loan invoice onscreen and then Print or Cancel.
4. **To print the Loan invoice,** click the “OK” button (Windows) or “Print” button (Mac OS) in the Print window.
- **If you requested Print Preview,** the Loan Invoice for the active Loan record appears in the Preview screen.

Header	Birds of the Galápagos Islands
Lender block	Charles Robert Darwin Down House Lupton Road Bromley, Kent United Kingdom Voice Phone 1: [Unlisted] E-Mail Address: cdarwin@geospizanet.uk
Borrower block	LOAN INVOICE LOAN NUMBER: NHM0051 LOAN DATE: May 12, 2003 LOAN PERIOD: Indefinite BORROWER: P. L. Sclater Cromwell Road The Natural History Museum London SW7 5BD United Kingdom Voice Phone 2: +44 (0)20 7942 5000 E-Mail Address: slater@heaven.nhm.ac.uk
DESCRIPTION AND CONDITIONS: See attached list.	
Approved By	Received by
Lender	Borrower

- ◊ **The header** at the top of the Loan Invoice shows the [Project]Heading for the Active Project. See “[Entering Project Data: The ‘General’ Tab](#)” in Chapter 16.
- ◊ **The lender block** displays address and contact information from the Project-Linked Personnel record (if any) for the Active Project. (Each Project record

may be linked, one-to-one, to a single Personnel record that provides contact information for the Project. See “[Personnel Input](#)” in Chapter 11.)

- ◊ **The remaining information on the Loan Invoice** comes from the corresponding fields of the Loan record, or from the Personnel record for the Borrower (*borrower block*, above). (*Loan Number* on the Invoice is the Loan Code for the record.)
- **To print the Invoice after previewing it**, click the Printer icon in the control panel at the top left of the Preview screen (see “[Printing and Previewing Procedures for Reports and Labels](#)” in Chapter 14 for details on the Preview screen).
- **To proceed without printing the Invoice**, after viewing the Invoice in the Preview screen, click the “X” icon in the control panel at the top left of the Preview screen.
- **If you choose to Print without previewing the invoice, or you clicked the “Print” button on the Preview screen**, the Loan Invoice is printed and the “Print and Export Options” screen appears.



5. **Choose Print and Export options and click the “OK” button**, or Cancel to dismiss the rest of the procedure.
 - **Either:** Choose “Sort taxonomically before printing.” This option sorts Specimen records taxonomically (see “[Sort Options](#)” in Chapter 15) before printing, if you select the “Print a list of Specimens loaned” option in the lower half of the Print and Export Options screen.
 - **Or:** Choose “Design and print a special report.” This option launches the Quick Report Editor (see “[Designing and Printing Reports with the Quick Report Editor](#)” in Chapter 14), with which you can create your own format for a report on the Specimen records in the Loan. Fields from the Loan record are not available, however, except for the Loan Code, which is reproduced in the [Specimen] Deposited field.
 - **If you chose “Sort taxonomically before printing,”** the two checkboxes in the Print and Export Options screen are enabled. You can check either or both.

- ◊ If you click the “Print a list of Specimens loaned” checkbox, Biota prints a special version of the standard Specimen report (see “[Printing a Standard or Custom Report Based on the Records in a Record Listing Screen](#)” in Chapter 14) that includes Loan information and lists all Specimen records in the Loan (below).

Birds of the Galápagos Islands Specimen Loan		Charles Robert Darwin Down House Leeds Road Bramley, Kent United Kingdom Voice Phone 1: [Unlisted] E-Mail Address: cdarwin@bigcatsplanet.uk	Loan Code NHM0051	P. L. Sclater Cromwell Road The Natural History Museum London SW7 5BD United Kingdom	Voice Phone 2: +44 (0)20 7942 5000 E-Mail Address: sclater@nhm.ac.uk																																																																																																																																																																																																																																																																																																																																																																																																																			
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Code</th> <th>Method</th> <th>Date Coll.</th> <th>Locality</th> <th>Source</th> <th>X</th> <th>Y</th> <th>Stage/Sex</th> <th>No.</th> <th>Medium</th> <th>Deposited</th> </tr> </thead> <tbody> <tr> <td>Class Aves</td> <td></td> </tr> <tr> <td>Order Passeriformes</td> <td></td> </tr> <tr> <td>Family Fringillidae</td> <td></td> </tr> <tr> <td>Genus <i>Cactospiza</i></td> <td></td> </tr> <tr> <td><i>bebbiae</i></td> <td></td> <td></td> <td></td> <td></td> <td>(Species Code: cactbebb)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>HMS8013</td> <td>RF003</td> <td></td> <td>Shalquin Sep 30, 1832</td> <td>Fernandina Island</td> <td></td> <td>0</td> <td>0</td> <td></td> <td>1</td> <td></td> <td>NHM0051</td> </tr> <tr> <td><i>pallida</i></td> <td></td> <td></td> <td></td> <td></td> <td>(Species Code: cactpall)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>HMS8014</td> <td>CD004</td> <td></td> <td>Shalquin Oct 9, 1832</td> <td>Santiago Island</td> <td></td> <td>0</td> <td>0</td> <td></td> <td>1</td> <td></td> <td>NHM0051</td> </tr> <tr> <td>Genus <i>Camarhynchus</i></td> <td></td> </tr> <tr> <td><i>parvulus</i></td> <td></td> <td></td> <td></td> <td></td> <td>(Species Code: camapary)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>HMS8008</td> <td>CD002</td> <td></td> <td>Shalquin Sep 24, 1832</td> <td>Floreana Island</td> <td></td> <td>0</td> <td>0</td> <td>Female</td> <td>1</td> <td></td> <td>NHM0051</td> </tr> <tr> <td>HMS8017</td> <td>CD004</td> <td></td> <td>Shalquin Oct 9, 1832</td> <td>Santiago Island</td> <td></td> <td>0</td> <td>0</td> <td>Male</td> <td>1</td> <td></td> <td>NHM0051</td> </tr> <tr> <td><i>caeruleopectus</i></td> <td></td> <td></td> <td></td> <td></td> <td>(Species Code: camapaup)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>HMS8007</td> <td>CD002</td> <td></td> <td>Shalquin Sep 24, 1832</td> <td>Floreana 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- ◊ If you click the “Export the Specimen list to a text file” checkbox, Biota presents the Export Specimen Flatfile tool. See “[Exporting Specimen Flatfiles](#)” in Chapter 27 for instructions on using this tool. The text Specimen flatfile exported for the Specimen records in the Loan includes a special header with Loan information.

The exported Specimen flatfile can include virtually any selection of fields from the Core tables that you wish, allowing you to provide the Borrower with a complete archival electronic record of the loan (with or without a printed version).

If the Borrower determines specimens in the Loan, he or she can add the new determination to the same text file and return it to you for updating the Specimen records, using the “Update records” option in the Import Editor (see “[Import Step 3: Set Up and Launch the Import or the Update](#)” in Chapter 28).

Displaying and Editing an Existing Loan

Records in the Loans table, like other Core tables in Biota, can be displayed in a Record Listing screen and grouped as Record Sets, and Record Sets can be saved as Record Set Pointer Files (see Chapter 3, “[Key Concepts](#)”). The commands “Display All Loans” and “Display Loan Record Set,” however, are located in the Loans menu, rather than the Find and Display menus, respectively, where the analogous commands for other Core tables can be found.

To display an existing Loan record, follow these steps:

- From the Loans menu, choose “Display All Loans.”** A list of all Loan records appears in the Loans Record Listing screen.

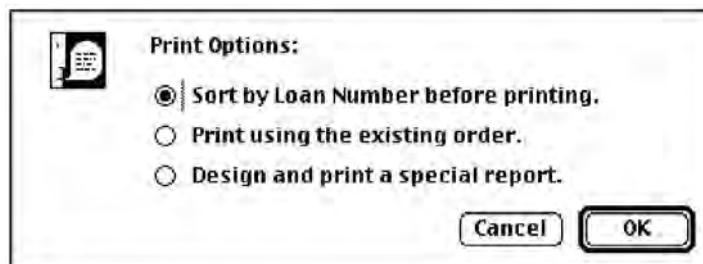
The screenshot shows a computer window titled "Loan Records". At the top, it says "Double Click a Loan to View It in the Loan Input Screen" and "15 Records". Below is a table with the following data:

Loan Code	Loan Date	Borrower	Last Name	Institution	Loan Period	Loaned	Returned
AgCan0073	Feb 16, 1994	E. Lindquist	Lindquist	Agriculture Canada	Indefinite	370	0
AgCan0079	Feb 16, 1994	Behan	Behan-Pelletier	Agriculture Canada	Indefinite	267	18
AMNH0038	Sep 3, 1993	Grimaldi	Grimaldi	American Museum of Natural	Indefinite	0	0
Anderson0249	Jan 26, 2002	R. S. Anderson	Anderson	Canadian Museum of Nature	6 months	0	4
Bergen0151	Sep 1, 1995	L. Kirkendall	Kirkendall	Univ. of Bergen	Indefinite	0	0
Bishop0030	Jul 25, 1993	L.W. Quate	Quate	Bishop Museum	Indefinite	0	0
BMNH0024	May 17, 1993	N. Stork	Stork	British Museum (Natural Histo	Indefinite	0	0
Bodner_Apr02	Apr 22, 2002	G. S. Bodner	Bodner	University of Arizona	One year	49	0
Furth_Nov02	Nov 11, 2002	D. Furth	Furth	Smithsonian	Indefinite	833	0
Hanson0278	Feb 18, 2001	P. Hanson	Hanson	Universidad de Costa Rica	One year	32	0
Hespeneide_Ago	Aug 16, 2002	HA Hespeneide	Hespeneide	University of California	Indefinite	265	3
Ibara0129	Feb 8, 1995	Kojima	Kojima	Ibaraki University	Indefinite	0	0
INBio0186	Mar 6, 1997	INBio	INBio	Instituto Nacional de Biodivers	Permanent	4066	400
JTLO218	Jan 27, 1999	J. Longino	Longino	The Evergreen State College	Indefinite	162	156
NHM0051	May 12, 2003	Natural History	Sclater	The Natural History Museum	Indefinite	16	0

Buttons at the bottom include: Sort, Print Loan List, Delete Selection, Sub-Selection, Done.

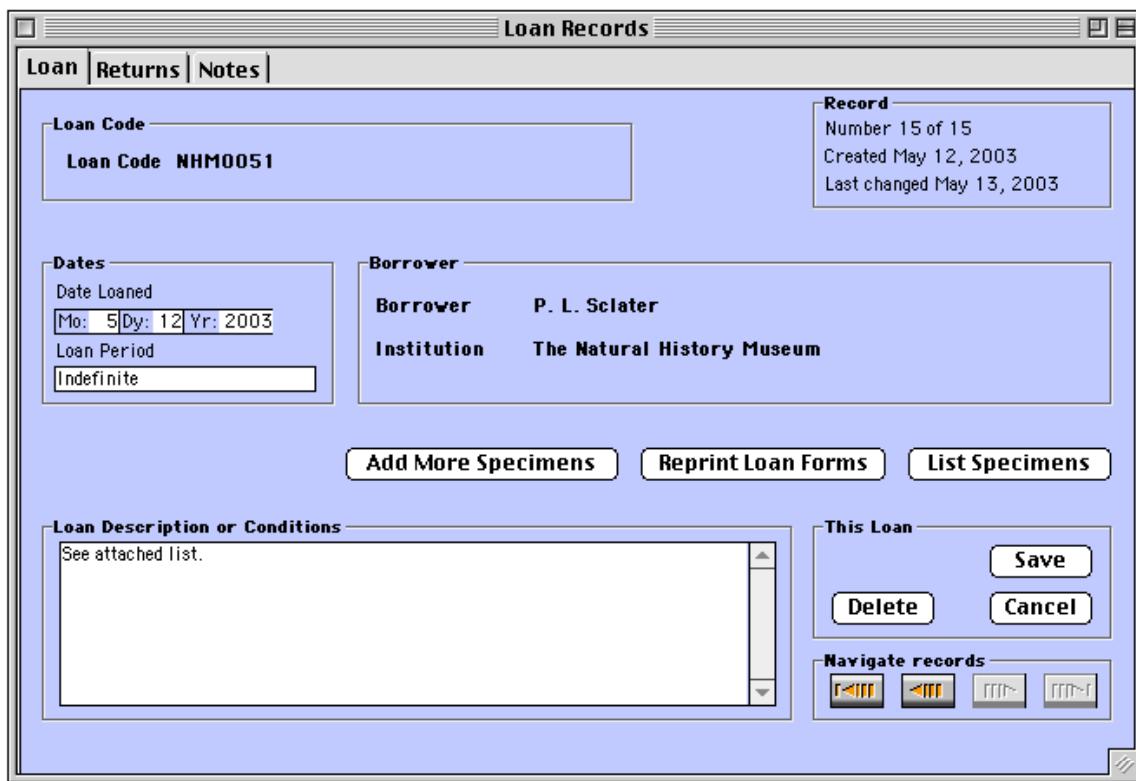
The Loans Record Listing screen differs from the standard Record Listing screens for other Core tables only in lacking a New Record button. (To create a new Loan record, choose New Loan from the Loans menu; see “[Recording a New Loan](#)” earlier in this chapter). The “Sort,” “Delete Selection,” and “Sub-Selection” buttons work in the same way as the analogous buttons for other Core tables (see Chapter 10, “[Working With Records in Record Listing and Input Screens](#).”).

- To print a list of the Loans displayed in the Record Listing screen,** click the “Print Loan List” button in the Record Listing screen, or select Print from the File menu while the screen is displayed. A print options window appears.



See Chapter 14, “[Printing Reports](#),” for help using these options.

3. To display an individual Loan record, double-click the record in the Record Listing screen. The record appears in a special version of the Loan Records Input screen.



This screen resembles the New Loan screen (see “[Recording a New Loan](#)” earlier in this chapter) but has a different set of tabs, buttons, and functions. This is the same screen used for recording Returns, by displaying the Returns tab (see “[Recording Specimen Returns](#),” later in this chapter).

In this screen you can edit the Date Loaned, Loan Period, Loan Description or Conditions, add a Loan Note, or add more specimens to the existing loan. You can also *manually* change the Number of Specimens Returned and Number of Specimens Loaned, if necessary, but these numbers are normally (and preferably) adjusted *automatically* when you record returns by the methods described in “[Recording Specimen Returns](#),” later in this chapter.

4. To add more Specimens to this Loan record, click the “Add More Specimens” button in the “Loan Records” screen (above). See the next section of this chapter, “[Adding More Specimens to an Existing Loan](#)” for details.
5. To display the Specimen records linked to this Loan record, click the “List Specimens” button in the screen above. The Specimen records are displayed in a special Specimen Record Listing screen entitled “Specimens in Loan.” (If the Loan is not linked to any Specimen records, a message appears, instead.)



Specimens in Loan

Loan Code NHM0051										16 Records	
Specimen Code	Genus	Species	Collection Code	Collector	Method	Stage/Sex	Host	Storage	Deposited		
HMSB001	Geospiza	fortis	CD001	C. Darwin	Shotgun				NHM0051		
HMSB002	Geospiza	fortis	RF001	R. Fitzroy	Shotgun				NHM0051		
HMSB003	Geospiza	fuliginosa	RF001	R. Fitzroy	Shotgun				NHM0051		
HMSB004	Geospiza	scandens	CD001	C. Darwin	Shotgun				NHM0051		
HMSB005	Geospiza	scandens	CD002	C. Darwin	Shotgun				NHM0051		
HMSB006	Camarhynchus	psittacula	CD002	C. Darwin	Shotgun				NHM0051		
HMSB007	Camarhynchus	pauper	CD002	C. Darwin	Shotgun				NHM0051		
HMSB008	Camarhynchus	parvulus	CD002	C. Darwin	Shotgun	Female			NHM0051		
HMSB009	Certhidea	olivacea	RF002	R. Fitzroy	Shotgun				NHM0051		
HMSB011	Geospiza	fortis	CD003	C. Darwin	Shotgun				NHM0051		
HMSB012	Geospiza	difficilis	CD003	C. Darwin	Shotgun				NHM0051		
HMSB013	Cactospiza	hellobates	RF003	R. Fitzroy	Shotgun				NHM0051		
HMSB014	Cactospiza	pallida	CD004	C. Darwin	Shotgun				NHM0051		
HMSB015	Certhidea	olivacea	CD004	C. Darwin	Shotgun				NHM0051		
HMSB016	Geospiza	difficilis	CD004	C. Darwin	Shotgun				NHM0051		
HMSB017	Camarhynchus	parvulus	CD004	C. Darwin	Shotgun	Male			NHM0051		

Double Click a Specimen to View or Modify Record
Resize Columns in the Header

Sort **Reprint Loan Forms**

Returns **Sub-Selection** **Done**

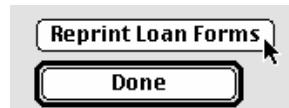
This screen has two special buttons, “Returns” (see “[Recording Specimen Returns](#)” later in this chapter) and “Reprint Loan Forms” (see the next step).

NOTE: If you wish, you can re-size the columns in the “Specimens in Loan” Record Listing screen (above) by dragging the column dividers in the header area. The cursor changes to a “splitter” icon.

Loan Code NHM0051

Specimen Code	<input type="button" value=""/>	Genus
---------------	---------------------------------	-------

- To reprint the Loan Invoice, reprint the list of Specimens in the Loan, or export a text file for the Specimen records in the Loan:
 - Either:** Click the “Reprint Loan Forms” button in the Loan Records Input screen.
 - Or:** Click the “Reprint Loan Forms” button in the Specimens in Loan Record Listing screen.
 Biota offers the same sequence of options and functions available for New Loans (see “[Previewing, Printing, and Exporting Loan Records](#)” earlier in this chapter for examples).
- If you clicked either “Reprint Loan” button, please continue with “[Previewing, Printing, and Exporting Loan Records](#)” earlier in this chapter.



Adding More Specimens to an Existing Loan

If you wish, you can incorporate additional Specimens in an existing Loan. This capability can be useful when you are preparing a complicated or extensive Loan over several Biota sessions and need to save your progress in the meantime.

- 1. Display the existing Loan record**, following the instructions in the section “[Displaying and Editing an Existing Loan](#)” earlier in this chapter.
- 2. To add more Specimens to the Loan record**, click the “Add More Specimens” button in the “Loan Records” screen. The “Loan Records” screen is replaced by a special version of the New Loan screen, with the special title “Add More Specimens to the Loan.”



Using this screen, you can incorporate additional Specimens into the existing Loan, using all the tools described in the section “[Recording a New Loan](#)” earlier in this chapter.

Note: The Loan Code and Borrower fields of the Loan record are not editable in the “Add More Specimens to the Loan” screen (above). Once a Loan record has been saved, these fields are protected from alteration, by design.

Recording Specimen Returns

Biota offers three alternative methods of recording the return of physical specimens represented by Specimen records in the Data File.

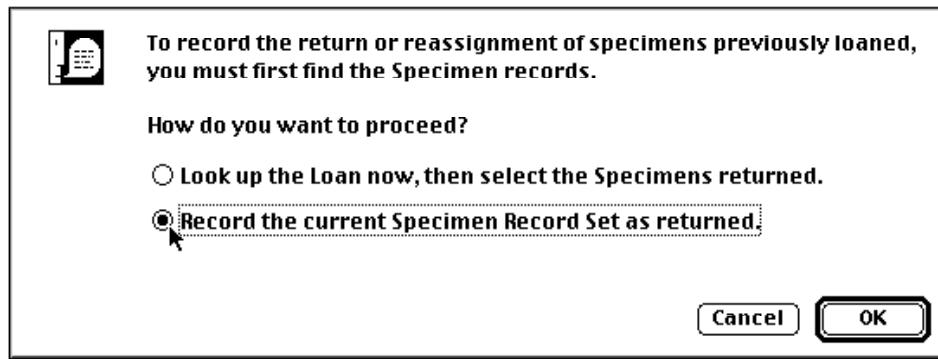
Using the Specimen Record Set to Record Returns

This is usually the most efficient method when a set of returned specimens represents several different Loan records. For example, you may have made several Loans to the same individual or institution, who then returns some or all of the specimens, determined and sorted by species, but each conspecific group is a mixture of specimens from several Loans.

1. **Gather the Specimen records for the returned specimens** using any of the tools in the Find or Series menus (see Chapter 12, “[Finding and Updating Records](#)”).

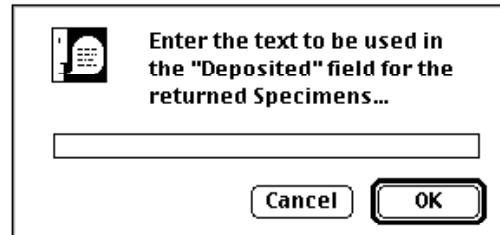
Probably the most useful tool for this purpose, especially when the specimens have barcodes, is the “Find Specimen Series” tool (Series menu; the same tool is called “By Specimen Code Series” in the Find menu). Use this tool with the “In any order” option and the “Auto Accept” button enabled. See “[Creating, Finding, and Updating Specimen Series](#)” in Chapter 13.

2. **Declare the Specimen records to be the current Specimen Record Set** (see “[The Record Set Options Screen](#)” in Chapter 3).
3. **From the Loans menu, select “Record Returns.”** The Loan returns option screen appears.



4. **Choose the second option, “Record the current Specimen Record Set as returned,”** then click the “OK” button in the option window. (If the Specimen Record Set is empty, this option is disabled and the window displays a help message; see [Step 1](#) in the next section, for an illustration.)

A window appears requesting a value to be entered in the “Deposited” field of the Specimen records returned.



Note: If the Specimen Record Set is empty, the second option is disabled and the window displays a help message.

- Look up the Loan now, then select the Specimens returned.**

- Record the current Specimen Record Set as returned.

There are no records in Specimen Record Set. Use tools from the Series or Find menu to gather the records to be registered as returned. Find Specimen Series is especially useful.

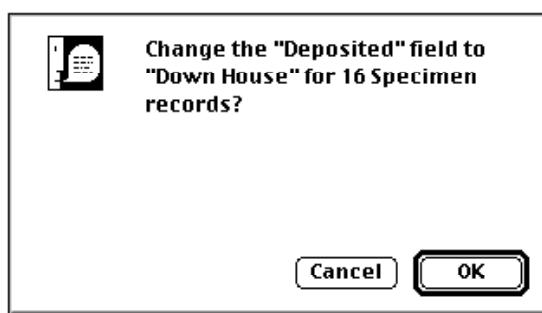
Cancel **OK**

5. Type in the value and click OK.



- **If you are recording returns to your own collection,** you would normally enter its code or name.
- **If you are recording the return of specimens loaned to you,** you would normally enter the code or name for the collection to which they have been returned.

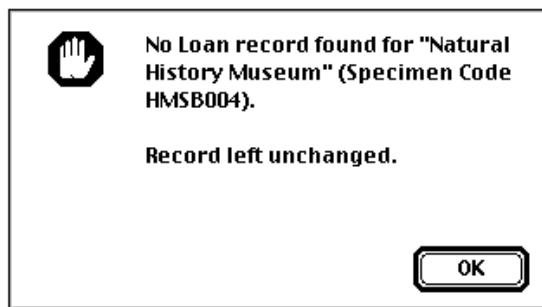
A confirmation message appears.



6. Click the “OK” button to confirm the changes, or Cancel to leave the records unchanged.

- **If you click OK,** Biota makes the changes in the Specimen records.

- If any of the Specimen records in the Record Set are not part of an existing Loan, Biota posts a message, for each such record.



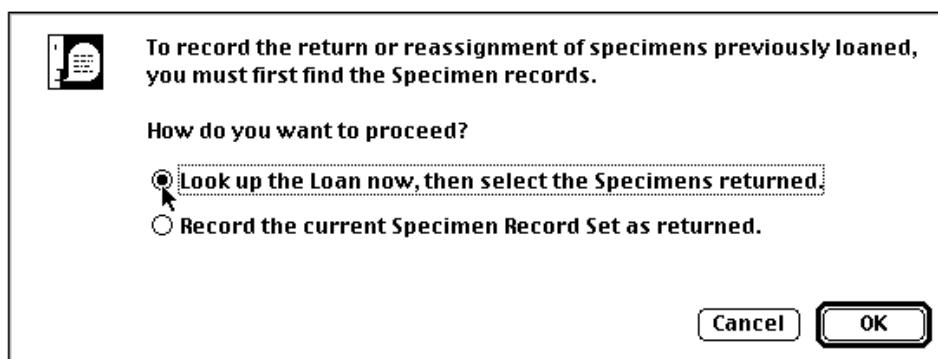
All records in the Record Set are then displayed in the Specimen Record Listing screen, whether changed or not.

NOTE: When you use this method to record Returns, the “Number Returned” field in the Loan record for each Loan involved in the return is automatically updated to reflect the number of specimens returned.

Two Ways to Use the Loan Records Screens to Record Returns

With either of the methods described in this section, you record returns of specimens from one Loan at time. If you need to record returned specimens mixed from several Loans, see “[Using the Specimen Record Set to Record Returns](#)” earlier in this chapter.

1. From the Loans menu, select “Record Returns.” The Loan Returns option screen appears.



NOTE: If the Specimen Record Set is empty, the second option is disabled and the window displays a help message, which you may ignore, for this method.

Look up the Loan now, then select the Specimens returned.

Record the current Specimen Record Set as returned.

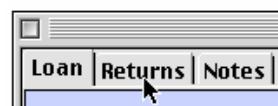
There are no records in Specimen Record Set. Use tools from the Series or Find menu to gather the records to be registered as returned. Find Specimen Series is especially useful.

Cancel

OK

2. Choose the first (default) option, “Look up the Loan now, then select the Specimens returned,” then click the “OK” button in the option window.
The Loans Record Listing screen appears, showing all Loan records.
3. Double-click the Loan record for which you need to record returns (above).
The Loan record appears in the Loan Records Input screen.

4. Click the Returns tab.



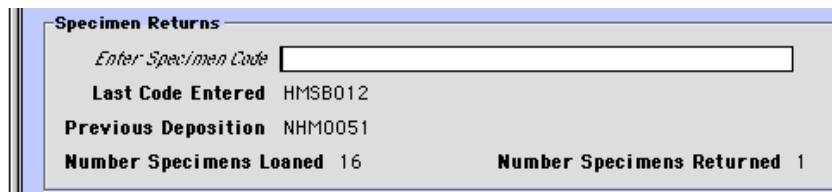
The Returns screen appears.

5. To record returns by Specimen Code:

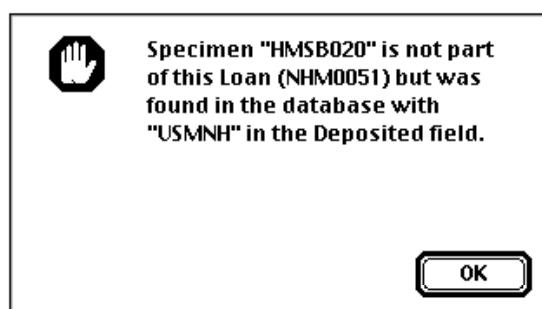
- Enter the Specimen Code for a returned specimen in the “Enter Specimen Code” area of the Returns screen.**

- Press TAB.** (If you are using a barcode reader and Specimen barcodes, and the reader is set to enter an end-of-line character automatically after each read, this step is not necessary.)

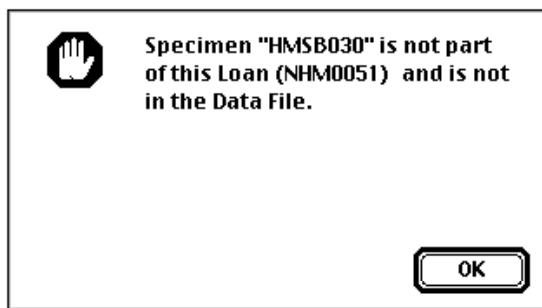
- ◊ If Biota determines that the Specimen Code is linked to this Loan record, the Specimen Code appears in the Last Code Entered display area, and the Enter Specimen Code area is cleared for the next Specimen Code. The Number Returned field is incremented by 1.



- ◊ If Biota finds the Specimen Code, but it is not linked to this Loan, the message below appears. The Specimen Code may be linked to a different Loan record, or to no Loan record.

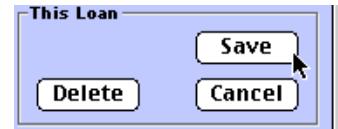


- ◊ If Biota determines that the Specimen record is not in the Data File, the message below appears.



- c. Enter the remaining Specimen Codes for the returned specimens in the same way.
- d. Click the “Save” button in the Loan Records Input screen.

A window appears requesting a value to be entered in the Deposited field of the Specimen records returned.





- e. Go to [Step 6](#), below.
6. To record returns by selecting them from a list of Specimen records:

- a. Click the “List Specimens” button in the Loan tab of the Loan Records Input screen.

The Specimen records will be displayed in the “Specimens in Loan” Record Listing screen. (If the Loan is not linked to any Specimen records, a message will inform you.)



- b. Select from the list all records for the returned Specimens, using the mouse (see “[Creating a Sub-Selection of Records](#)” in Chapter 10, for selection techniques).

Specimens in Loan

Loan Code **NHM0051**

17 Records

Specimen Code	Genus	Species	Collection Code	Collector	Method	Stage/Sex	Host	Storage	Deposited
HMSB001	Geospiza	fortis	CD001	C. Darwin	Shotgun				NHM0051
HMSB002	Geospiza	fortis	RF001	R. Fitzroy	Shotgun				NHM0051
HMSB003	Geospiza	fuliginosa	RF001	R. Fitzroy	Shotgun				NHM0051
HMSB004	Geospiza	scandens	CD001	C. Darwin	Shotgun				NHM0051
HMSB005	Geospiza	scandens	CD002	C. Darwin	Shotgun				NHM0051
HMSB006	Camarhynchus	psittacula	CD002	C. Darwin	Shotgun				NHM0051
HMSB007	Camarhynchus	pauper	CD002	C. Darwin	Shotgun				NHM0051
HMSB008	Camarhynchus	parvulus	CD002	C. Darwin	Shotgun	Female			NHM0051
HMSB009	Certhidea	olivacea	RF002	R. Fitzroy	Shotgun				NHM0051
HMSB010	Geospiza	magnirostris	CD003	C. Darwin	Shotgun				NHM0051
HMSB011	Geospiza	fortis	CD003	C. Darwin	Shotgun				NHM0051
HMSB012	Geospiza	difficilis	CD003	C. Darwin	Shotgun				NHM0051
HMSB013	Cactospiza	heliobates	RF003	R. Fitzroy	Shotgun				NHM0051
HMSB014	Cactospiza	pallida	CD004	C. Darwin	Shotgun				NHM0051
HMSB015	Certhidea	olivacea	CD004	C. Darwin	Shotgun				NHM0051
HMSB016	Geospiza	difficilis	CD004	C. Darwin	Shotgun				NHM0051
HMSB017	Camarhynchus	parvulus	CD004	C. Darwin	Shotgun	Male			NHM0051

Double Click a Specimen to View or Modify Record

Resize Columns in the Header

Sort Reprint Loan Forms

Returns Sub-Selection Done

- c. Click the “Returns” button at the bottom of the “Specimens in Loan” screen (shown above).

A window appears requesting a value to be entered in the Deposited field of the Specimen records returned.



NOTES:

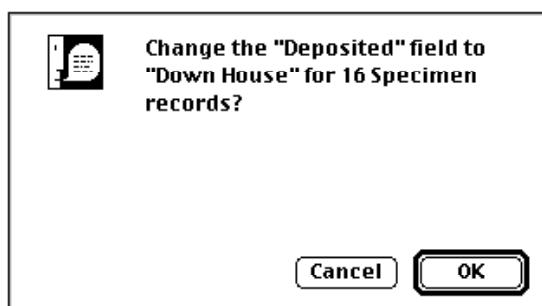
- a. You can select a few Specimen records at a time, then click the "Returns" button for each group, if more convenient. Each time, you will need to fill in the request window, above.
 - b. As with all methods for recording Returns, when you use this method the "Number Returned" field in the Loan record for each Loan involved in the return is automatically updated to reflect the number of specimens returned.
-

7. Type in the value for the Deposited field.



- **If you are recording returns to your own collection,** you would normally enter its code or name.
- **If you are recording the return of specimens loaned to you,** you would normally enter the code or name for the collection to which they have been returned.

A confirmation message appears.



8. Click the “OK” button to confirm the changes, or Cancel to leave the records unchanged. When you click OK, Biota makes the changes in the Specimen records and displays them again in the Specimens in Loan Record Listing screen.
9. Click the “Done” button in the “Specimens in Loan” Record Listing screen. The Record Set Options screen appears (see “[The Record Set Options Screen](#)” in Chapter 3).
10. Select a Record Set Option and click the “OK” button. The “Loan Records” Record Listing screen reappears. (It has been open all along, but hidden by the “Specimens in Loan” screen.) The “Loan Records” screen allows you to work with another Loan now, if you wish.
11. When you are through, click the “Done” button in the “Loan Records” screen and choose a Record Set option for the Loans records displayed.



Chapter 22

Determination Histories

In the management of biological collections and in systematic revisions, the determination of individual specimens often changes as knowledge increases, nomenclature is corrected, or opinions shift. Botanists often record such changes right on the herbarium sheet, vertebrate biologists annotate tags or add secondary tags, whereas entomologists generally update determinations by adding secondary labels to specimens.

In biotic surveys and inventories, information on the taxonomic identity of a specimen is useful even when imprecise. A trained non-specialist assistant can correctly identify most insects to order or family, for example. (See Chapter 25, “[Temporary Taxa for Approximate Determinations](#).”) A specialist may at first determine the same specimens to genus, and later determine some of the same specimens to species while others await description as types for new taxa.

If you enable the Determination History system (see “[Enabling or Disabling the Determination History System](#)” later in this chapter), Biota keeps track of all sources of change in specimen determination automatically.

Determination History Records

Determination History records have a child-parent (many-to-one) relation with Specimen records (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). Each Determination History record (in the Determination History table) records the following information:

- **The Specimen Code field of the parent record** (the linking field for the child-parent relation between a Determination History table and the Specimen table). If you change the parent record’s Specimen Code, this field in the Determination History table is automatically updated to keep the records linked.
- **The Determined By and Date Determined fields of the parent Specimen record**, at the time the determination change was recorded in the Determination History record.
- **The Species Code, Species Name, and Species Author fields of the Species record** to which the Specimen record was linked at the time of the determination change was recorded in the Determination History record.
- **The Genus field of the Genus record** to which the Species record was linked, at the time of the determination change was recorded in the Determination History record.
- **A record of who entered the change** (the Changed By field of the Determination History table). The person entering the change may or may not be the same person who changed the determination. This entry is made automatically based on who signed on when Biota was launched. If the User Password system has not been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#).”) Biota records “Administrator” in the Changed By field of the Determination History record.

NOTE: If it is important to know who entered each change in Specimen determination, be sure to set up sign-on names and passwords for each user, with appropriate privileges (see Chapter 26, “[Security: Passwords and Access Privileges](#)”).

- **The date the change was entered** (the Date Changed field of the Determination History table), entered automatically from the computer’s internal clock.
- **A record of where the change was made.** (See “[How and When Changes in Determination Are Recorded](#),” later in this chapter, for details.)
 - ◊ **In an individual Specimen record**, by changing the Species Code linking field of the Specimen record.
 - ◊ **In a series of Specimen records**, by changing the Species Code linking field of several Specimen records by means of the “Find and Identify Specimen Series” tool (see “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13).
 - ◊ **In the linked Species record**, by changing the Species Name field, the Species Author field, or the [Species] Genus linking field, then choosing to update linked Specimen records (see “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12).
 - ◊ **In the linked Genus record**, by changing the [Genus] Genus field and choosing to update linked Species records (see “[Automatically Updating Child Records by Changing a Parent Record](#)” in Chapter 12).
 - ◊ **In the Synonymy screen**, by reassigning Specimen records to a Species that has been declared a senior synonym (see Chapter 23, “[Synonymy System](#)”).
- **The Sequence Number of the record** in the Determination History table. The only purpose for this field is to sort the records in the reverse order they were created (see illustrations below).

NOTE: The sequence number is the number of records entered in the table since the Data File was created. The number increases by one every time a record is created, no matter how many records are later deleted. (The Date Changed field cannot be used to sort by entry order since more than one change can occur on the same date.)

Enabling or Disabling the Determination History System

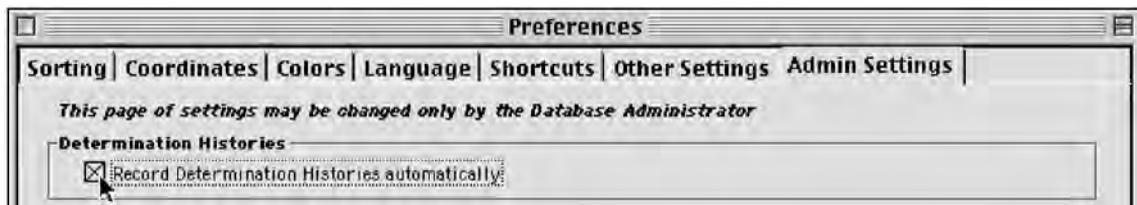
NOTE: If the User Password System has been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), you must have Administration access privileges to enable or disable the Determination History system.

1. **From the Special menu, select Preferences.**
2. **Click on the “Admin Settings” tab.**

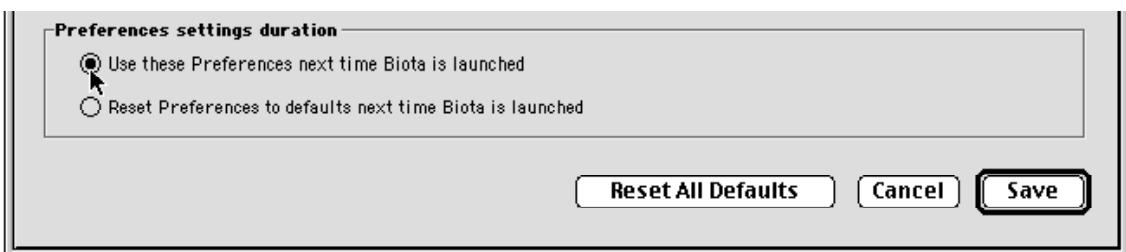


The Admin Settings tab screen appears.

3. **Check to enable, or uncheck to disable** the option “Record Determination Histories automatically.”



4. **Choose an option for saving any changes** in Preference settings made during this Biota session.



- **If you want the changes to remain in force until altered** regardless of how many times Biota is launched in the meantime, choose the option “Use these Preferences next time Biota is launched.”
- **If you want the changes to be in force only for this session**, choose the option “Reset Preferences to defaults next time Biota is launched.”

The default setting for Determination Histories is unchecked (off).

5. Click the “Save” button on the Preferences screen.

Displaying the Determination History for a Specimen Record

You can display previously recorded Determination History records, whether or not the system is currently enabled (see “[Enabling or Disabling the Determination History System](#)” earlier in this chapter).

1. **Display a Specimen record in the Specimen Input screen** (see Chapter 10, “[Working With Records in Record Listing and Input Screens](#)”).
2. **Click the Determination tab.**



The Determination History tab screen for this Specimen appears, displaying a record of all previous determinations for this Specimen (in reverse chronological order, most recent to earliest). Each line (after the first) shows data from a separate record in the Determination History table.

In addition, the Determination tab screen has a data entry area for “Last Determined by” and “Date Last Determined.”

Species Code	Genus	Species	Sp. Author	Determined By	Date Detrmd.	Where	Date	By Whom
AL1248074	Steirodon	robertsorum	Emsley, 1970	P.Naskrecki	Jul 28, 1996	← Current Record		
AL1248074	Steirodon	sp. 2		P. Naskrecki	Oct 26, 1995	Species Rec	Jul 29, 1996	P. Naskrecki
AL1248074	cf. Lamprophy	sp. 2		P. Naskrecki	Oct 24, 1995	Species Rec	Oct 26, 1995	P. Naskrecki

- **The Determination History Record list has two groups of columns:**
 - ◊ **The “Historical Data” panel**, on the left, shows the history of changes in Species Code, Genus, Species (specific name), Author, Determined by, and Date Determined.
 - ◊ **The “Record Change Data” panel**, on the right, shows, for each line of Historical Data, the table in which the determination in the left panel was changed (Where), when the change was made (Date), and who made it (By Whom).
- *Keep in mind the convention used in this screen: “Record Change Data” in the right panel refers to changes made to the Historical Data on the same line in the left panel. See the historical summary for this Specimen record, below, for an illustration.*
- **The first data row of the screen**, labeled “Current Record” in the Record Change Date panel, is not a Determination History record. It shows fields from the parent Specimen record.
- **The rest of the data rows**, which are Determination History records, are listed from most recent to the earliest.

In the illustration above, the Determination History of Specimen INBIOCRI001248084 can be fully reconstructed, as follows:

- **On October 24, 1995**, the Specimen was tentatively identified as “cf. *Lamprophyllum* sp. 2” (Species Code AL1248074) by P. Naskrecki.
 - **On October 26, 1995**, Naskrecki determined the correct genus to be *Steirodon*. He himself entered this information in Genus field in the Species record (Species Code AL1248074) on the same date (shown on the *last* line of the display in the Record Change Date panel).
 - **On July 28, 1996**, Naskrecki updated the determination again, by identifying the species as *Steirodon robertsorum* Emsley, 1970. On July 29, 1996, R. Colwell entered this change in the Species record, replacing “sp. 2” in the Species Name field with Naskrecki’s definitive determination, “*robertsorum*,” adding the Author (and date), “Emsley, 1970.”
3. **To display an individual Determination History record**, double-click the row. (Clicking the Current Record row has no effect.)

The record appears in a special, read-only Determination History Input screen. You can use the navigation buttons to look at the sequence of Determination History records for this Specimen.

In the illustration, for example, “cf. *Lamprophyllum*” is too long to fit in the Genus column of the Determination listing pane, but can be read in the Input screen.

Specimen Record

Specimen Code: INBIOCRI001248084
Steirodon robertsorum Emsley, 1970

Species Code	AL1248074
Genus	cf. <i>Lamprophyllum</i>
Specific Name	sp. 2
Species Author	
Subspecific Name	
Subspecies Author	
Variety	
Variety Author	
Determined By	P. Naskrecki
Date Determined	Mo 10 Dy: 24 Yr: 1995
Where Changed	Species Rec
Date Changed	Mo 10 Dy: 26 Yr: 1995
Changed By	P. Naskrecki
Sequence Number	0

This Det History record

Save Delete Cancel

Navigate records

NOTE: If you need to edit or delete a Determination History record, you must do so using commands from the Special menu. See “Displaying, Editing, or Deleting Determination History Records,” later in this chapter.

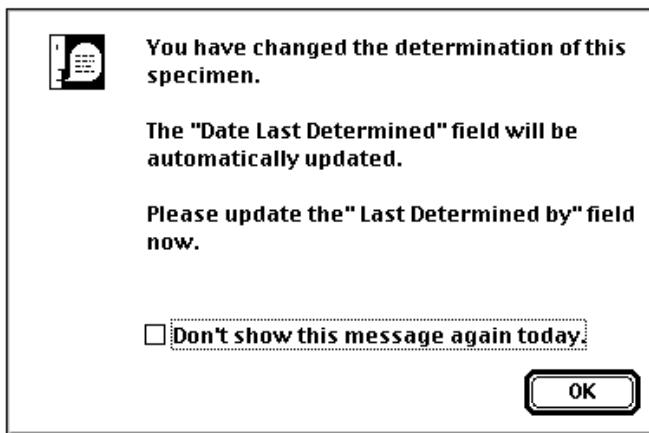
How and When Changes in Determination Are Recorded

Because Biota is a relational database, it records changes in Specimen determination made not only in Specimen records but also in the parent Species and Genus records.

Changing a Determination in an Individual Specimen Record

Make sure you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#),” earlier in this chapter).

1. **Display the existing Specimen record** in the Specimen Input screen (see “[Viewing, Editing, Printing, or Deleting Individual Records from an Input Screen](#)” in Chapter 10).
2. **Change the existing Species Code in the Specimen record to a new value.** See “[Entering Specimen Data: The ‘General’ Tab](#)” in Chapter 11 for help in finding and entering a Species Code in a Specimen record.
 - **Biota enters today’s date automatically** in the Date Last Determined area. You can change the date if necessary. (See “[Entering Specimen Data: The ‘Determination’ Tab](#)” in Chapter 11.)
 - **Biota prompts you to enter a new value for “Last Determined by.”**



When you click the “OK” button in this window, Biota highlights the “Last Determined by” entry area. If the new determination was made by the same person as the previous one, you need not make an entry. See “[Entering Specimen Data: The ‘Determination’ Tab](#)” in Chapter 11 for help in finding and entering a “Last Determined by” value.

If you don’t want Biota to remind you to update the “Last Determined by” field again during this session, check the “Don’t show me this message again today” box.

NOTE: If there was no previous Species Code entry in the Specimen record, no Determination History record is created when you enter one, and the window above does not appear.

3. Accept the revised Specimen record.

- If you did not update the “Last Determined by” area after changing the determination, Biota prompts you again.



- If you updated the “Last Determined by” area or you click OK in the window above, Biota creates a linked record automatically in the Determination History based on information from the *old* Specimen determination. The new information then replaces the old in the Specimen record.

4. To check that the Determination History record was created, re-display the Specimen record in the Input screen and click the Determination History tab

The “Where Changed” field for the new Determination History record will now read “Spcmn Rec,” to indicate where the change was made.

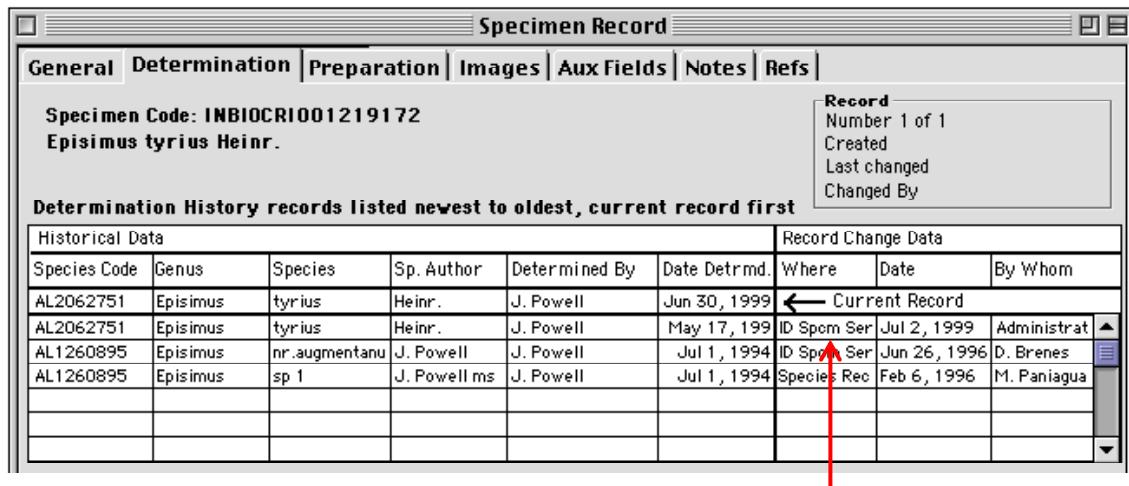
Changing a Determination in a Specimen Record Series

Changing the determination for groups of specimens efficiently is the special function of the “Find and Identify Specimen Series” tool. The group of specimens may have sequential or non-sequential Specimen Codes. See “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13.

Make sure you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#)” earlier in this chapter).

1. From the Series menu, choose “Find and Identify Specimen Series.” Following the instructions in “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” (Chapter 13), set up the screen to find a group of Specimen records.
2. Set up the Species Code for the new determination. Follow the instructions in “[Changing a Determination in an Individual Specimen Record](#),” earlier in this chapter.
3. Accept the revisions to the Specimen series. Biota automatically creates a Determination History record for each Specimen record in the Series.
4. To check that the Determination History records were created:
 - a. Click the “Cancel” button in the “Find and Identify Specimen Series” screen to dismiss it.

- b. Display a Specimen record in the Input screen and click the Determination tab.



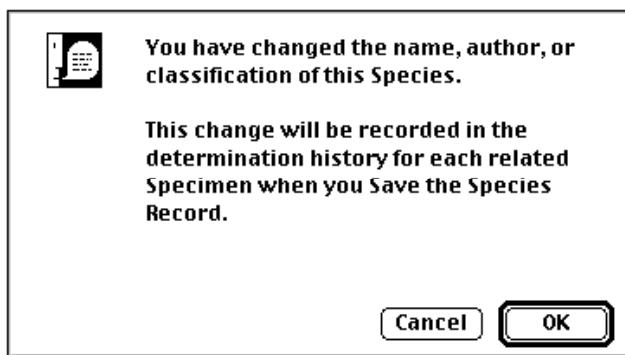
The “Where Changed” field for the new Determination History record will read “ID Spcm Ser,” to indicate where the change was made.

Changing a Determination in a Species Record

If you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#)” earlier in this chapter), any of the following changes in an existing Species record generates a new Determination History record for all linked Specimen records:

- **Changing the Species Code.**
- **Changing the Genus field.** (Changing the Genus field in a Genus record also generates a Determination History record. See “[Changing a Determination in a Genus Record](#)” later in this chapter.)
- **Changing the specific name (Species Name) or the Species Author field.**
- **Changing the Subspecies or the Subspecies Author field.**
- **Changing the Variety or the Variety Author field.**

Biota posts the following confirmation message:



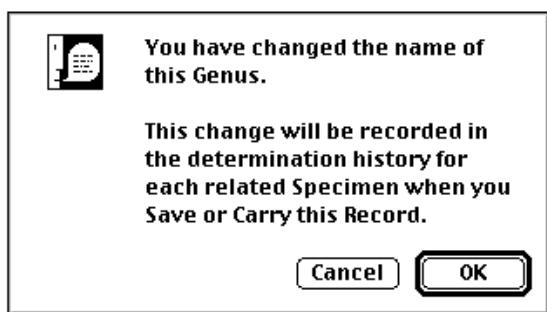
The “Where Changed” field in the Determination History record will read “Species Rec,” to indicate where the change was made.

Changing a Determination in a Genus Record

If you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#)” earlier in this chapter), the following action generates a Determination History record for each Specimen linked to a Genus record through any Species record:

- **Changing the Genus field in a Genus record.**

Biota posts a confirmation message:



After you click the “OK” button, the “Where Changed” field in the Determination History record will read “Genus Rec.”

Changing a Determination Using the Synonymy Tool

Using the Synonymy tool, you can automatically reassign Specimen records to a Species that has been declared a senior synonym (see Chapter 23, “[Synonymy System](#)”), unlinking those records from the junior synonym you specify.

If you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#)” earlier in this chapter), this action generates a Determination History record for each Specimen affected.

The “Where Changed” field in the Determination History record will read “Species Syn.”

Displaying, Editing, or Deleting Determination History Records

Generally, the purpose of Determination History records is to keep a complete “audit trail” for all actions that affect the identification of Specimen records, including errors and corrections of errors.

Nonetheless, circumstances may arise that require editing or deletion of Determination History records. This section describes the tools available in Biota for working with existing Determination History records directly. The creation of *new* Determination History records occurs only through the mechanisms described in the previous section.

NOTE: If the User Password system has been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), you must have Administration access privileges to use the tools described in this section. If the User Password system has not been activated, any user will have Administration privileges, by default, and may use these tools.

- **To display all Determination History records,** choose “All Determination Histories” from the Special menu.
- **To display the Determination History records linked to the Specimen records in the active Specimen Record Set,** choose “Determination Histories for the Specimen Record Set” from the Special menu (abbreviated “Det Hists for the Spcm Rec Set” in the menu).



In either case, the records are displayed in a standard Biota Record Listing screen, with columns arranged in the same way as in the special Determination History Record Listing screen used to display Determination History records for an individual Specimen Record.

DetHistory Records

Double click a DetHistory to view or modify record

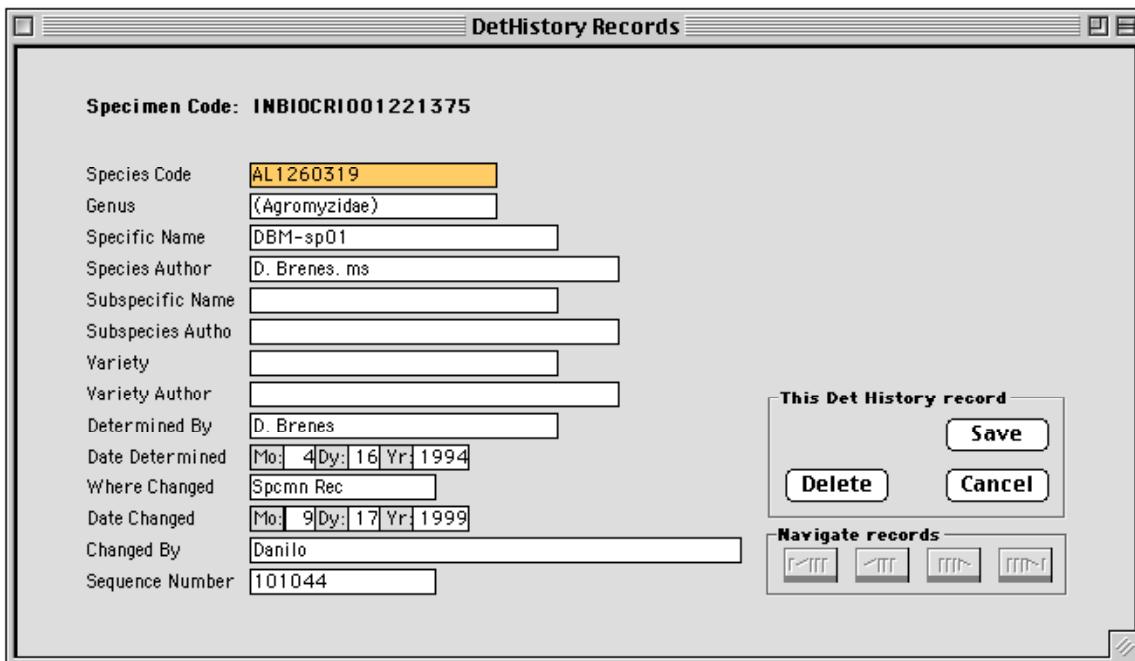
17 Records

Historical Data							Record Change Data		
Specimen Code	Species Code	Genus	Species	Sp. Author	Det. By	Date Detrmed.	Where	Date	By Whom
063716	AL1248087	Lamprophyll	bugabae	Hebard, 1927	D. Nickle	Nov 7, 1995	Species Re	Aug 20, 1999	Administrator
063717	AL1247952	Vallea	orienta	(Burmeister, 1	P. Naskeoki	Nov 8, 1995	Species Re	Nov 9, 1995	P. Naskeoki
ALAS201923	AL012319	Acrochaeta	sp		W.U.Hanson	1989	Species Re	Nov 29, 2000	Danilo
ALAS201924	AL012220	Merosargus	banksii	Janzen	W.U.Hanson		Species Re	Oct 13, 1999	Administrator
ALAS201925	AL012321	Merosargus	brunnipes	McFad.	W.U.Hanson		Species Re	Oct 13, 1999	Administrator
ALAS201940	AL012336	Sargus	fasciatus	Fab	W.U.Hanson	1989	Species Re	Nov 29, 2000	Danilo
INBICR1001236420	AL1261687	(Gelechia)	sp 5	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	May 23, 199	Ronald
INBICR1001236422	AL1261885	(Bonkleta)	sp 8	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	May 22, 199	Maylin
INBICR1001236428	AL1261882	"Goniostiza"	sp 5	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	Jan 24, 1999	Tack
INBICR1001236429	AL1261655	"Dichomeris	sp 23	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	Sep 11, 1996	Administrator
INBICR1001236432	AL1261790	(Stenoma)	sp 5	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	Jun 3, 1996	Danilo
INBICR1001236456	AL1261681	(Anacampsis)	sp 24	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	May 23, 199	Ronald
INBICR1001236456	AL1261681	"Anacampsi	sp 24	J. Powell ms.	J. Powell	Jul 1, 1994	Genus Rec	Sep 11, 1996	Administrator
INBICR1001236461	AL1243091	Argyrtaeni	sp 001	J.Powell ms.	J. Powell	Jul 1, 1994	Species Re	Jul 1, 1999	Administrator
INBICR1002265971	AL2270660	Macroctptur	CP/MCD90		HA Hespenheide	Jul 1, 1997	Species Re	Jul 22, 1998	Danilo
INBICR1002265971	AL2270660	Macroctptur	CP/MCD90		HA Hespenheide	Jul 1, 1997	Species Re	Aug 5, 1998	Danilo
INBICR1002265985	AL1248088	Macroctptur	MCD98		HA Hespenheide	Jul 22, 1998	ID Spm Se	Jul 25, 1998	Danilo

Sort Print
Delete Selection Sub-Selection Done

The screen includes all the standard Record Listing screen buttons except for the “Add Record” button (see “[Using the Add Record Button](#)” in Chapter 10). You can Sort the records, Print them, Delete a Selection, or create a Sub-Selection.

- To display an individual Determination History record, double-click the record. The record appears in the Determination History Input screen.



In this screen, you can edit any field except Specimen Code. (Editing the Specimen Code field in a Determination History record could create an orphan Determination History record, an action that would render the record useless.)

- To create a Determination History Record Set or Record Set Pointer File, click the “Done” button in the Determination History Record Listing screen and choose an option in the standard Record Set option screen (see “[The Record Set Options Screen](#)” in Chapter 3).
- To display the current Determination History Record Set, choose “Display Determination Histories” from the Special menu.
- To Save or Load a Record Set Pointer File for Determination History records, use the appropriate command from the File menu. See the note below.
- To use the Query Editor to find Determination History records by their content, choose “Using the Query Editor” from the Find menu (see “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12). See the note below.

Note: If the User Password system has been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), the Determination History table is accessible to the “Save Record Set Pointer File” and “Load Record Set Pointer File” tools and the Query Editor only for users with Administration access privileges.

Importing and Exporting Determination History Records

Determination History records can be exported to text files using the “Export by Tables and Fields” tool from the Im/Export menu. There are no special considerations; just follow the general instructions in Chapter 27, “[Exporting Data by Tables and Fields](#).”

Determination History records can be imported from text files using the Import by Tables and Fields tool from the Im/Export menu. Be sure to consult the section “[Importing Data to Notes Tables or the Determination History Table](#)” in Chapter 28.

Chapter 23

Synonymy System

The Synonymy system can help you keep track of synonymies among Species records.

- **If your work is in systematics**, you can use the system to record historical synonymies from the literature. The same system is easily used in managing your own specimen data: you can update Species and linked Specimen records, in your own active database, when you conclude that two groups of specimens are conspecific. Biota keeps a record of the junior synonym by *synonymizing*—but retaining—its original Species record.

With your confirmation, Biota automatically switches the links for Specimen records from the junior synonym to the senior synonym. If you have activated the Determination History system (see “[Enabling or Disabling the Determination History System](#)” in Chapter 22), the switch is recorded for each Specimen.

- **In biotic surveys and inventories**, Biota’s Synonymy system can be used to resolve and document the “synonymies” that often arise in pooling two or more temporarily determined groups of Specimens, when each group was initially identified as representing a different Species (which may well have only a temporary name in the Species Name field; see Chapter 25, “[Temporary Taxa for Approximate Determinations](#)”).

If you determine that both groups of Specimens represent the same Species, the Synonymy system can “move” all Specimens from one of the two Species to the other instantaneously. If you have enabled the Determination History system (see “[Enabling or Disabling the Determination History System](#)” in Chapter 22), Biota documents the move for each Specimen affected.

Biota’s Synonymy system is not designed to handle all the complexities that arise under the rules of nomenclature, nor does Biota have an explicit system for synonymies at higher ranks. But it does well with the commonest case: simple synonymies at the Species level.

How Biota Keeps Track of Species Synonymies

Biota uses Species Codes to uniquely identify each record in the Species table (the section “[Why Does Biota Require Species Codes?](#)” in Chapter 8 explains how and why). In addition to the Species Code field, however, each Species record has a separate field called *Valid Sp Code* (for Valid Species Code; see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

In each new or imported Species record, the *Valid Sp Code* field is automatically initialized with the same value as the Species Code—each Species record thus begins life as a *valid Species record*, defined in Biota as any record in which the *Valid Sp Code* is the same as the Species Code.

When you *synonymize Species Z with Species Y*, Species Z becomes a *junior synonym record* and Species Y becomes the *senior synonym record*. Biota replaces the *Valid Sp Code* in the record for the junior synonym (Species Z) with the Species Code of the

senior synonym (Species Y). No change is made in the record of the senior synonym, which remains a valid Species record.

NOTE: Unfortunately there is no agreement between different Codes of Nomenclature regarding what to call Species Z and Y in the previous sentence. With apologies to those to whom these terms sound non-standard, this Manual uses them consistently in senses defined above.

Thus Biota recognizes junior synonyms by the presence of a Valid Sp Code that does not match the Species Code. Of course, the Valid Sp Code need not be unique; several Species records may share the same Valid Sp Code when there are several junior synonyms of the same senior synonym.

Biota recognizes senior synonyms by searching for junior synonyms—that is, searching for other Species records that carry the Species Code of the senior synonym in their Valid Sp Code field.

To summarize, there are three *proper* kinds of Species records, with regard to the Synonymy system:

- **Species X is a valid Species with no synonyms in the database** if its Valid Sp Code matches its own Species Code, but the Valid Sp Code of no other Species in the database matches Species X's Species Code.
- **Species Y is a valid Species and a senior synonym** if its Valid Sp Code matches its own Species Code, and the Valid Sp Code for at least one other Species in the database matches Species Y's Species Code.
- **Species Z is a junior synonym** if its Valid Sp Code does not match its own Species Code, but instead matches the Species Code of a valid Species in the database.

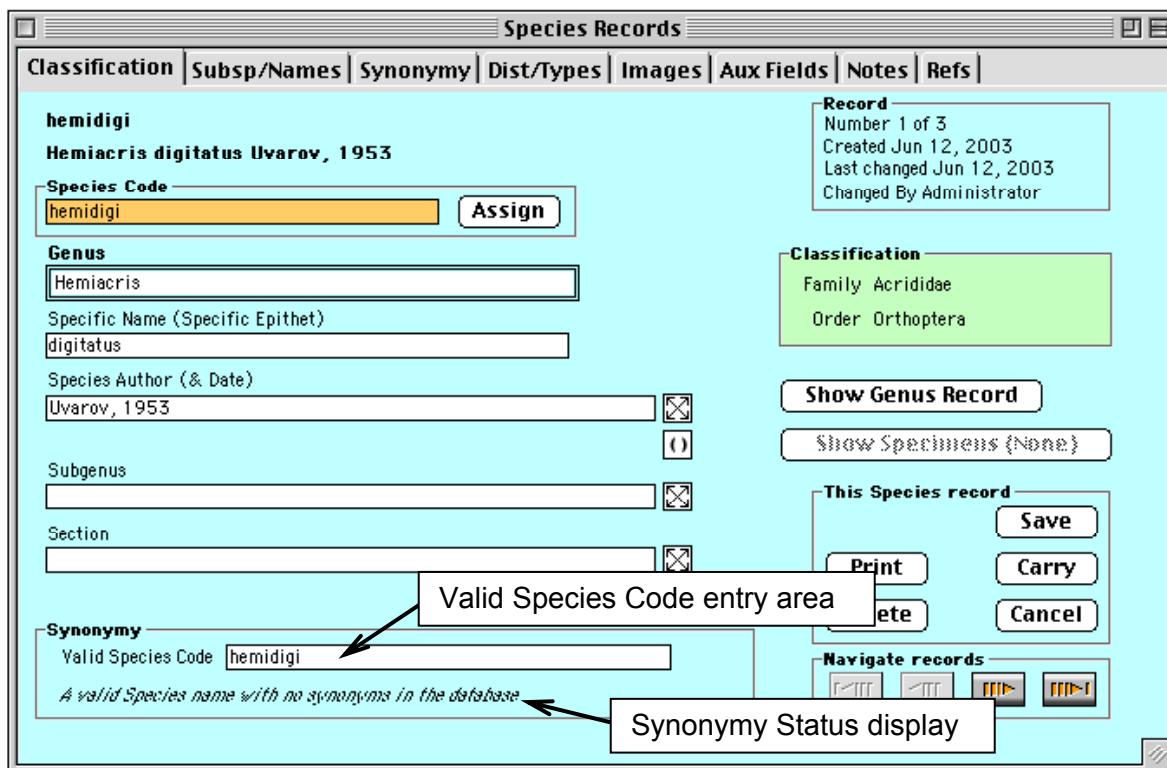
In addition, there are two *improper* kinds of Species records, with regard to the Synonymy system. Biota safeguards against the *inadvertent* creation of either of these categories of junior synonyms, while permitting you to do so *intentionally* anyway, if you wish.

- **Species A is an orphan junior synonym** if its Valid Sp Code matches neither its own Species Code nor the Species Code of any other Species in the database. When you change the Species Code of a senior synonym, the Valid Sp Code of all its junior synonyms is automatically updated to prevent this anomaly.
- **Species B is a compound junior synonym** if its Valid Sp Code does not match its own Species Code, but instead matches the Species Code of a junior synonym in the database. When you synonymize a Species record that was previously a senior synonym using the “Synonymize This Species” button, Biota automatically updates the Valid Sp Code of its former junior synonyms to the Species Code of the new senior synonym. If you wish to create compound synonyms, intentionally, to keep track of historical changes in nomenclature, you can do so by entering manual changes in Valid Sp Code.

Displaying the Synonymy Status of a Species Record

Each Species record falls into one of the five categories outlined in the previous section (“[How Biota Keeps Track of Species Synonyms](#)” earlier in this chapter). To display complete information for a Species record, follow these steps.

1. **Display the Species record** in the Species Input screen (see “[Viewing, Editing, Printing, or Deleting Individual Records from an Input Screen](#)” in Chapter 10).



The Classification (main) tab of the Species Input screen includes a “Synonymy” panel at the bottom of the screen that includes two elements:

- **The Valid Species Code entry area.** Although the Synonymy system normally takes care of assigning values to the Valid Sp Code field, you can change the value manually in this entry area if necessary (for example, to correct an orphan or compound synonym anomaly).
- **The Synonymy Status display.** This line summarizes the Synonymy Status of the Species record. The degree of detail depends on the setting of the “Show full Synonymy Status in Species Input screen” checkbox in the Preferences screen. See the section “[The Synonymy Status display](#)” later in this chapter.

2. To display full synonymy information for the current Species record, click the Synonymy tab in the Species Input screen.



The Synonymy tab screen appears.

The screenshot shows the Species Records window with the Synonymy tab selected. The main area displays the species name **hemidigi** and its authority **Hemiacris digitatus Uvarov, 1953**. A note below states "The name..." followed by the scientific name *Hemiacris digitatus*, author **Uvarov, 1953**, and species code **Sp. Code: hemidigi**. To the right, a "Record" box shows details: Number 1 of 3, Created Jun 12, 2003, Last changed Jun 12, 2003, and Changed By Administrator. Below this is a table with columns **Genus**, **Species**, **Author**, and **Species Code**. A note below the table says "Is a valid Species name with the following junior synonyms in the database." A checkbox next to this note is unchecked. Another checkbox below it, labeled "Is a junior synonym of...", is also unchecked. A third checkbox, labeled "Is a valid Species name with no synonyms in the database.", has a red arrow pointing to it and is checked. At the bottom are buttons for **Synonymize This Species**, **Accept New Synonymy**, and **Cancel New Synonymy**. On the right, there are buttons for **This Species record**: **Save**, **Print**, **Delete**, and **Cancel**. Below these are buttons for **Navigate records**.

The synonymy screen displays complete synonymy information for the Species. There are no data entry areas—the screen is used only for display and to create new synonymies using the “Synonymize This Species” button in the lower-left corner of the screen (see the section [“Declaring a Species Junior Synonym and Transferring Its Specimens,” later in this chapter](#)).

To indicate the Synonymy Status of the current Species record, a check appears next to one of the three alternatives, completing the statement:

“The name...” [Genus, Specific Name, Author, Species Code]...

- **“Is a valid Species name with no synonyms in the database.”** This alternative is illustrated above.

- “Is a valid Species name with the following junior synonyms in the database,” followed by a scrollable list of junior synonyms. This alternative is illustrated below.

Species Records

Classification Subsp/Names Synonymy Dist/Types Images Aux Fields Notes Refs																			
hemiferv Hemiacris fervens Walker, 1870 The name... <i>Hemiacris fervens</i> Walker, 1870 Sp. Code: hemiferv																			
<input checked="" type="checkbox"/> Is a valid Species name with the following junior synonyms in the database: <table border="1"> <thead> <tr> <th>Genus</th> <th>Species</th> <th>Author</th> <th>Species Code</th> </tr> </thead> <tbody> <tr> <td>Hemiacris</td> <td>femoralis</td> <td>Kirby, 1902</td> <td>hemifemo</td> </tr> <tr> <td>Hemiacris</td> <td>prognathica</td> <td>Uvarov, 1953</td> <td>hemiprog</td> </tr> <tr> <td>Phalinus</td> <td>Rehn, 1944</td> <td></td> <td>phalreli</td> </tr> </tbody> </table> <input type="checkbox"/> Is a junior synonym of...				Genus	Species	Author	Species Code	Hemiacris	femoralis	Kirby, 1902	hemifemo	Hemiacris	prognathica	Uvarov, 1953	hemiprog	Phalinus	Rehn, 1944		phalreli
Genus	Species	Author	Species Code																
Hemiacris	femoralis	Kirby, 1902	hemifemo																
Hemiacris	prognathica	Uvarov, 1953	hemiprog																
Phalinus	Rehn, 1944		phalreli																
<input type="checkbox"/> Is a valid Species name with no synonyms in the database.																			
<input type="button" value="Synonymize This Species"/>		<input type="button" value="Accept New Synonymy"/> <input type="button" value="Cancel New Synonymy"/>																	
This Species record <input type="button" value="Save"/> <input type="button" value="Print"/> <input type="button" value="Delete"/> <input type="button" value="Cancel"/> Navigate records 																			

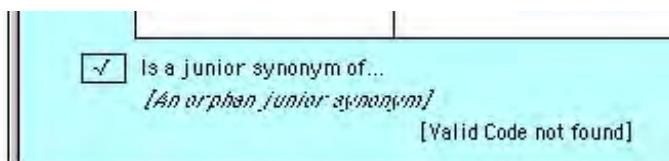
- “Is a junior synonym of...” [Genus, Specific Name, Author, Species Code]. This alternative is illustrated below for a proper junior synonym

Species Records

Classification Subsp/Names Synonymy Dist/Types Images Aux Fields Notes Refs											
hemiprog Hemiacris prognathica Uvarov, 1953 The name... <i>Hemiacris prognathica</i> Uvarov, 1953 Sp. Code: hemiprog											
<input type="checkbox"/> Is a valid Species name with the following junior synonyms in the database: <table border="1"> <thead> <tr> <th>Genus</th> <th>Species</th> <th>Author</th> <th>Species Code</th> </tr> </thead> <tbody> <tr> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table> <input checked="" type="checkbox"/> Is a junior synonym of...				Genus	Species	Author	Species Code				
Genus	Species	Author	Species Code								
<i>Hemiacris fervens</i> Walker, 1870 Sp. Code: hemiferv		<input type="button" value="Accept New Synonymy"/> <input type="button" value="Cancel New Synonymy"/>									
This Species record <input type="button" value="Save"/> <input type="button" value="Print"/> <input type="button" value="Delete"/> <input type="button" value="Cancel"/> Navigate records 											

The three alternatives correspond to the three *proper* forms of Synonymy Status, detailed the section “[How Biota Keeps Track of Species Synonymies](#),” earlier in this chapter. The next three steps explain what happens if a Species record falls into the *improper* categories of *orphan junior synonym* or *compound junior synonym*, or if it has compound junior synonyms linked to it.

3. If the Species is an **orphan junior synonym**, the junior synonym alternative is checked, but the message indicates orphan status.

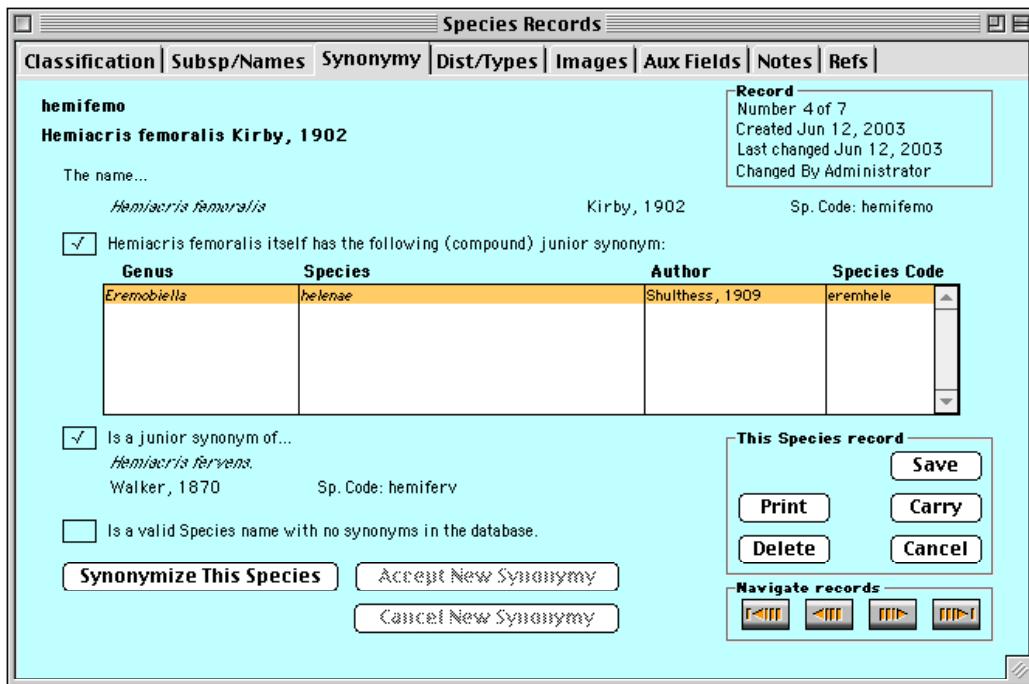


4. If the Species is a **compound junior synonym**, both the first and second checkboxes are checked. The first has the special legend “...which is itself a junior synonym of...” followed by the Valid Species Code for the record of which the current record is a junior synonym. The second checkbox legend details the Valid Species of which the “linking” species is a proper junior synonym.

Species Records

Species Records			
Classification	Subsp/Names	Synonymy	Dist/Types
eremhele Eremobiella helenae Shulthess, 1909			
The name... <i>Eremobiella helenae</i> Shulthess, 1909 Sp. Code: eremhele			
<input checked="" type="checkbox"/> ...which is itself a junior synonym of Species Code: hemiferv.			
Genus	Species	Author	Species Code
<input checked="" type="checkbox"/> Is a junior synonym of... <i>Hemacryia femoralis</i> . Kirby, 1902 Sp. Code: hemifemo			
<input type="checkbox"/> Is a valid Species name with no synonyms in the database.			
<input type="button" value="Synonymize This Species"/>		<input type="button" value="Accept New Synonymy"/> <input type="button" value="Cancel New Synonymy"/>	
This Species record <input type="button" value="Save"/> <input type="button" value="Print"/> <input type="button" value="Delete"/> <input type="button" value="Carry"/> <input type="button" value="Cancel"/>			
Navigate records <input type="button" value="First"/> <input type="button" value="Previous"/> <input type="button" value="Next"/> <input type="button" value="Last"/>			

5. If the Species itself is a proper junior synonym, but has one or more compound junior synonyms linked to it, both the first and second checkboxes are checked. The first has the special legend "...which itself has the following compound junior synonym..." followed by a scrollable list of compound junior synonyms. The second checkbox legend details the Valid Species of which the species is a proper junior synonym.



The Synonymy Status display

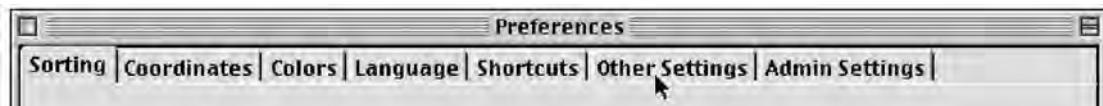
The small “Synonymy” display area in the “Classification” (primary) tab of the Species Input screen, the *Synonymy Status display*, shows the Synonymy Status for the current Species record. The five possible status alternatives are discussed in the section “How Biota Keeps Track of Species Synonyms,” earlier in this chapter.

The level of detail shown in the Synonymy Status display depends on whether or not the “Show full Synonymy Status in Species Input screen” checkbox in the Preferences screen has been checked and on whether or not you have already used the Synonymy tab for the current Species record. The only advantage of leaving the Full Synonymy checkbox unchecked (disabled—the default setting) is a slightly faster display of Species records in the Species Input screen.

NOTE: If you use the Synonymy system, it is recommended that you enable the Full Synonymy Display. The slight cost in display time is worth it.

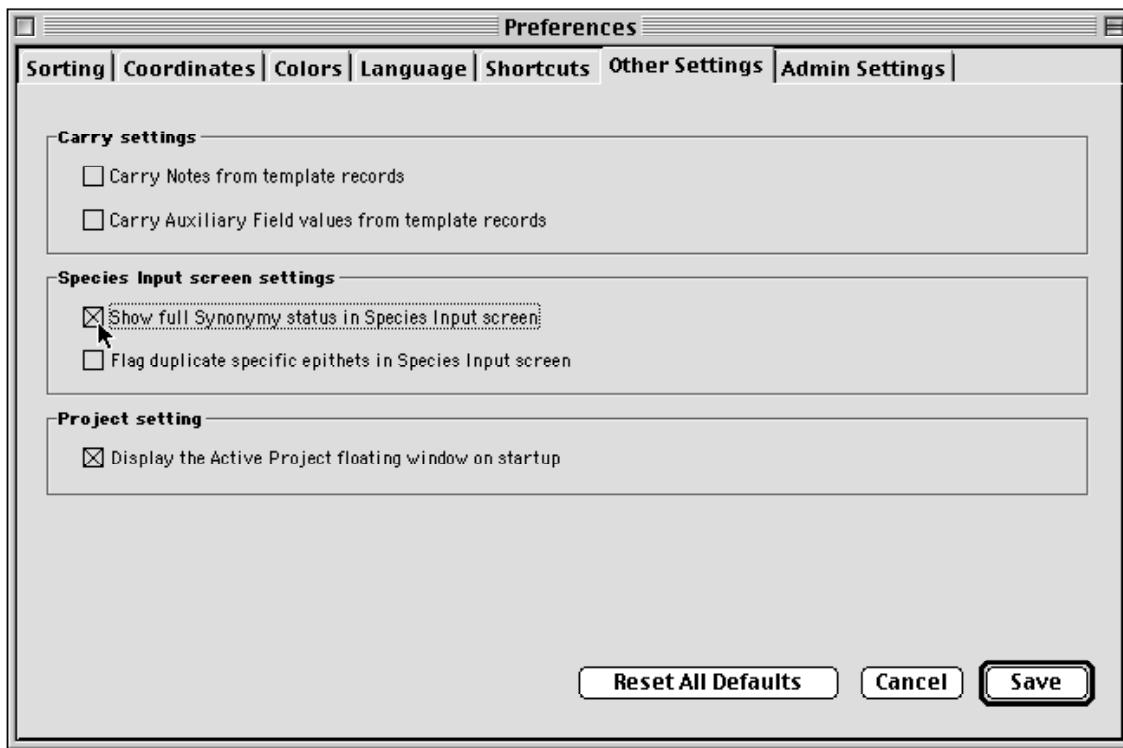
To Enable or Disable Full Synonymy Display

1. From the Special menu, select Preferences. The Preferences screen appears.
2. Click the “Other Settings” tab.



3. Check or uncheck the box labeled “Show full Synonymy Status in Species Input screen.” The default setting is unchecked, to allow faster display of Species records in the Species Input screen.
4. Click the “Save” button in the Preferences screen.

NOTE: To keep the setting between Biota sessions, click the “Admin Settings” tab (if you have Administrative privileges) and select “Use these Preferences next time Biota is launched.”

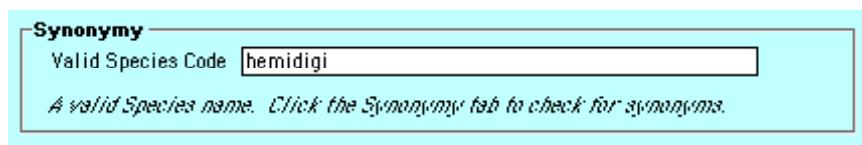


If Full Synonymy Display Is Not Enabled

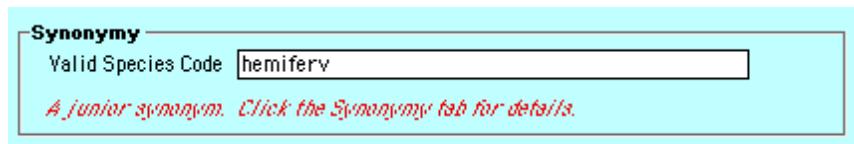
If you have not enabled the Full Synonymy option (see “To Enable or Disable Full Synonymy Display” earlier in this chapter), Biota makes a *preliminary* check of

Synonymy Status of each Species record just before it is displayed in the Species Input screen and reports accordingly in the Synonymy Status display area.

- If the Valid Species Code matches the Species Code for the record, the Synonymy Status display reads “A valid Species name. Click the Synonymy tab to check for synonyms.”



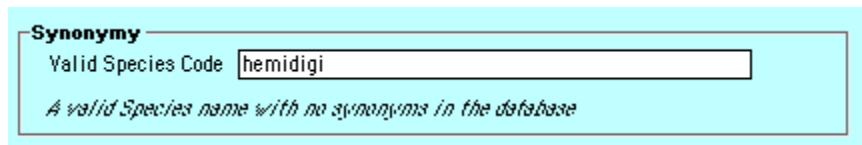
- If the Valid Species Code does not match the Species Code for the record, the Synonymy Status display reads “A junior synonym. Click the Synonymy tab for details.” The message is in red type, to alert you not to link Specimen records to a junior synonym (unintentionally).



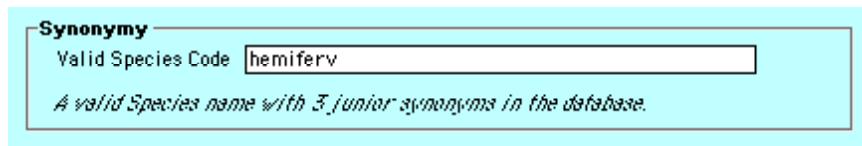
If Full Synonymy Display Is Enabled

If you have enabled the Full Synonymy option (see “[To Enable or Disable Full Synonymy Display](#)” earlier in this chapter), Biota investigates the full Synonymy Status of each Species record just before it is displayed in the Species Input screen and reports accordingly in the Synonymy Status display area.

- If the Valid Species Code matches the Species Code for the record and no junior synonyms are found, the Synonymy Status display reads “A valid Species name with no synonyms in the database.”

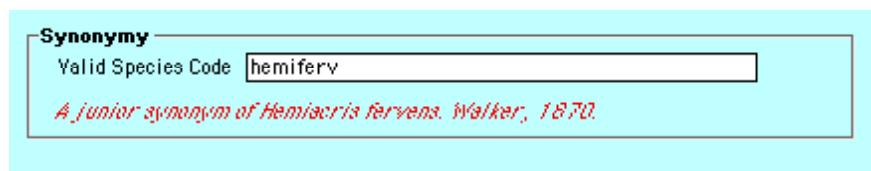


- If the Valid Species Code matches the Species Code for the record and *n* junior synonyms are found, the Synonymy Status display reads “A valid Species name with *n* junior synonyms in the database.” (Three were found in the example below).



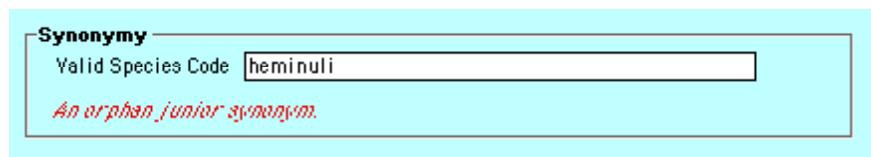
To display the full list of junior synonyms, click the Synonymy tab. (See “[Displaying the Synonymy Status of a Species Record](#).” earlier in this chapter.)

- If the Valid Species Code does not match the Species Code for the record but matches the Species Code of a valid Species, the Synonymy Status display reads “A junior synonym of [full name of the senior synonym].” The message is in red type, to alert you not to link Specimen records to a junior synonym (unintentionally).



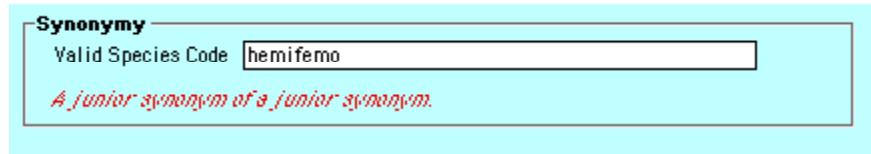
To display the full list of junior synonyms, click the Synonymy tab. (See “[Displaying the Synonymy Status of a Species Record](#).” earlier in this chapter.)

- If the Species is an orphan synonym, the Synonymy Status display reads “An orphan junior synonym.” The message is in red type, to alert you not to link Specimen records to an orphan junior synonym and to highlight the need to correct this anomaly.



For more information, click the Synonymy tab. (See “[Displaying the Synonymy Status of a Species Record](#).” earlier in this chapter.)

- If the Species is a compound junior synonym, the Synonymy Status display reads “A junior synonym of a junior synonym.” The message is in red type, to alert you not to link Specimen records to a junior synonym and to highlight the need to correct this anomaly.



For more information, click the Synonymy tab. (See “[Displaying the Synonymy Status of a Species Record](#).” earlier in this chapter.)

The Synonymy Display after Using the Synonymy Screen

Regardless of whether you have enabled the Full Synonymy option (see “[To Enable or Disable Full Synonymy Display](#),” earlier in this chapter), Biota investigates the complete Synonymy Status of a Species record when you click the Synonymy tab. (See “[Displaying the Synonymy Status of a Species Record](#).” earlier in this chapter.)

When you return to the Classification tab of the Species Input screen, Biota displays full information on synonymy, as described in the preceding section (“[If Full Synonymy Display Is Enabled](#)” earlier in this chapter).

Declaring a Species a Junior Synonym and Transferring Its Specimens

In systematics, you may need to record that two species names are synonymous. In survey or inventory work, you may conclude that two groups of specimens linked to different temporary Species (morphospecies) records are, in fact, conspecific.

Biota makes it easy to synonymize two Species records. As explained in detail earlier in this chapter (see “[How Biota Keeps Track of Species Synonymies](#)”), Biota keeps a record of the junior synonym by *synonymizing*—but retaining—its original Species record.

With your confirmation, Biota automatically switches the links for Specimen records from the junior synonym to the senior synonym. If you have activated the Determination History system (see “[Enabling or Disabling the Determination History System](#)” in Chapter 22), the switch will be recorded for each Specimen (see “[Changing a Determination Using the Synonymy Tool](#)” in Chapter 22).

Here are the steps to take to synonymize one Species record with another:

- Display the Species record** in the Species Input screen (see “[Viewing, Editing, Printing, or Deleting Individual Records from an Input Screen](#)” in Chapter 10).
- Click the Synonymy tab in the Species Input screen.**

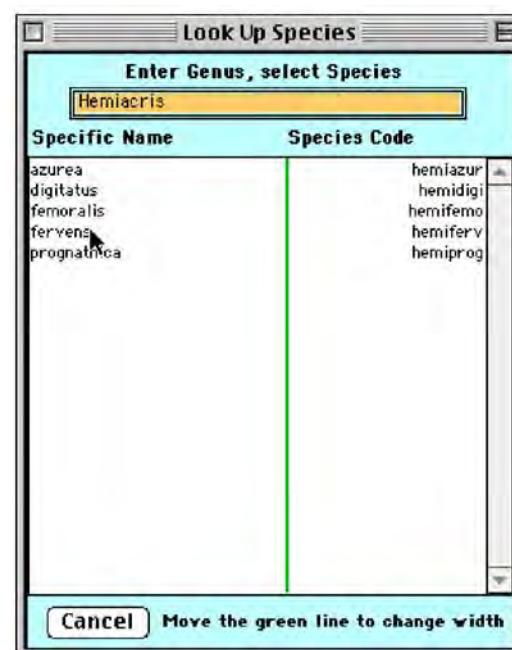
The Synonymy tab screen appears, with a complete report on the Synonymy Status of the Species record. (See “[Displaying the Synonymy Status of a Species Record](#),” earlier in this chapter, for details.)

- Click the “Synonymize This Species” button** in the bottom left corner of the Synonymy screen.

The standard “Look Up Species” screen appears. (See “[Entering Specimen Data: The ‘General’ Tab](#)” in Chapter 11 if you need help with this tool.)

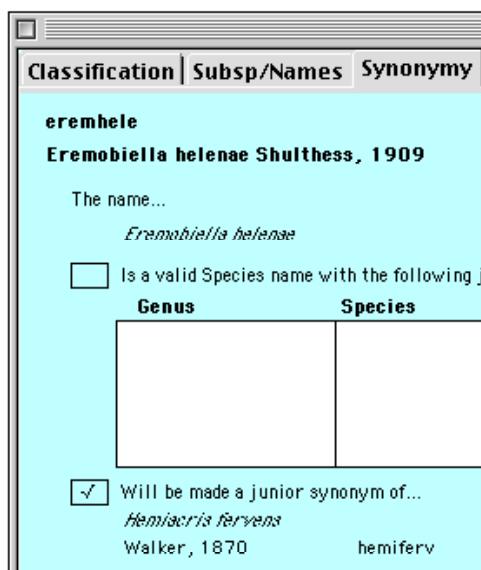
- Enter the Genus** (or the first letters of the Genus) of the Species with which the current Species is to be synonymized, then press TAB.

The scrolling list in the Look Up Species tool displays all specific names (Species Names) linked to the Genus.

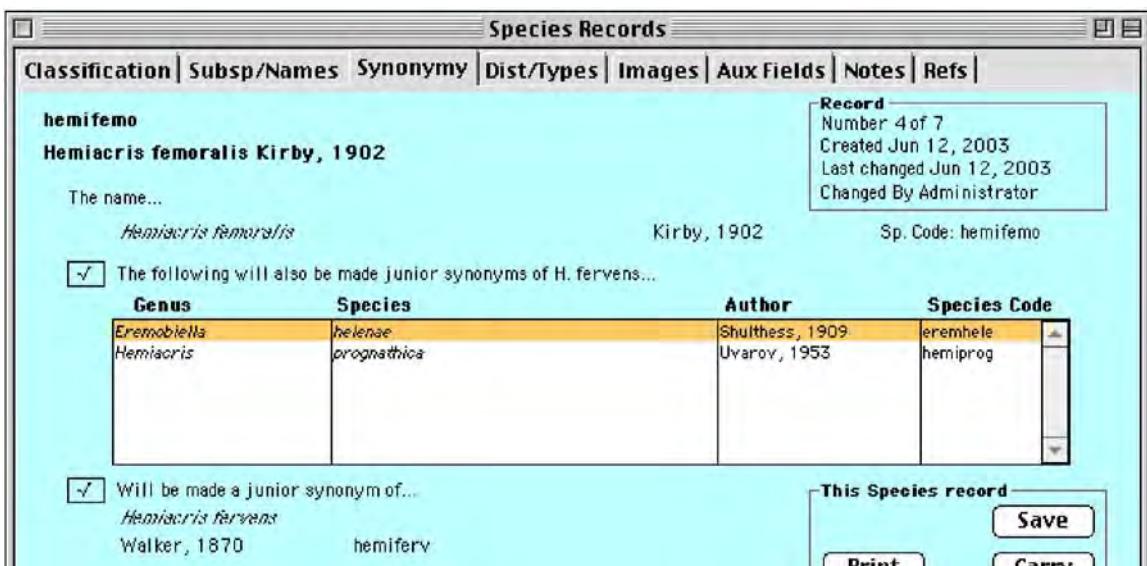


5. Click the specific name of the valid Species (senior synonym) of which the current Species is to be declared a junior synonym.

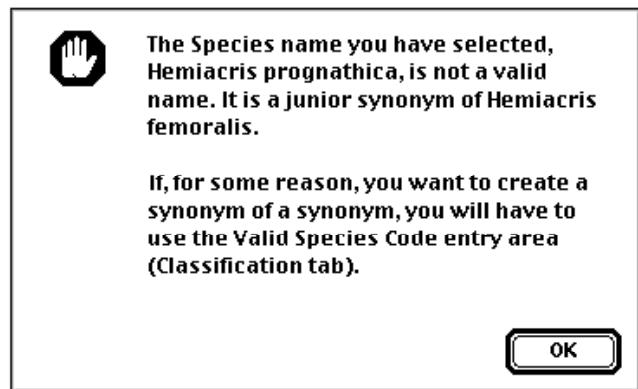
- If the Species you clicked is a valid Species, and the Species to be synonymized has no junior synonyms of its own, Biota posts the report below. “The name... [Genus, Specific Name, Author, Species Code]...Will be made a junior synonym of... [Genus, Specific Name, Author, Species Code].”



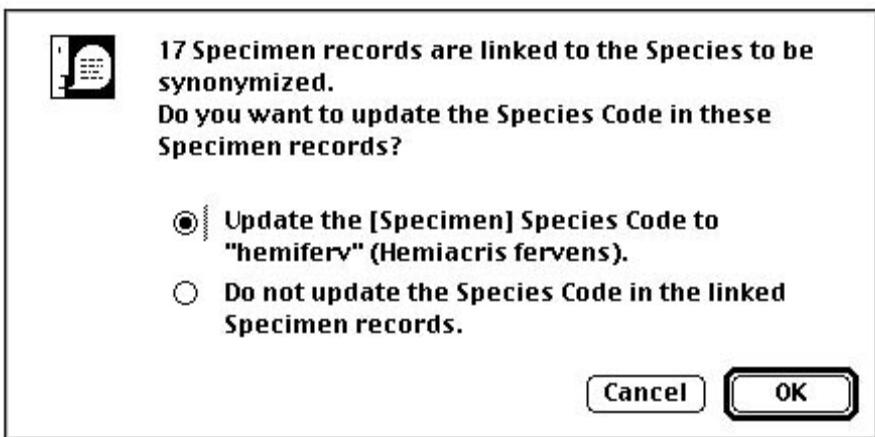
- If the Species you clicked is a valid species, and the Species to be synonymized has one or more junior synonyms of its own, Biota posts the report below. The species to be synonymized and all its own junior synonyms will be declared junior synonyms of the designated valid species.



- If you attempt to make a Species record a junior synonym of an existing junior synonym (i.e., if you attempt to create a compound junior synonym), Biota posts the following message:



6. Accept or Cancel the proposed changes by clicking the appropriate button (“Accept New Synonymy” or “Cancel New Synonymy”) in the Synonymy screen.
7. If you clicked “Accept the New Synonymy” and the Species destined to become a junior synonym has linked Specimen records, Biota offers to update the Species Code in the Specimen records to match the Species Code of the senior synonym.



- If you choose “Update the [Specimen] Species Code...,” Biota “moves” the Specimens from the junior synonym to the senior synonym, automatically, by changing the [Specimen] Species Code field in the Specimen records.
- If you choose “Do not update the Species Code...,” no change will be made in any Specimen record. The Specimens linked to the junior synonym’s Species record will remain linked to it.

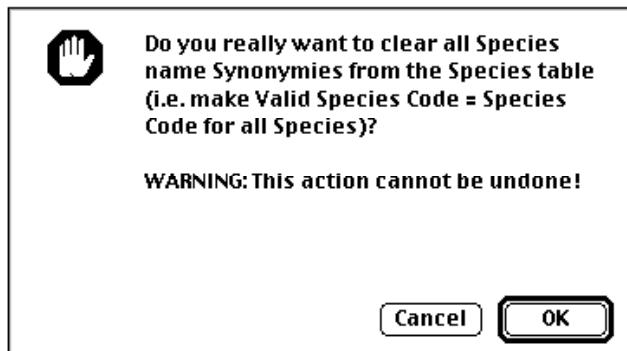
NOTE: If you have enabled the Determination History system, and you choose the first option above, Biota records the change in Specimen determination for each Specimen record that was “moved” to the senior synonym. See “[Enabling or Disabling the Determination History System](#)” in Chapter 22.

8. Select an option and click OK.

Clearing All Synonyms

You can undo any synonymy by setting the Valid Species Code equal to the Species Code for an individual Species record. In addition, Biota offers a tool to do this for every Species record in a Biota Data File, all at once.

1. From the Special menu, choose “Clear All Synonyms.” A warning appears.
2. *Understanding that this action cannot be undone*, click OK to confirm the proposed action or Cancel to dismiss it.



NOTE: If the User Password system has been enabled (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), only a user with Administration access privileges can use this command.

Displaying Specimen Records for Junior Synonyms

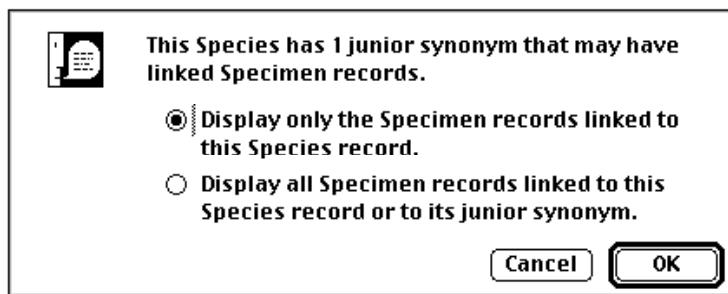
When you display the Species record for a senior synonym (a Valid Species record with one or more junior synonyms in the Data File), you can use the “Specimens” button to display not only all Specimen records linked to the Species record for the senior synonym, but (as an option) all Specimen records linked to the Species records for its junior synonyms as well. You must first enable the “Full Synonymy” option.

1. In the Preferences screen (Special menu), enable the “Show full Synonymy status in Species Input screen” checkbox (see “[To Enable or Disable Full Synonymy Display](#)” earlier in this chapter).

2. **Display the Species record for a senior synonym and click the “Show Specimens” button.** The number shown on the button includes *all* linked Specimens, both those linked to the Species displayed (if any), plus any Specimens linked to junior synonyms.

An option screen appears.

Show Specimens (17)

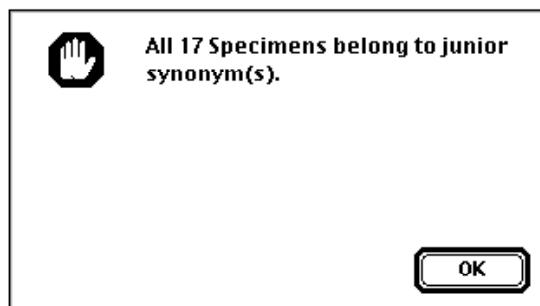


3. **Choose an option:**

- Either:** “Display only the Specimen records linked to this Species record.”

Normally, if a Species record has no linked Specimens, the “Show Specimens” button is not enabled, but if one or more junior synonyms has linked specimens, it is enabled whether or not the valid Species has linked Specimens (if you have enabled this feature).

If you select this option, and only the junior synonyms have linked Specimens, Biota displays this message.



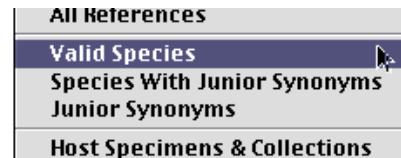
- Or:** “Display all Specimen records linked to this Species record or to its junior synonym.”

4. **Click the “OK” button in the option screen.** Biota displays the Specimen records in a new window.

Finding Valid Species, Species With Synonyms, or Junior Synonym Records

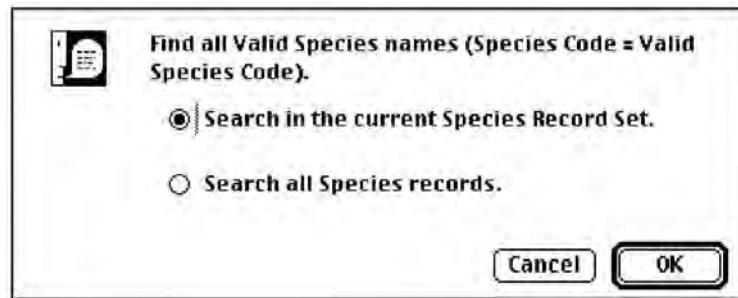
Sometimes you may want to work only with valid Species, rather than both valid Species and junior synonyms. Or, you might want to work only with senior synonyms (valid species that have junior synonyms) or just with junior synonyms.

In the Find menu, Biota offers special tools to find valid Species records (with or without junior synonyms), valid Species with junior synonyms, and junior synonym Species records.



1. If you want to search within a Species Record Set, establish the Record Set first (see “[Record Sets](#)” in Chapter 3).
2. From the Find menu, choose one of these commands:
 - “**Valid Species**.” This category includes all species for which the Species Code is identical to Valid Sp Code, whether or not a Species has any Junior Synonyms.
 - “**Species With Junior Synonyms**.” This category includes all Species for which the Species Code is identical to Valid Sp Code that have at least one Junior Synonym.
 - “**Junior Synonyms**.” This category includes all species for which the Species Code differs from the Valid Sp Code, whether or not the Valid Sp Code matches the Species Code of a senior synonym.

Biota presents an option screen. The opening statement differs appropriately depending on the command you chose, but the options are the same for all three commands. If the Species Record Set is empty, Biota will inform you.



3. Choose an option and click OK. Biota displays the requested records in the Species Record Listing screen.

NOTE: If you need to find all valid Species that have no junior synonyms:

- a. Choose the command “Valid Species” from the Find menu.
 - b. Establish the Species found as a Record Set.
 - c. Choose the command “Species With Junior Synonyms” from the Find menu.
 - d. In the Record Set Options screen, click “More Choices” then “Subtract it from the Species Record Set” (the difference operation).
-

Finding Orphan Junior Synonym Records

An orphan junior synonym is a Species record for which the Valid Sp Code value is either blank or does not match the Species Code for any Species record in the database. The “Orphan Records” command in the Find menu (see “[Finding Orphan Records](#)” in Chapter 12) offers a tool to find such records.

1. From the Find menu, choose “Orphan Records.”

The “Find Orphan Records” selection screen appears.



2. Click the popup and choose “Junior Synonym.”



3. Click the “Find” button. Biota displays the requested records in the Species Record Listing screen.

Chapter 24

Host-Guest Relations

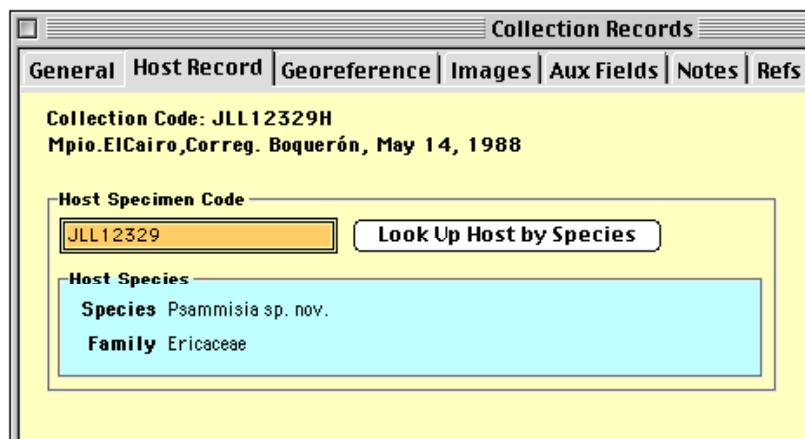
In the web of life, biological interactions link one species with another in myriad patterns. A relational database offers a natural way to document these links, enriching the biological information you record about specimens or living individuals.

In addition, organs, tissues, or molecules derived from whole-organism specimens are specimens in their own right and often require their own records, but these records should be linked to the master record for the whole-organism specimen.

How Biota Handles Links Between Specimens

Biota uses a *host–guest* metaphor to express linkage between two Specimen records—whether the “guest” is a welcome one or not. The relationship may be an interspecific one, such as between a host and a parasite, pathogen, commensal, or mutualist (guests); or between a food plant (host) and an herbivore (guest). Alternatively, the relationship may be intraspecific, such as between a parent (host) and its several offspring (guests). Using the same metaphor, organ, tissue, or molecular specimens are considered “guests” of the individual organism to which they belonged—the host specimen.

Structurally, Biota handles relationships between Specimen records through a recursive (circular) relationship mediated by the Collection table (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). The justification is simple: the collection *site* for a guest specimen is its host specimen. Thus, Host Specimen Code appears as a field in the Collection table, as illustrated in the “Host Record” tab of the Collection Input screen below. (The field is abbreviated *Host Spcm Code* in Biota’s internal structure.)



Host–Guest Relations: An Example

Suppose, for example, that a caterpillar (the guest specimen) has been collected from its food plant (the host specimen), and a Specimen record has been created for each.

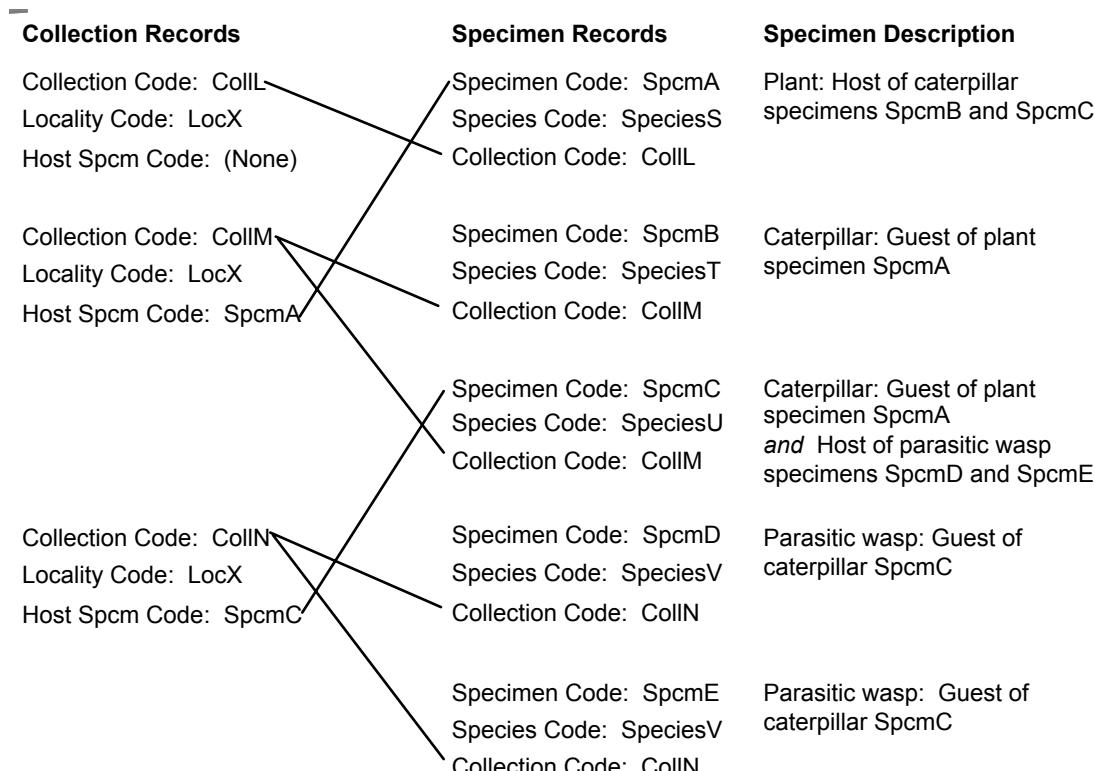
To begin with, you link the Specimen record for the plant (the *host Specimen record*) to an ordinary Collection record (the *host Collection record*) through the Collection Code field, defining details of the collecting event (collector, date collected, etc.). Of course, additional Specimen records, such as duplicate plant specimens, may be linked to the same Collection record. These are simply the normal procedures for data entry (see “[Specimen Input](#)” in Chapter 11).

To use Biota’s Host-Guest system, you then link the Specimen record for the caterpillar (the *guest Specimen record*), however, to a *separate* Collection record (the *guest Collection record*).

The guest Collection record includes the Specimen Code for the host plant in the [Collection] Host Specimen Code field (illustrated here). If Specimen records exist for additional guest specimens collected from the same plant host, you would link them to the same guest Collection record. These links are depicted in the illustration that follows the next paragraph.

Host Specimen Code
JLL12329
Host Species
Species Psammisia sp. nov.
Family
Ericaceae

Host–guest relations are recursive in Biota. Most often, you will need to use only a single level of host–guest relations, but you can link Specimen records recursively to any level necessary. For each level in a recursive host–guest relationship, a guest Collection record—distinct from the host Collection record—must be created. The illustration below shows the Specimen and Collection records necessary to link the Specimen records for two host–guest levels: (1) a *host plant and its caterpillar “guests”*; and (2) one of those caterpillars, now as a host, and its parasitic wasp “guests.” (Only the linking fields are shown.)



Notice that, at each level in this hypothetical example, guest Specimen records potentially bear a *many-to-one* relationship with the guest Collection record, and thus also with the host Specimen record. Specifically, two caterpillar specimens (SpcmB and SpcmC) are linked to a single guest Collection record (CollM), and thus to a single plant host Specimen record (Spcm A). Likewise, two wasp specimens (SpcmD and SpcmE) are linked to a single guest Collection record (CollN), and thus to a single caterpillar host Specimen record (SpcmC). Moreover, multiple guests of a single host need not be conspecific. In the illustration, caterpillar SpcmB has been identified as a representative of SpeciesT whereas caterpillar SpcmC belongs to SpeciesU.

Notice, also, that all three Collection records in the illustration are linked to the same Locality record (LocX).

Recording Information in the Guest Collection Record

If the guest specimen was collected by the same person at the same time and place as the host specimen, then most of the fields of the host Collection record can be repeated in the guest Collection record. Biota offers a quick way to transfer this information (see “[Creating Guest Collection Records Automatically](#)” later in this chapter). Even so, you may wish to add details in the Site or Source fields specifying the precise collection site or collection method for the guest specimen: “Reared from host pupa,” “Under bark of the host tree,” “Recovered by washing leaves,” “Attached to the third gill arch,” “Extracted by centrifugation,” or “Amplified by PCR.”

On the other hand, the guest specimen may have been collected or extracted from the host specimen at a later date by a different person than the collector of the host specimen. In this case the appropriate place to record this collection information is in the guest Collection record. Collection data for the host can still be located, if needed, by first following the link from the guest Collection record (Host Record tab) to the host Specimen record. Then follow the link from the host Specimen record to the host Collection record.

Host Information in Guest Specimen Labels and Printed Reports

As an option, Biota will include host information on printed locality labels for guest Specimens. See Chapter 15, “[Printing Labels](#),” especially the section on “[Data Options](#).”

In printed reports for Specimen records, you can choose to include host information for each guest Specimen record. See Chapter 14, “[Printing Reports](#),” especially the section on “[Printing a Standard or Custom Report Based on the Records in a Record Listing Screen](#).”

Creating a Host Specimen Link

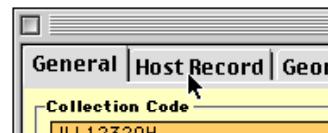
As explained and illustrated in the section “[Host–Guest Relations: An Example](#),” earlier in this chapter, to link a guest Specimen record to a host Specimen record, you enter the Host Specimen Code in the Collection record for the guest. Here are the steps to take.

1. Display a Collection record in the Collection Input screen.

- ***Either:*** Create a new guest Collection record. You can do this by selecting Collection from the Input menu, by clicking the “New Collection” button on the Collection output (record listing) screen, or “on the fly” from the Specimen Input screen (with the guest Specimen record displayed). See “[Specimen Input](#)” in Chapter 11.

- **Or: Find and display the existing, linked guest Collection record from a Specimen record.** You can do this by clicking the “Show Collection Record” button in the Collection panel of the Specimen Input screen with the guest Specimen record displayed (see “[Moving Up the Table Hierarchies from an Input Screen: Parent Record Buttons](#)” in Chapter 10), or by using tools from the Find menu (see Chapter 12, “[Finding and Updating Records](#)”).
2. Complete or update the fields of the Collection record, except for the Host Specimen Code tab, following the instructions in the section “[Collection Input](#)” in Chapter 11.
3. Click the “Host Record” tab.

The Host Record tab screen appears.



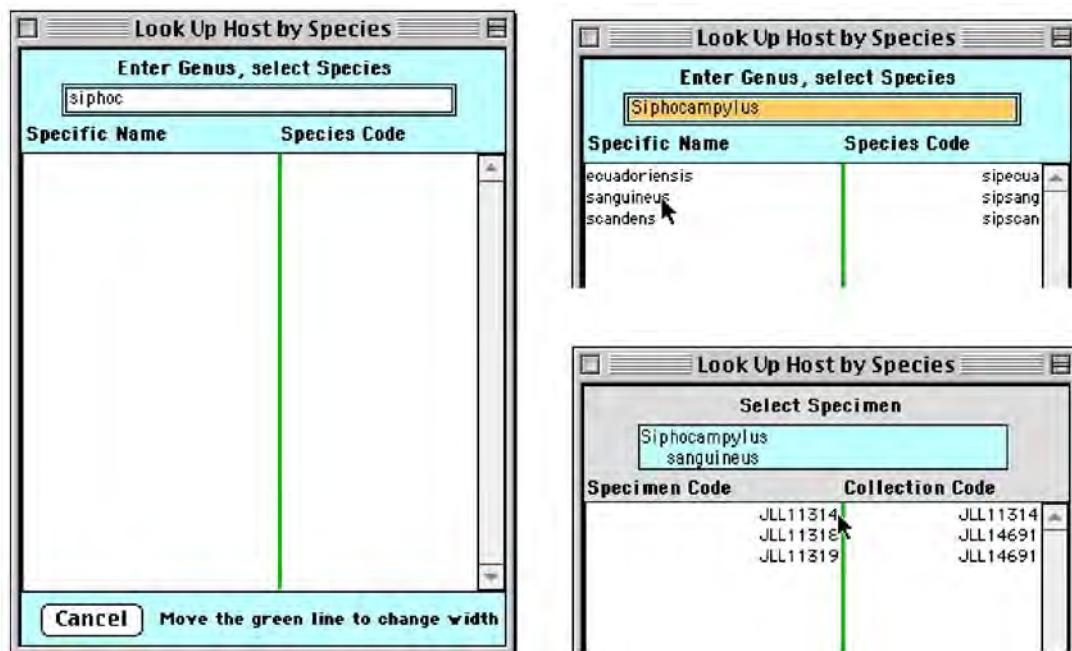
4. Enter the Host Specimen Code.

- **Either: Enter the Host Specimen Code manually.** When you press TAB to complete the entry, the Genus, Species Name (specific name), and Family for the host Specimen should appear in the Host Specimen display area, as illustrated below.

Host Specimen Code
JLL12329
Look Up Host by Species
Host Species
Species Psammisia sp. nov.
Family Ericaceae

- ◊ **If the information is correct,** click the “Save” button in the Collection Input screen. You are done; skip the rest of the steps in this section.
- ◊ **If the host specimen information does not appear or is incorrect,** you have probably entered the wrong Specimen Code. Try the alternative method below.

- **Or: Click the “Look Up Host by Species” button in the Host Specimen Code panel of the Collection Input screen (illustrated above). The Look Up Host by Species window appears (left illustration below).**



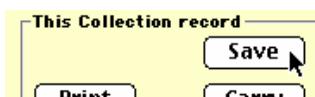
- a. Enter a Genus, or the first letter or letters of a Genus and press TAB** (above left illustration). If a matching Genus record is found, all Species records for the Genus appear in the scrollable area of the Lookup window (above, upper right illustration). If more than one match is found, a list of matches appears from which you can select the correct Genus (not illustrated here.)
- b. When you find the Species you want, click it** (above, upper right illustration). A list of all Specimen records for that Species will appear (above, lower right illustration).
- c. Click the host Specimen record in the scrollable list** (above, lower right illustration).

The information for the selected host Specimen record appears in the Host Specimen Code panel in the guest Collection record.

This screenshot shows the "Host Specimen Code" panel. It contains the following fields:

- Host Specimen Code:** A text input field containing "JLL11314".
- Look Up Host by Species:** A button next to the host code.
- Host Species:** A section containing "Species Siphocampylus sanguineus" and "Family Campanulaceae".

- d. If the information is correct, click the “Save” button in the Collection Input screen.**



Creating Guest Collection Records Automatically

Commonly, most fields of a guest Collection record require the same values as the corresponding fields in the linked host Collection record. For example, if a collector removes and preserves ectoparasites from a host when the host is collected, or collects herbivores and food plant vouchers at the same time and place, then the Locality Code, Collected By, Date Collected, Coordinates, and perhaps other fields of the host and guest Collection records will share the same values.

Biota takes advantage of this circumstance to offer a quick way to create guest Collection records, using the corresponding host Collection records as templates. For this reason, you must first have linked each host Specimen record to a host Collection record (through the Collection Code field) before using this tool, although Biota will warn you if you fail to create the appropriate links.

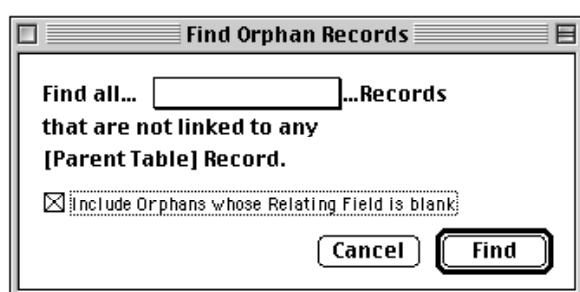
Creating Guest Collection Records Automatically: Step by Step

NOTE: If the User Password system has been enabled, only a user with Administration access privileges can use this tool (see Chapter 26, “[Security: Passwords and Access Privileges](#)”).

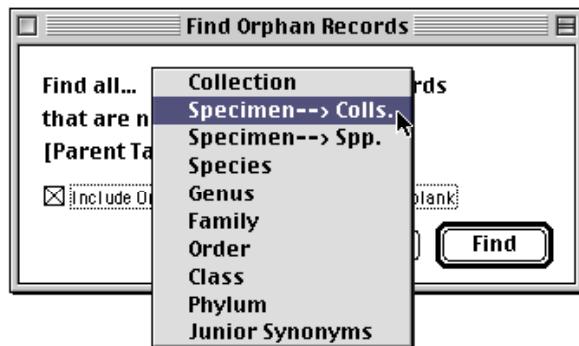
Here are the steps to take to create guest Collection records automatically, based on information in host Specimen and host Collection records.

1. In the Specimen Record Listing screen, display only the host Specimen records that will be referenced by the guest Collection records that you want to create. You can use any of the tools of the Find menu to find the host Specimen records. If other Specimen records are also displayed, select the host Specimen records and use the “Sub-Selection” button (see “[Creating a Sub-Selection of Records](#)” in Chapter 10) to dismiss the other records.
2. Make a note of how many host Specimen records are displayed.
3. Click the “Done” button and declare the host Specimen records the current Specimen Record Set. See “[The Record Set Options Screen](#)” in Chapter 3 if you need help.
4. If you wish to confirm that a host Collection record already exists for each host Specimen record, follow the lettered steps below. (If you are reasonably confident that each host Specimen is linked to a host Collection record, proceed directly to [Step 5](#), instead. Biota checks for missing links in any case.)
 - a. From the bottom of the Find menu, choose “Orphan Records.”

The query screen for this tool appears.



- b. From the popup, choose “Specimen→Colls.”

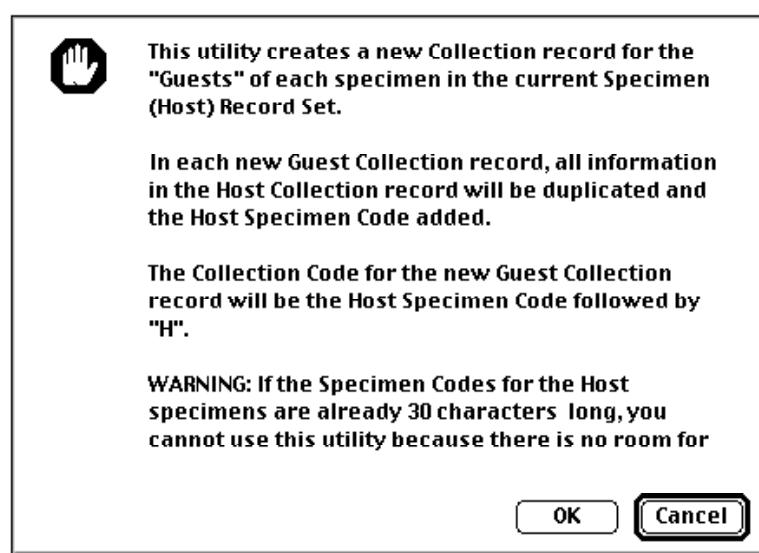
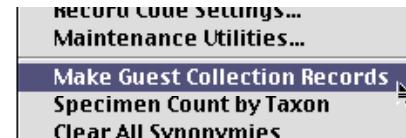


If any of the records in the (host) Specimen Record Set appear in the list of orphan records, it means they lack a linked Collection record.

NOTE: If there are many orphan records to scan, you could use the Record Set Options screen (“More Choices,” then “Make shared records the new Record Set”) to find the offending records. (Make a Record Set Point file for the host Specimen records first, to recover the set after this procedure.) See “[The Record Set Options Screen](#)” and “[Record Set Pointer Files](#)” in Chapter 3

5. From the Special menu, choose “Make Guest Collection Records.”

An instruction and warning message appears.



6. Click the “OK” button to proceed, or Cancel to dismiss the procedure. (Notice that Cancel is the default button, for safety.) If you click OK, Biota creates one new

guest Collection record based on each host Specimen record in the current Specimen Record Set, with the following characteristics:

- **The Collection Code of the new guest Collection record** is composed of the Specimen Code of the host Specimen record, with the letter *H* appended.
- **The Host Specimen Code field of the guest Collection record** contains the Specimen Code of the host Specimen record.
- **All other fields of the guest Collection record** have the same value as the corresponding fields of the *host Collection record*.

The new guest Collection records are displayed in the Collection Record Listing screen.

Creating Guest Collection Records Automatically: Error Messages

Two error messages may appear during the process of creating new guest Collection records.

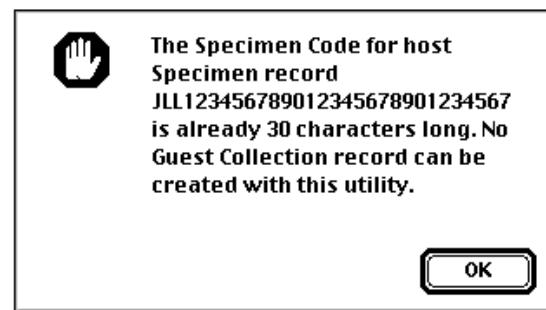
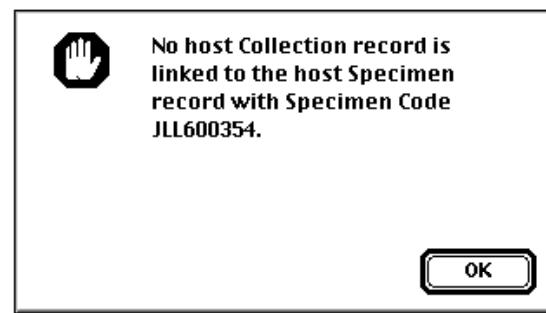
- **No host Collection record.** For each Specimen record in the current Specimen Record Set that is not linked to any Collection record (through the Collection Code field) Biota displays the message shown here.

Make a note of the Specimen Code. The creation of other new guest Collection records proceeds when you click the “OK” button.

When the process is complete, create the missing link for each Specimen record flagged for this error, declare them the current Specimen Record Set, then repeat the steps in the previous section to create guest Collection records based on the Specimen records that were flagged.

- **Host Specimen Code already maximum length.** If the Specimen Code for any host Specimen is already 30 characters in length (the maximum length allowed), you cannot use this tool to create a corresponding guest Specimen record because there is no room to append the *H*. If the Specimen Code is already 30 characters long for a host Specimen record, Biota displays the alert shown here, but proceeds with the rest of the records.

In this circumstance, you will have to create a guest Collection record manually. You can use the existing host Collection record as a template and the “Carry” button (see “[Using an Existing Record as a Template for a New Record](#)” in Chapter 10) to speed the process.



- **Duplicate Key Error.** If Biota attempts to create a new guest Collection record using a Collection Code that matches the Collection Code for an existing Collection record, you will receive the warning below.

Make a note of the Collection Code. The creation of other new guest Collection records proceeds when you click the “OK” button.

A Duplicate Key Error probably means that the guest Collection record you want to create already exists, perhaps because you have inadvertently used this tool with the same host Specimen record previously. In this case, just ignore the warning.

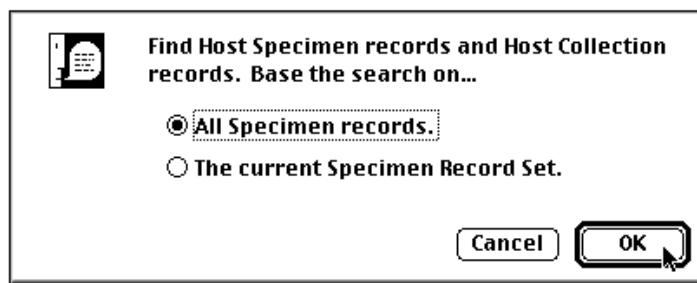


Finding Host and Guest Records

You can find linked host and guest records by following, one link at a time, the links shown in the illustration in the section “[Host–Guest Relations: An Example](#),” earlier in this chapter. However, the Find menu provides four tools to help trace host–guest links much more efficiently.

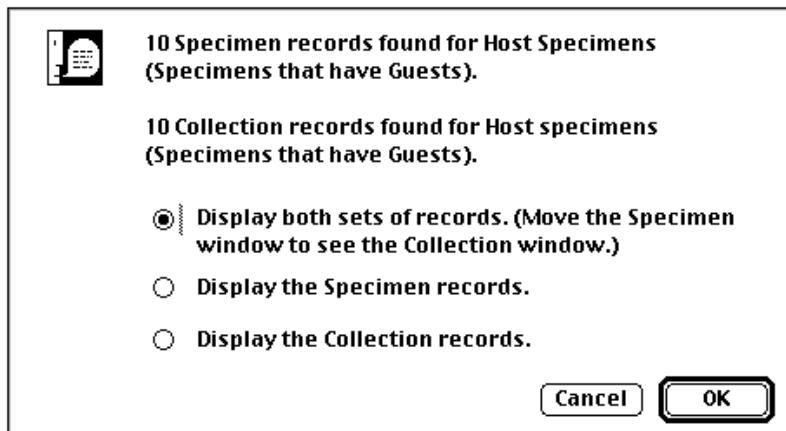
Finding Host Specimens and Host Collections

1. **If you want to base the search for host Specimen and host Collection records** on a certain group of Specimen records (or even just one host Specimen record), find the Specimen records and declare them the current Specimen Record Set (see “[Record Sets](#)” in Chapter 3).
2. **From the Find menu, choose “Host Specimens & Collections.”** An option window appears. (See the next step.)
3. **Choose a search option.**



- **If the active Specimen Record Set is not empty,** the search option window offers two alternatives (below).

- ◊ **All Specimen records.** If you choose this option (the default) Biota finds and displays : **(1)** All Specimen records in the Data File for which the Specimen Code appears in the Host Specimen Code field of any Collection record (all host Specimen records) and **(2)** the Collection records linked to those Specimen records through the Collection Code field (all host Collection records).
 - ◊ **The current Specimen Record Set.** If you choose this option Biota finds and displays **(1)** all Specimen records in the current Specimen Record Set (which may contain only a single record, if you wish) for which the Specimen Code appears in the Host Specimen Code field of any Collection record (host Specimen records) and **(2)** the Collection records linked to those Specimen records through the Collection Code field (host Collection records).
- **If the active Specimen Record Set is empty,** the search option window offers only the first alternative (below). The second alternative is disabled.
4. **Click the “OK” button in the search option window to launch the search.** When the search is complete, Biota reports the results and offers three display options.



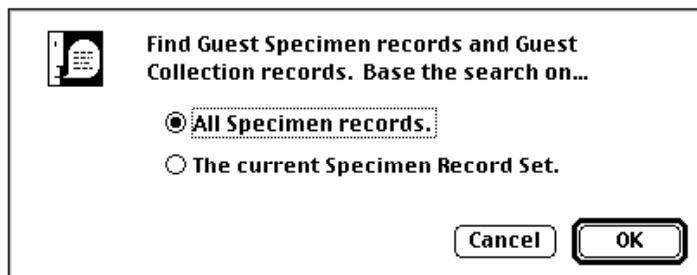
You can choose to display Specimen and Collection records, only the Specimen records, or only the Collection records.

5. **Click the “OK” button to display the records.** The records appear in the standard Record Listing screen for each table. When you click the “Done” button in the Record Listing screen, the usual Record Set options are made available (see “[The Record Set Options Screen](#)” in Chapter 3).

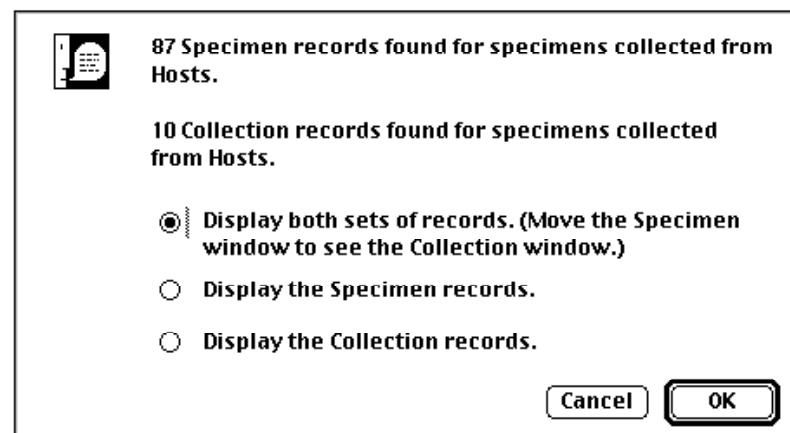
Finding Guest Specimens and Guest Collections

1. **If you want to base the search for guest Specimen and guest Collection records** on a certain group of Specimen records (or even just one guest Specimen record), find the Specimen records and declare them the current Specimen Record Set (see “[Record Sets](#)” in Chapter 3).
2. **From the Find menu, choose “Guest Specimens & Collections.”** An option window appears. (See the next step.)

3. Choose a search option.



- If the active Specimen Record Set is not empty, the search option window offers two alternatives (below).
 - ◊ All Specimen records. If you choose this option (the default), Biota finds and displays (1) all Collection records in the Data File that have a non-blank value in the Host Specimen Code field (guest Collection records) and (2) all Specimen records linked to those Collection records through the Collection Code field (guest Specimen records).
 - ◊ The current Specimen Record Set. If you choose this option, Biota finds and displays (1) all Collection records in the Data File that have a nonblank value in the Host Specimen Code field (guest Collection records) and are linked through the Collection Code field to a record in the current Specimen Record Set, and (2) the Specimen records linked to those Collection records through the Collection Code field (guest Specimen records).
 - If the active Specimen Record Set is empty, the search option window offers only the first alternative. The second alternative is disabled.
4. Click OK in the search option window to launch the search. When the search is complete, Biota reports the results and offers three display options.



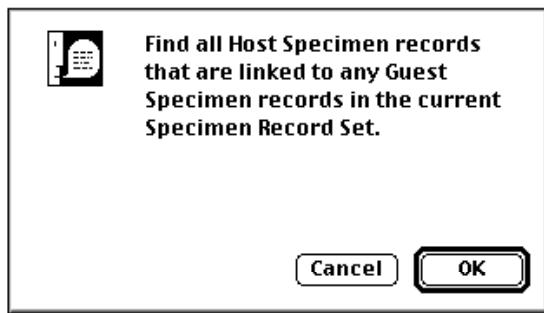
You can choose to display Specimen and Collection records, only the Specimen records, or only the Collection records.

5. Click the “OK” button to display the records. The records appear in the standard Record Listing screen for each table. When you click the “Done” button in the Record Listing screen, the usual Record Set options are made available (see “[The Record Set Options Screen](#)” in Chapter 3).

Finding Host Specimens for Guest Specimens

This tool finds the host Specimen record linked to the Specimen record for a guest or the host Specimen records linked to a group of guest Specimen records.

1. Create a Specimen Record Set for a guest Specimen record or records (see “[Record Sets](#)” in Chapter 3). If you wish, you can first ensure that all the putative guests are linked to host records by using the Guest Specimens and Collections tool (see “[Finding Guest Specimens and Guest Collections](#)” earlier in this chapter).
2. From the Find menu, choose “Host Spcms for Guest Spcms.” An explanatory message appears.



3. Click the “OK” button. Biota finds the Host Specimen records and displays them in the Specimen Record Listing screen. When you click the “Done” button in the Record Listing screen, the usual Record Set options are made available (see “[The Record Set Options Screen](#)” in Chapter 3).

Finding Guest Specimens for Host Specimens

This tool finds the guest Specimen records linked to the Specimen record for a host or to a group of host Specimen records.

1. Create a Specimen Record Set for a host Specimen record or records (see “[Record Sets](#)” in Chapter 3). If you wish, you can first ensure that all the putative hosts are linked to guest records by using the Host Specimens and Collections tool (see “[Finding Host Specimens and Host Collections](#)” earlier in this chapter).

2. From the Find menu, choose “Guest Spcms for Host Spcms.” An explanatory message appears.



3. Click the “OK” button. Biota finds the Guest Specimen records and displays them in the Specimen Record Listing screen. When you click the “Done” button in the Record Listing screen, the usual Record Set options are made available (see “[The Record Set Options Screen](#)” in Chapter 3).

Chapter 25

Temporary Taxa for Approximate Determinations

In virtually any study that involves new collections, many specimens will initially be undetermined (unidentified) to the species level, particularly if you work with highly diverse or poorly known taxa or with groups that are unfamiliar to you. Nonetheless, it is often useful to record approximate identifications of specimens that can later be made more precise as new information or authoritative determinations become available.

A natural (and familiar) way to provide an approximate identification is to identify a specimen accurately at a higher taxonomic rank—"Drosophila sp.," "drosophilid fly" (Family Drosophilidae), "fly" (Order Diptera), or simply "insect" (Class Insecta). In fact, *not* recording known, accurate determinations at higher ranks, when specific identities are unknown, means a loss of potentially useful information that is already in hand.

The problem with recording approximate determinations in a relational database, like Biota, is that records for higher taxa must be linked to Specimen records through the appropriate records at all intervening ranks. Otherwise, the Specimen record remains an orphan record (see "[Linking Fields: Parent and Child Records](#)" in Chapter 3), invisible to searches based on higher ranks, even though the physical specimen may have been identified accurately at a higher rank.

The easiest solution to this dilemma is to link any Specimen record that you have identified as representing a higher taxon (a taxon at a rank above species) to the record for that taxon through *temporary taxon* records at all intervening ranks. (The term refers to the temporary nature of the specimen determination. Temporary taxon records themselves need not be temporary.)

Biota's Convention for Temporary Taxon Records

Biota uses a specific convention to indicate a temporary taxon: its name is enclosed in parentheses.

Suppose, for example, that you have identified a particular plant specimen as a composite—a member of the Family Asteraceae—but you do not know its genus and specific name. Using Biota's convention, you would link it to a Species record (with any unique Species Code) for the Species "(Asteraceae)" (*with* the parentheses but *without* the quotation marks). The Species record would be linked to a Genus record for the Genus "(Asteraceae)," which, in turn, would be linked to the Family record for "Asteraceae" (no parentheses, since this is indeed a family). Subsequently, you would link all Specimen records identified only as members of the Family Asteraceae the same temporary taxon record in the Species table: the Species "(Asteraceae)."

With this approach, if you set up the query "Find all Specimens of the Family Asteraceae" in the "Lower Taxon for Higher Taxa" search tool (see "[Finding Records for Lower Taxa Based on Higher Taxa](#)" in Chapter 12), for example, Biota would find and display not only all Specimens fully determined to Species within Genera of the Family Asteraceae, but also all Specimen records identified only as "(Asteraceae)."

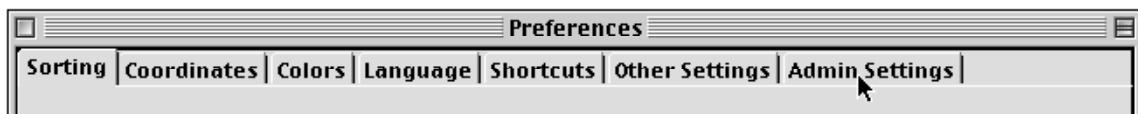
Automatic Creation of Temporary Taxon Records

If you decide to use Biota's convention for temporary taxa (see the previous section in this chapter, “[Biota's Convention for Temporary Taxon Records](#)”), you need not create the temporary taxon records one by one, although there is nothing wrong with that approach. Biota offers an option for the automatic creation of temporary taxon records, either by manual input or importing of higher taxon “master” records.

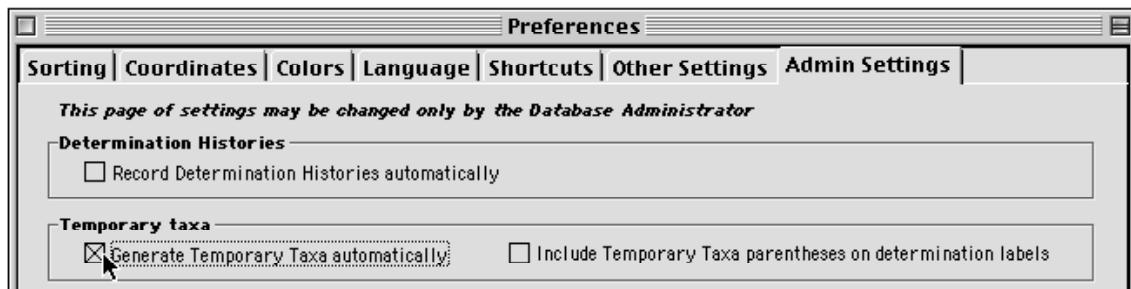
Enabling or Disabling Automatic Creation of Temporary Taxon Records

NOTE: If the User Password System has been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), you must have Administration access privileges to enable or disable the Determination History system.

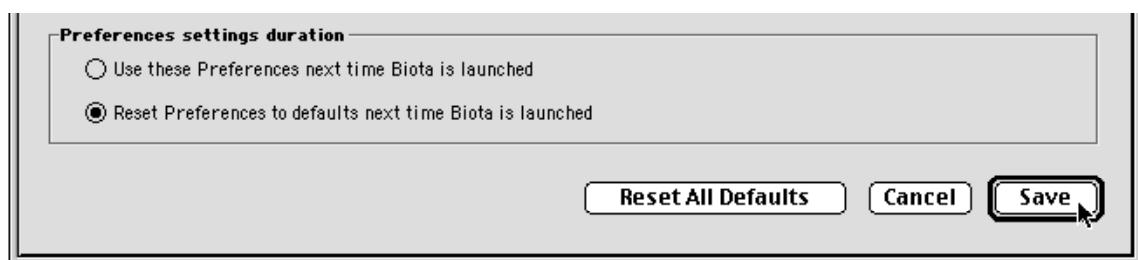
1. From the Special menu, select Preferences.
2. Click on the “Admin Settings” tab.



The Admin Settings tab screen appears.



3. To enable the automatic creation of temporary taxon records, click the checkbox labeled “Generate Temporary Taxa automatically” to check it. To disable this option, click the checkbox to uncheck it (illustrated above).
4. Choose an option for saving any changes in Preference settings made during this Biota session.



- If you want the changes to remain in force until altered regardless of how many times Biota is launched in the meantime, choose the option “Use these Preferences next time Biota is launched.”
- If you want the changes to be in force only for this session, choose the option “Reset Preferences to defaults next time Biota is launched.”

The default setting for Determination Histories is unchecked (off).

5. Click the “Save” button on the Preferences screen.

How Biota Creates Temporary Taxon Records

If you have enabled the automatic creation of temporary taxon records (see the previous section in this chapter, “[Enabling or Disabling Automatic Creation of Temporary Taxon Records](#)”), each time you create or import a new record for any of Biota’s taxon tables above the rank of Species (Kingdom, Phylum, Class, Order, Family, or Genus), a temporary taxon record is created automatically for all tables of lower rank, including Species.

For example, if you create or import a new record in the Order table for (Asterales), Biota immediately creates each of the following records, automatically:

Table	Key Field	Key Field Value	Linking Field	Linking Field Value
Family	Family	(Asterales)	Order	Asterales
Genus	Genus	(Asterales)	Family	(Asterales)
Species	Species Code	Aster001234	Genus	(Asterales)

Biota assigns a Species Code for the Species record (in the table above) automatically, prefixing the first five characters of the taxon name (Aster, in this example) to a six-digit integer based on the Species table sequence number (0001234 is just an example; see “[The Format of Automatically Generated Record Codes](#)” in Chapter 8 for information on sequence numbers). The Species Name field of the automatically created Species record is also assigned the temporary taxon name—(Asterales) in this example.

NOTE: There is a second option for the format of automatically created Species Code for temporary taxa for imported records. See the next section of this chapter, “Automatic Creation of Temporary Taxon Records for Imported Records.”

If instead or in addition, you create or import a Family record for Asteraceae, Biota automatically creates the following records:

Table	Key Field	Key Field Value	Linking Field	Linking Field Value
Genus	Genus	(Asteraceae)	Family	Asteraceae
Species	Species Code	Aster009946	Genus	(Asteraceae)

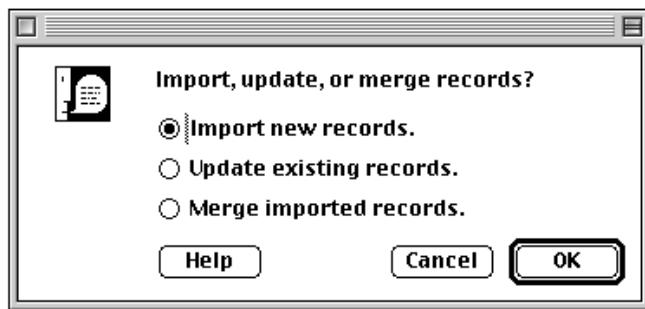
The Species Name field of the automatically created Species record is also assigned the temporary taxon name—(Asteraceae) in this example.

Automatic Creation of Temporary Taxon Records for Imported Records

For manually created records, if the Temporary Taxon option is enabled (see “[Enabling or Disabling Automatic Creation of Temporary Taxon Records](#)” earlier in this chapter), Biota simply creates the records without confirmation.

To create temporary taxon records for imported higher taxon records, take the following steps.

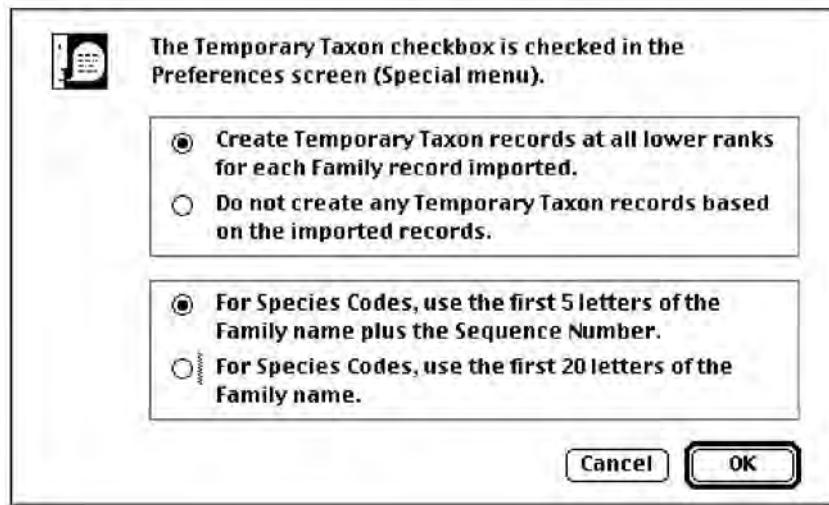
1. **Enable automatic creation of temporary taxon records** in the Preferences screen (Special menu), following the instructions in the section “[Enabling or Disabling Automatic Creation of Temporary Taxon Records](#)” earlier in this chapter.
2. **Prepare a delimited text file for importing taxon records** (Genus or above), following instructions in Chapter 28, “[Importing Data by Tables and Fields](#).”
3. **From the Im/Export menu, choose “Import by Tables and Field.”** The Import Option screen appears.



4. **Choose “Import new records” or “Merge imported records”** (the “Update existing records” option does not create temporary taxon records) and click the “OK” button.
Biota displays the Import Editor.
5. **Set up the Import Editor to import the higher taxon records** (Genus, Family, Order, Class, Phylum, or Kingdom), following the instructions in Chapter 28, “[Importing Data by Tables and Fields](#).”
6. **Click the “Import” button in the Import Editor** to launch the import process.

Biota displays an option screen for the creation of temporary taxon records (see next page).





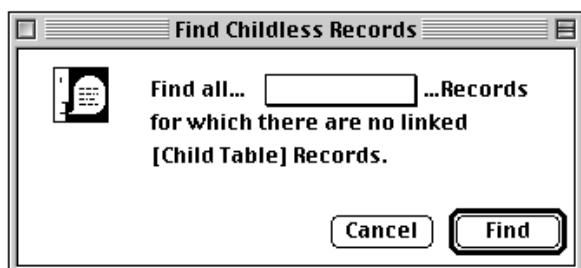
- The upper pair of options allows you to confirm or suppress the automatic creation of temporary taxon records for each imported record.
 - ◊ “Create Temporary Taxon records at all lower ranks for each [higher taxon] record imported.” The name of the taxonomic rank you are importing (Family, in the example above) appears in the option text.
 - ◊ “Do not create any Temporary Taxon records based on the imported records.” If you choose not to create the temporary taxon records, the lower pair of buttons is disabled.
 - The lower pair of options controls the format of Species Codes in automatically created Species records. (You must choose to create temporary taxon records, as explained above, to enable these options.)
 - ◊ “For Species Codes use the first 5 letters of the [higher taxon] name plus the Sequence Number.” The name of the taxonomic rank you are importing (Family, in the example above) appears in the option text. This is the same format Biota uses for automatically created Species records based on manually entered higher taxon records. See “[How Biota Creates Temporary Taxon Records](#)” earlier in this chapter.
 - ◊ “For Species Codes use the first 20 letters of the [higher taxon] name.” This option provides more alphabetic information, but leaves less room for long sequence numbers. (The maximum number of characters allowed in a Species code is 30.)
5. Click the “OK” button to proceed with the import, under the settings you have selected. Or, click the “Cancel” button to abort the import.

Eliminating Unused Temporary Taxon Records

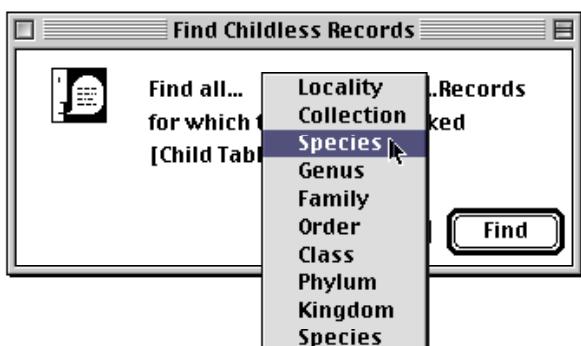
If you leave the option for the automatic creation of temporary taxon records enabled over a long period, you may discover that some of the temporary taxon records that Biota has created are not needed to link undetermined Specimen records with higher taxa.

You can find all currently unused temporary taxon records quite easily with the Childless Records tool in the Find menu (“[Finding Childless Records](#)” in Chapter 12).

1. From the Find menu, choose “Childless Records.” A table selection screen appears.



2. From the popup, select “Species.”

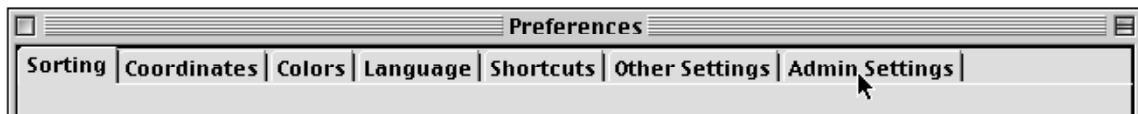


3. Click the “Find” button. Biota finds and displays childless Species records.
Depending on your Preference settings, Species records may already be sorted by Genus + Species Name. If not, use the “Sort” button in the Species Record Listing screen to order the records in this way (see “[Sorting Records in Record Listing Screens](#)” in Chapter 10 if you need help) or reset the Preferences (“Sorting” tab) to do so. Temporary taxon Species records, for which both Genus and Species begin with “(“ (the left parenthesis character) should sort at (or near) the top of the list.)
4. Delete all childless temporary taxon Species records that you do not anticipate using to link records for undetermined specimens.
5. Repeat the process with the Genus table, then the Family table, and so on up the taxonomic hierarchy.

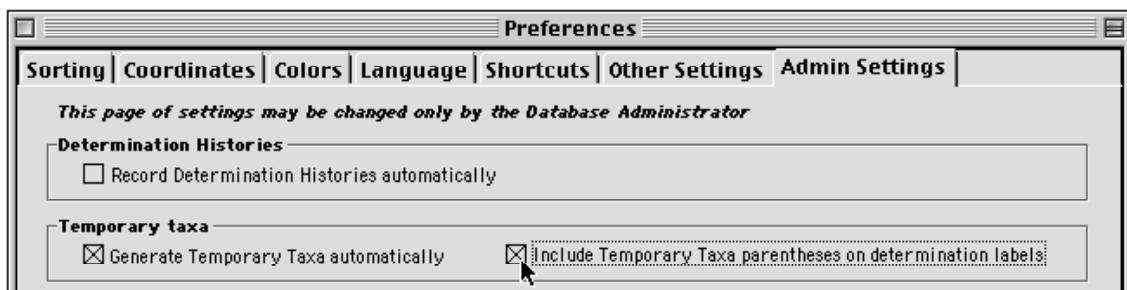
Temporary Taxa on Determination Labels

If you follow Biota's parenthesis convention for temporary taxon names (see “[Biota's Convention for Temporary Taxon Records](#)” earlier in this chapter), you can decide whether or not you want to print temporary taxon names on determination labels (see Chapter 15, “[Printing Labels](#)” for general information on printing determination labels of various kinds).

1. From the Special menu, select Preferences.
2. Click on the “Admin Settings” tab.



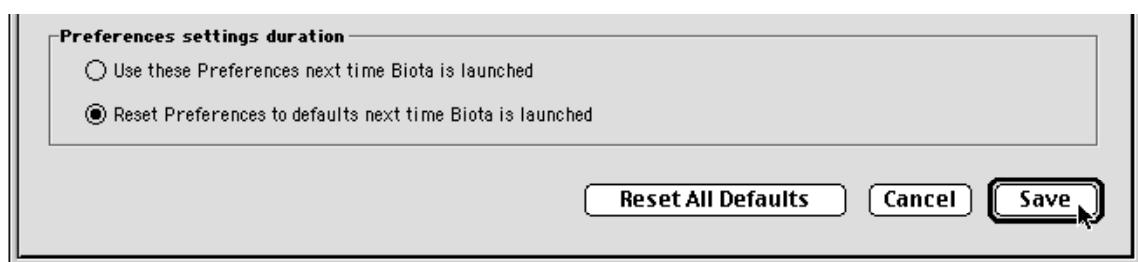
The Admin Settings tab screen appears.



3. To enable or disable the printing of temporary taxa parentheses on determination labels, click the checkbox labeled “Include Temporary Taxa parentheses on determination labels” to check it. To disable this option, click the checkbox to uncheck it (illustrated above).

Biota looks for an initial left parenthesis in specific names (Species Name), Genus names, and Family names (if you have checked the data option to include Family on the labels, see “[Data Options](#)” in Chapter 15), and includes or suppresses the opening and closing parentheses according to the setting of this preference.

4. Choose an option for saving any changes in Preference settings made during this Biota session.



- **If you want the changes to remain in force until altered** regardless of how many times Biota is launched in the meantime, choose the option “Use these Preferences next time Biota is launched.”
- **If you want the changes to be in force only for this session**, choose the option “Reset Preferences to defaults next time Biota is launched.”

The default setting for Determination Histories is unchecked (off).

5. **Click the “Save” button** on the Preferences screen.

Chapter 26

Security: Passwords and Access Privileges

Biota offers an optional *User Password system* that can be configured to your needs. You can use the Password Editor to set up a system of user passwords for yourself and other users and assign each user individualized access privileges. Each user can change his or her own password, but the Administrator has “Super User” privileges to change any password or access privileges. (See “[Using the Password Editor](#)” later in this chapter.)

If your database requires extra security, the Administrator can also activate an optional, secure link between your active copy of Biota and one or more Data Files (see “[Using the Data File Password Link](#)” later in this chapter).

For the highest level of security, running Biota4D under 4D Server in a secure room with password-protected access from remote clients is recommended (see “[If You Need High Security](#),” later in this chapter).

Activating and Deactivating the User Password System

When you first launch a new copy of Biota from the distribution disks, the User Password system is not activated. Biota opens without displaying the Password screen, shown here. You may choose to leave the User Password system deactivated if you are the only user or if you have confidence that no one else with access to your computer will launch Biota and alter a Data File in unintended or undesirable ways.



The cue Biota looks for to activate or deactivate the User Password system is the current password of the Administrator.

If the Administrator’s current password is the null string (no characters at all—not one or more space characters), the User Password system is deactivated. Assigning any other value to the Administrator’s password activates the User Password system. You can deactivate the system at any time by reassigning the null string as the Administrator’s password.

Activating the User Password System

1. **If Biota is not already launched, launch Biota, opening any Data File.** (If Biota is already launched, proceed to Step 2 instead.) You have been automatically signed on as “Administrator.”
2. **From the Special menu in Biota, choose “Change User Password.”**
The “Enter new password” request window appears (illustrated in the next step).
3. **Enter a password and click the “OK” button.** The password may consist of up to 15 characters, including letters, numbers, and symbols.



WARNINGS:

- a. This will be the Administrator’s password—*don’t forget it!*
 - b. Passwords are case sensitive. If you create a password that includes uppercase and/or lowercase letters, you must always reproduce the case of each letter precisely.
-

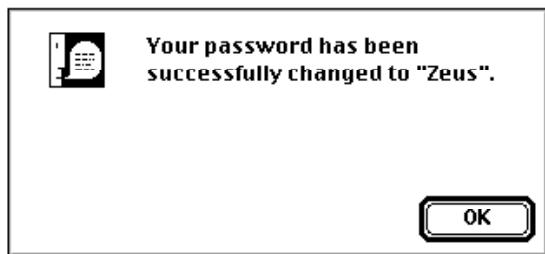
Biota responds by requesting the new password a second time (illustrated in the next step).

4. **Enter the same password again,** carefully repeating the case of each letter.



Click the “OK” button.

- If the two entries match, Biota confirms the new password.



- If the two entries do not match, Biota posts the message below. Your “old password” in this case is the null string (no characters at all) and the User Password system remains inactivated. To activate the User Password system, begin again with [Step 2](#), above.



Deactivating the User Password System

1. If Biota is not already launched, launch Biota with any Data File. (If Biota is already launched, proceed to [Step 2](#) instead.)
 - When the Password screen appears, enter the Administrator's User Name and the Administrator's current password, then click the “Connect” button.



NOTE: “Administrator” is the User Name assigned to the database Administrator when you first activate the User Password system. You can change the Administrator’s User Name (see “[Editing a User’s Password and Profile](#)” later in this chapter).

WARNING: Passwords are case sensitive. If the password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely. User Names are not case sensitive.

- **If the Password screen does not appear** during the launch, the User Password system has not been activated. Skip the rest of this section.
2. **From the Special menu in Biota, choose “Change User Password.”** The Password screen appears.
 3. **Enter the Administrator’s User Name and the Administrator’s *current password*** (as shown in [Step 1](#), above), then click the “Connect” button. If the password is correct, the “Enter new password” request window appears (illustrated in the next step).
 4. **Enter nothing at all and click the “OK” button.**



Biota responds by requesting the new “password” a second time (illustrated in the next step).

5. **Again, enter nothing at all and click the “OK” button.**



- **If the two null entries match,** Biota confirms the “new password” (the null string), indicated by two sets of double quotation marks, with no character between them.



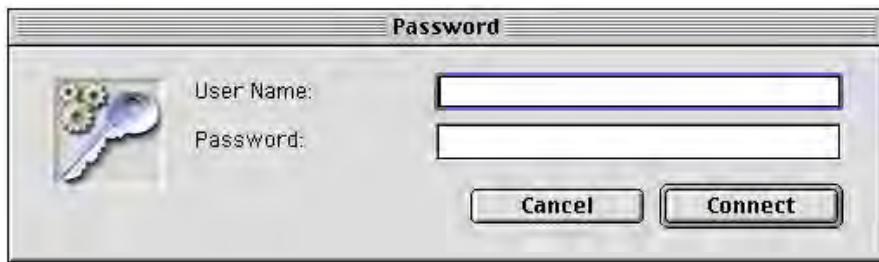
- If you made a mistake, Biota posts the message below. The old Administrator's password is still in force and the User Password system is still activated. To deactivate the User Password system, begin again with [Step 2](#), above.



Launching a Password-Protected Copy of Biota

If the User Password system has been activated, you must launch Biota by following these steps.

1. Double-click the Biota icon or application name (Or in Windows, select it from the Programs menu.) The Password screen appears.



2. Enter your User Name and press TAB. User Names are not case sensitive.
3. Enter your user password and press TAB. Passwords are case sensitive. If the password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely.

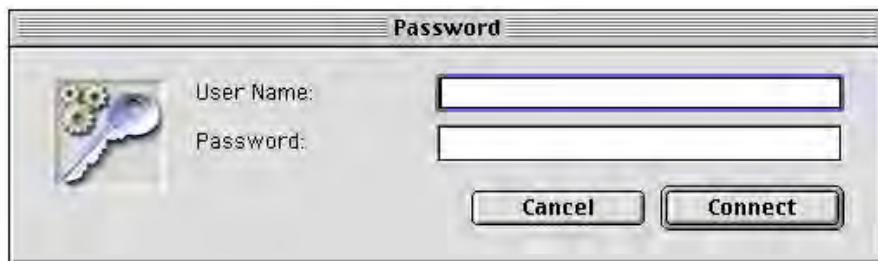


- **If you want to open the same Biota Data File** used the last time this copy of Biota was launched, click the “Connect” button in the Password window.
- **If you want to open a different Biota Data File** (or verify that the correct file will be opened), hold down the ALT key (Windows) or the OPTION key (Macintosh) while you click the “Connect” button in the Password window. Use the navigation window to find the correct Data File.

Changing Your User Password

If the User Password system has been activated, any user can change his or her own password at any time by following these steps.

1. **If Biota is not already launched, launch Biota with any Data File.** (If Biota is already launched, proceed to the next step.)
2. **From the Special menu in Biota, choose Change Password.** The Password screen appears.



3. **Enter your User Name and your *current* password,** then click the “Connect” button. If the password is correct, the “Enter new password” request window appears.



WARNING: Passwords are case sensitive. If the password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely. User Names are not case sensitive.

4. Enter the same password again, carefully repeating the case of each letter.
Click the “OK” button.



- If the two entries match, Biota confirms the new password.



- If the two entries do not match, Biota posts the message below. Your “old password” in this case is the null string (no characters at all) and the User Password system remains inactivated. To activate the User Password system, begin again with [Step 2](#), above.



Using the Password Editor

The Password Editor (an off-the-shelf 4th Dimension utility) is easy to use, once mastered, but the interface is not particularly intuitive. You will probably save time by reading or at least skimming this section before using the Password Editor.

NOTE: Once the User Password system has been activated, only the database Administrator can access the Password Editor.

Users, User Names, Passwords, Access Levels, and Privileges

Biota's implementation of the 4th Dimension User Password system is built on several key concepts.

- **A user record** is an individual record in the User Password system. (The User Password system is not an ordinary database table but, rather, an internal one that is not accessible to Biota's import and export tools.)
Each user record has an assigned *User Name*, *password*, and *Access Level*.
- **The User Name** can be any name the Administrator assigns to the user record, up to 30 characters, including letters, numbers, and symbols.
- **The password** can consist of up to 15 characters, including letters, numbers, and symbols.

WARNING: Passwords are case sensitive. If you create a password that includes uppercase and/or lowercase letters, you must always reproduce the case of each letter precisely.

- **The Access Level.** Biota offers five Access Levels, each with its own set of privileges. The privileges and Access Levels are outlined below and detailed in the table that follows. To assign an Access Level to a user, you assign the user to an *Access Group* that has those privileges.
 - ◊ **Super User.** The database Administrator, *only*, is assigned to the “Super User” Access Level, which allows the Administrator to use the Password Editor and enable or disable the Data File Password Link (see “[Using the Data File Password Link](#)” later in this chapter). The Administrator also has all the privileges of the Administration level (below).
 - ◊ **Administration.** Any user assigned to the “Administration” Access Level can find, display, print, export, create, modify, delete, or import records; change master settings; and use all the tools of the Special menu, with the exception of Edit Password System and Edit Data File Password Link. Only the Administrator can assign passwords and Access Levels using the Password Editor and enable or disable the Data File Password Link (see “[Using the Data File Password Link](#)” later in this chapter). Other users assigned to the Administration Access Level do not have these privileges.
 - ◊ **Read Write Export.** A user assigned to the “Read Write Export” Access Level can find, display, print, export, create, modify, or delete records, change certain settings in the Preferences screen, and change his or her own password. The Administrator, or another user with Administration privileges, can set limits on the number of records that can be deleted or created (see Appendix B, “[Setting Preferences](#)”) by users with Read Write Export privileges.
 - ◊ **Read Export.** A user assigned to the “Read Export” Access Level can find, display, print, or export records, change certain settings in the Preferences screen, and change his or her own password.
 - ◊ **Read Only.** A user assigned to the “Read Only” Access Level can find and display records, change certain settings in the Preferences screen, and change his or her own password.

Privilege	Super User	Administration	Read Write Export	Read Export	Read Only
Find records	✓	✓	✓	✓	✓
Display records	✓	✓	✓	✓	✓
Change password	✓	✓	✓	✓	✓
Print records, reports, & labels	✓	✓	✓	✓	
Use all export tools	✓	✓	✓	✓	
Create records	✓	✓	✓		
Modify records	✓	✓	✓		
Delete records	✓	✓	✓		
<i>Set Preferences for:</i> Determination Histories, Temporary Taxa, “Record Changed By” display, Record Deletion and Record Series Creation limits	✓	✓			
All other Preference settings	✓	✓	✓	✓	✓
Use Import Editor	✓	✓			
Web Server settings	✓	✓			
Use Find & Replace tool	✓	✓			
Set Field Value Defaults	✓	✓			
Enable/Disable Choice Lists	✓	✓			
Set Core Field Aliases	✓	✓			
Set default Record Code Prefixes	✓	✓			
Use Maintenance Utilities	✓	✓			
Create Guest Collection Records automatically	✓	✓			
Clear All Synonyms	✓	✓			
Delete Images by Record Set					
Find, modify, or delete Determination Histories using tools of the Special menu	✓	✓			
Use the Password Editor; Set the Data File Password Link	✓				
Add a Data File Segment	✓				
Enter/view Biota License Code	✓				

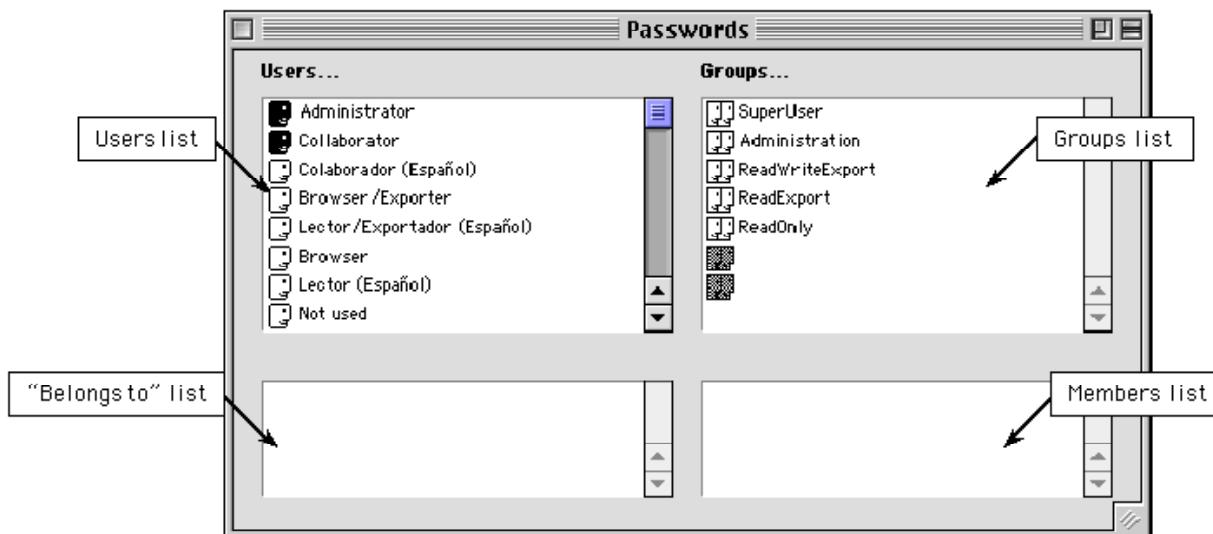
Opening and Closing the Password Editor

1. **Launch Biota and sign on as Administrator.** If you are already signed on as a different user, you need not quit Biota. Choose “Change Password” from the Special menu and sign on as Administrator without shutting down Biota. *Be sure to reenter the Administrator’s password correctly if you use this trick.*

NOTE: “Administrator” is the User Name assigned to the database Administrator when you first activate the User Password system. You can change the Administrator’s User Name (see “[Editing a User’s Password and Profile](#)” later in this chapter).

WARNING: Passwords are case sensitive. If a password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely. User Names are not case sensitive.

2. **From the Special menu, choose Edit Password System.** The Password Editor appears.



The Password Editor consists of four scrollable lists: the “Users” list, the “Belongs To” list, the “Groups” list, and the “Members” list. When you first display the Password Editor, the lower two list panels are blank.

The Password Editor has its own menu bar with a Passwords menu.

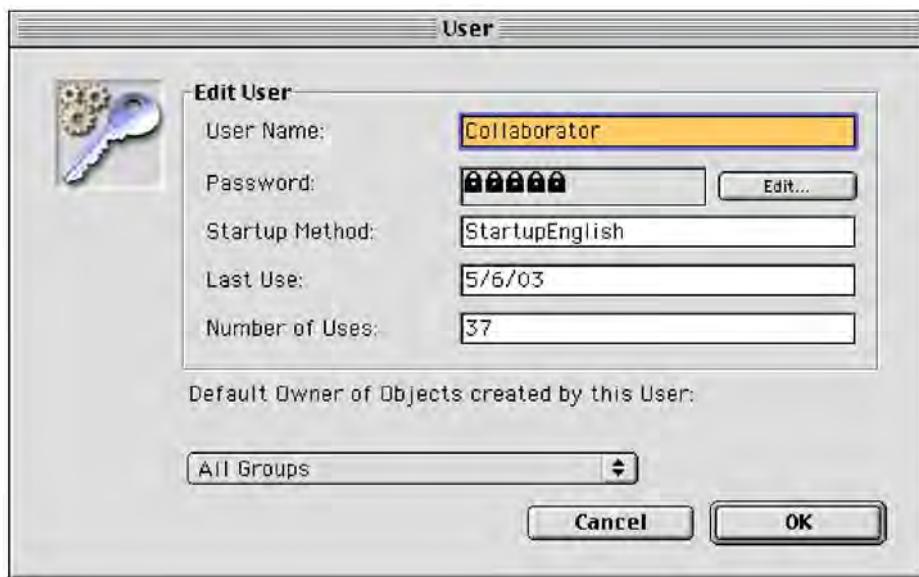
When you first activate the User Password system (see “[Activating the User Password system](#)” earlier in this chapter), Biota offers a set of generic User Names (e.g., Collaborator, Browser, etc.), in addition to Administrator, as shown above. These default user records have different access privileges and startup Language settings that you can use as models. You can use the Password Editor to change these entries to suit your own needs, or leave them as they stand.



3. To close the Password Editor and save any changes, click the close box in the Password Editor window. (There is no Save or Close command in the menus.)

Editing a User's Password and Profile

1. Open the Password Editor (see the previous section, "[Opening and Closing the Password Editor](#)").
2. Double-click a User Name in the Users list or select a User Name and choose "Edit User" from the Passwords menu. The "User" screen appears.



In the "User" screen, you can assign or modify the following settings:

- **User Name.** A User Name can include up to 30 characters, including letters, numbers, and symbols.
 - ◊ You can change any of the default User Names to suit your needs.
 - ◊ You cannot delete user records themselves, although you can add additional user records (see "[Adding a New User Record](#)" later in this chapter).

WARNING: You may change the User Name for the Administrator. However, the first record in the User Password system, and only that record, is permanently assigned the privilege of access to the Password Editor and Data File Password Link. Furthermore, the first record must be assigned to the Super User group to activate these privileges (see "[Users, User Names, Passwords, Access Levels, and Privileges](#)" earlier in this chapter).

- **Password.** A password can include up to 15 characters, including letters, numbers, and symbols.
 - ◊ When you first activate the User Password system in Biota, each of the default users has a nonsense password assigned, for safety's sake. You will

need to replace the password for any of the default user records you want to use.

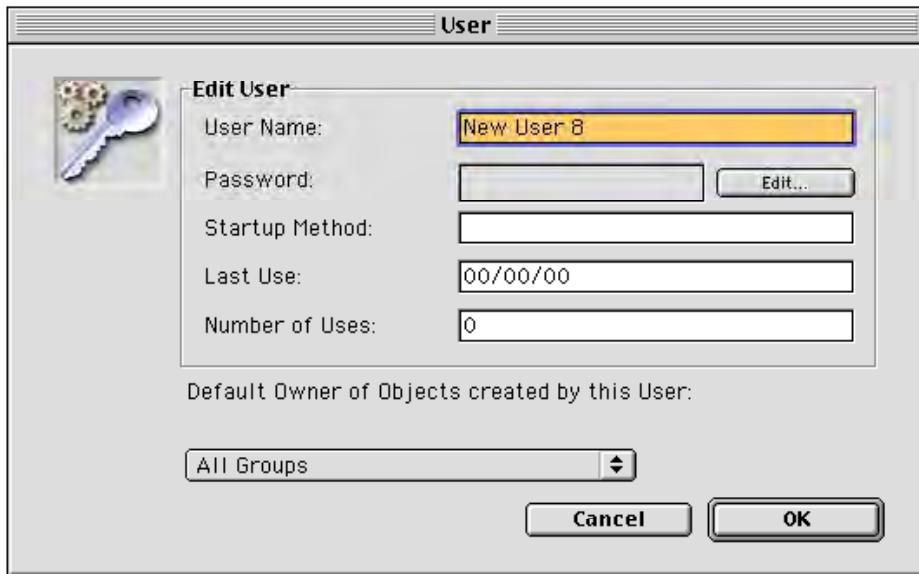
- ◊ **Once you assign a password**, it will appear as a string of "lock" symbols in the "User" screen, as shown above. If you are not sure about an existing password (the user may have changed it), delete the characters and reenter the correct password.
 - **Startup procedure.** Biota has two alternative startup procedures, *StartupEnglish* (no spaces) and *StartupSpanish* (no spaces).
 - ◊ **If you assign StartupEnglish** (no spaces) to a particular user, Biota displays the English language version of all dialogue screens (instructions, options, warnings, errors, and result reports) for that user, regardless of the saved Language setting in the Preferences screen (Special menu) (See "[The 'Language' Tab](#)" in Appendix B.)
 - ◊ **If you assign StartupSpanish** (no spaces) to a particular user, Biota displays a Spanish language version of all dialogue screens (instructions, options, warnings, errors, and result reports) that are accessible to users with Read Write Export, Read Export, or Read Only privileges, regardless of the saved Language setting in the Preferences screen (Special menu). Dialogue screens accessible only to users with Administration access privileges are displayed in English for all users. (The justification for this policy is the Administrator needs to be able to read this manual, which is not available in Spanish.) All menus are in English for all users.
 - ◊ **If you leave the "Startup procedure" blank**, Biota displays dialogue screens in English or Spanish, depending on the saved Language setting in the Preferences screen. If no user is likely to change the Language setting in the Preferences screen, you can leave the Startup procedure setting blank for all users.
 - **"Last use" and "Number of uses."** These areas display usage statistics for the user. You can delete the displayed value to reset the counters. (Oddly, the counters are also editable, if you can think of some legitimate reason to edit them.)
 - **"Default owner of objects created by this user."** This panel has no function in a compiled application such as Biota. Ignore it.
3. **When the user profile is complete, click the "OK" button** in the User screen to record it.
 4. **To close the Password Editor and save any changes**, click the close box of the Password Editor window. (There is no Close or Save command in the menus.)

Adding a New User Record

You can add as many new user records as necessary to the User Password system. However, once a user record is added, it can be edited but cannot be deleted. (This puzzling limitation is built into 4th Dimension.) Although user records require very little additional memory, you may wish to "recycle" the existing user records by editing them, before adding any new ones.

1. **Open the Password Editor** (see "[Opening and Closing the Password Editor](#)," earlier in this chapter).

- From the Password menu, choose “New User.” The User screen appears with a temporary name for the new user.

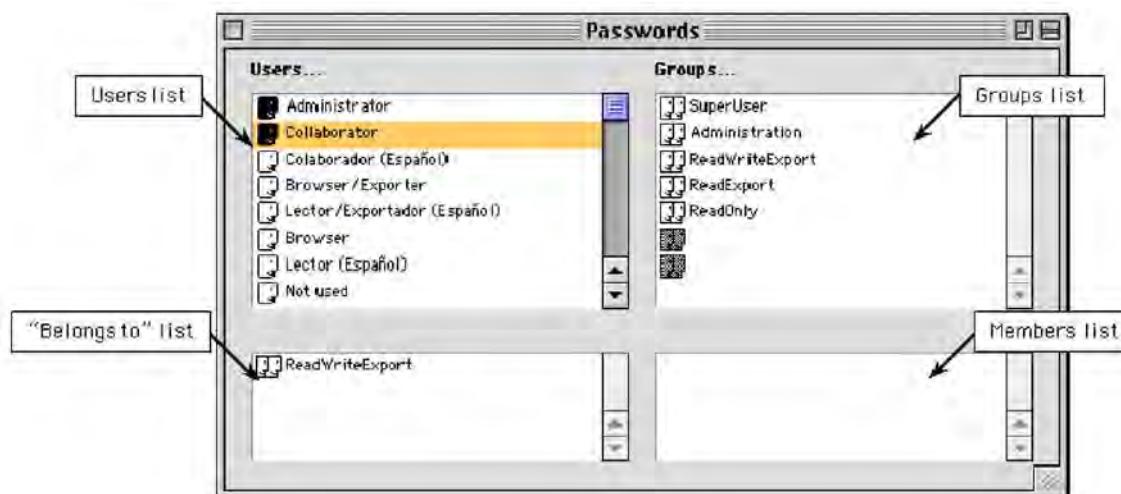


- Follow the guidelines in the previous section ([“Editing a User’s Password and Profile”](#)) to complete the new user record and close the Password Editor.

Assigning Users to and Removing Users from Access Groups

Access Levels (see [“Users, User Names, Passwords, and Access Levels”](#) earlier in this chapter) are determined for individual users in the Users list by assigning users to **Access Groups**. Biota has five preset Access Groups, each named for the Access Level assigned to the group. These Access Groups appear in the Groups list when you open the Password Editor.

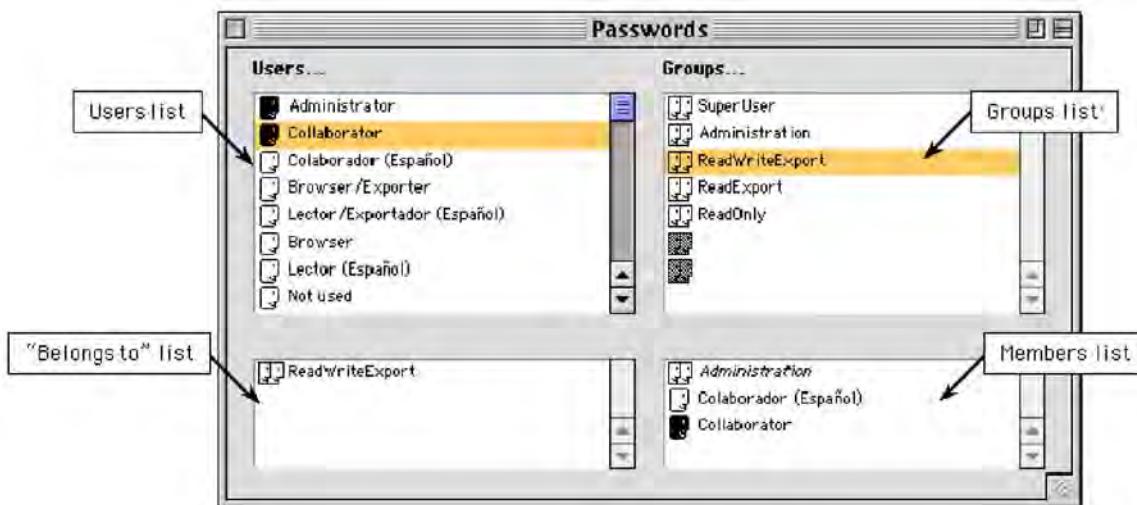
- Open the Password Editor (see [“Opening and Closing the Password Editor”](#) earlier in this chapter).
- Select a User Name in the Users list by clicking it once. The “Belongs to” list shows the Access Group (or groups) to which the user currently belongs.



In the example above, the User Named Collaborator belongs to the Read Write Export Access Group.

The “Belongs to” list will be blank if the selected user has not been assigned to any Access Group.

3. To remove a user from an Access Group, follow these steps:
 - a. In the Users list, select (single-click) the user to verify which group or groups the user belongs to (see [Step 2](#), above).
 - b. In the Groups list, select (single-click) the Access Group from which you wish to remove the user. The user’s name should appear in the Members list in the lower right panel.



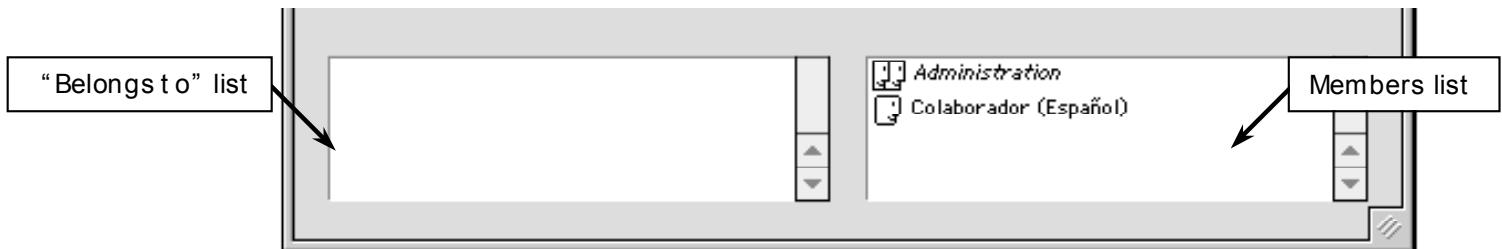
Notice that Collaborator is included in the Members list for the Read Write Export group along with Colaborador and Administration—the Administration group. (Groups that are members of other groups are shown in italics with a “double-head” icon; see [“Pitfalls to Beware and Features to Ignore in the Password Editor”](#) later in this chapter.)

- c. Using the mouse, select the name of the user in the Members list and drag it anywhere outside the Members list panel. In the illustration below, the user



called Collaborator is being removed from the Read Write Export group.

When you release the mouse button, the user's name disappears from the Members list, and the Access Group name disappears from the “Belongs to” list.

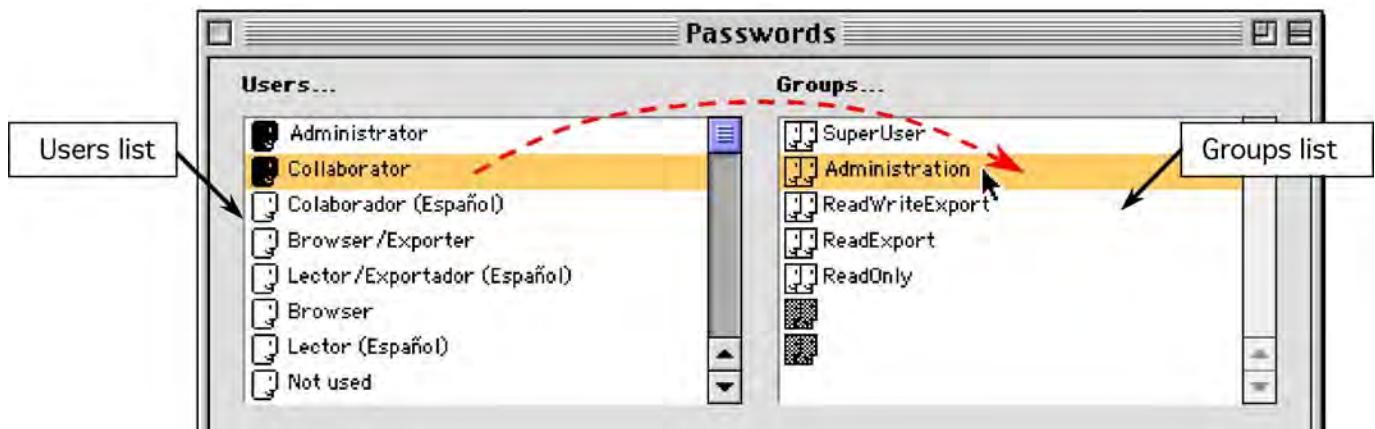


4. To add a user to an Access Group, follow these steps:

- In the Users list, select (single-click) the user to verify to which Access Group or groups the user currently belongs (see [Step 2](#), above). If the user belongs to the wrong group, remove the user from the group using the technique in [Step 3](#), above, before proceeding.

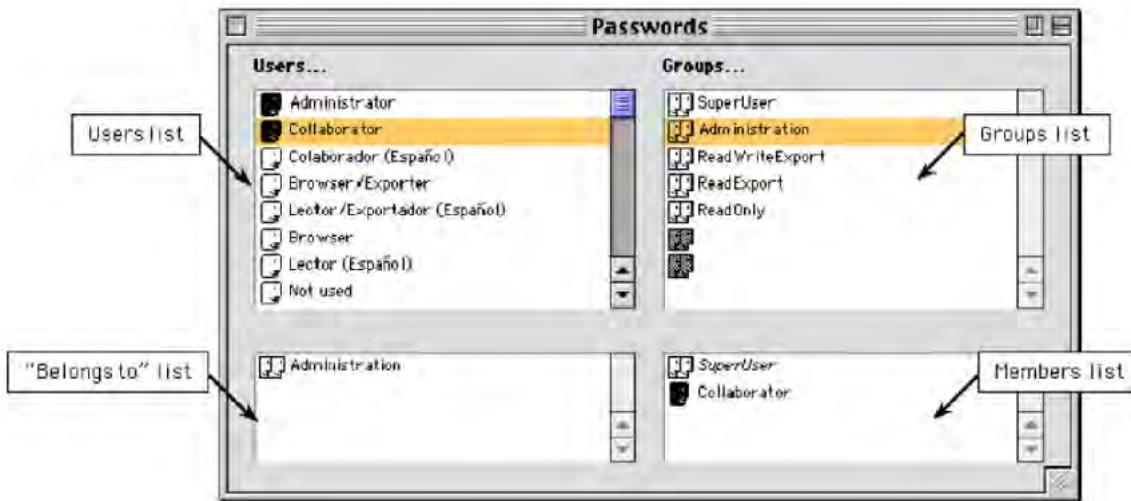
NOTE: In Biota, since access privileges are strictly hierarchical, there is no point in a user belonging to more than one Access Group (although the Password Editor permits it).

- Drag the user's name from the Users list over the name of the group (in the Groups list) to which you want to assign the user. In the illustration below, the user called Collaborator is being dragged over the "Administration" Group name in the Groups list.



- When the correct Access Group name is highlighted, release the mouse button ("drag and drop").

As shown below, the user's name now appears in the Members list, along with all other members of the group. The name of the Access Group now appears in the "Belongs to" list.



- To add a new user, click the 'New User' button at the bottom of the 'Users...' list. A 'New User' dialog box appears, prompting for a name and password. Click 'OK' to add the user.
- To add a new group, click the 'New Group' button at the bottom of the 'Groups...' list. A 'New Group' dialog box appears, prompting for a name and password. Click 'OK' to add the group.
- To change the password for a user or group, select the user or group in the list and click the 'Edit' button at the bottom of the list. An 'Edit User' or 'Edit Group' dialog box appears, allowing you to change the password. Click 'OK' to save changes.
- d. To close the Password Editor and save any changes, click the close box of the Password Editor window. (There is no Close or Save command in the menus.)**

Pitfalls to Beware and Features to Ignore in the Password Editor

The Password Editor and its Password menu include a number of features that have no application in Biota. This section of the chapter is intended to warn against certain changes and satisfy the curious.

- If you double-click the name of a group or select “Edit Group” from the Password menu, an “Edit group” window appears, in which you can change the name of the group. *Do not change the name of Biota’s preset Access Groups, or the access restrictions will not work.* Biota looks for these particular group names in order to limit access appropriately. *There is absolutely nothing useful you can do with the Edit Group tool.*
- Do not change the hierarchical (italicized) group memberships for higher Access Groups (although the Password Editor permits it). Specifically, the Super User group must remain a member of the Administration group, the Administration group must remain a member of the Read Write Export group, and the Read Write Export group must remain a member of the Read Export group for the hierarchical privilege system to work.

If you accidentally change these settings, drag the appropriate group name in the Groups list and drop it on the name of the group (also in the Groups list) of which it should be a member, to recreate the hierarchy—or install a fresh copy of Biota from the distribution CD or online source.

- If you select the “New Group” command from the Password menu, a new group icon will appear in the Groups list. *The Password Editor does not allow you to remove groups, once created.*

You can use this command to create your own groups, if you can think of a reason to do so.

- The “Save Groups,” “Load Groups,” and “External Package Access” commands in the Password menu have no function in Biota.

Moving User Names, User Passwords and Access Group Assignments to a New Copy of Biota

For security reasons, the User Password system is part of the Biota application itself, not a component of Biota Data Files. If you have set up a custom list of User Names, passwords, and Access Group assignments, and you need to install a fresh copy or a new version of Biota, you will have to move the information to the new copy manually. Here is a suggested strategy:

1. **Launch the old copy or old version of Biota** (sign on as the Administrator).
2. **Open the Password Editor** (see “[Opening and Closing the Password Editor](#)” earlier in this chapter).
3. **Copy down the list of User Names** (or, better, use the screen capture utility in your operating system to copy it and paste it in a document). You can expand the Password Editor window as large as your monitor screen permits.
4. **Select each user, one at a time, and record his or her group membership** from the “Belongs to” list.
5. **Double-click each user, one at a time, and record his or her Startup procedure**, if any.
6. **Quit the old copy or version of Biota and launch the new one.**
7. **Recreate the password and access scheme** in the new version, based on your notes or screen captures.

Using the Data File Password Link

The User Password system protects your copy of the Biota application from unauthorized use, as detailed in the previous sections of this chapter. By assigning access privileges to each user, authorized users can be restricted to activities appropriate to their training and responsibilities (see “[Assigning Users to and Removing Users from Access Groups](#)” earlier in this chapter). The password and User Access system, however, does not in itself protect Biota *Data Files* from unintended or unauthorized access, which could occur by means of the unauthorized or accidental installation of an unprotected copy of Biota.

You can create a secure link between a *particular* copy of Biota and a *particular* Data File (or Files) using a *Data File Password Link*, as detailed below. You need not activate the User Password system in order to activate the Data File Password Link, although it usually makes sense to activate the User Password system if the Data File Password Link is used. (The two systems are technically independent.)

Here's how the Data File Password functions:

- **New Biota Data Files** do not have the Data File Password Link activated.

- Any Biota Data File that has not had the Data File Password Link activated can be opened by any copy of Biota. (If the User Password system has been activated, however, the user must have a valid User Name and password to launch Biota. Such a user is referred to, below, as an *authorized user*.)
- Once you activate the Data File Password Link for a particular Data File (see “[Activating the Data File Password Link](#)” later in this chapter), the copy of Biota that you used to activate the Link opens *that particular Data File* without requiring authorized users to enter the Data File Password.
- If you use a fresh copy or a new version of Biota to open a protected Data File, Biota will request the Data File Password at startup (see “[Opening a Password-Protected Data File with a New Copy or New Version of Biota](#)” later in this chapter).
 - ◊ If the correct Data File Password is entered, that copy of Biota will open the file thereafter without requiring authorized users to enter the Data File Password.
 - ◊ If the correct password is not entered (in up to three attempts), Biota quits without opening the Data File.
- If you assign the same Data File Password to more than one Data File, using the same copy of Biota, all such files will open for any authorized user, without requesting the Data File Password.

Activating the Data File Password Link

When you create an empty Biota Data File (see “[Creating an Empty Biota Data File While Launching Biota](#)” in Chapter 3), the Data File Password in the Data File is blank (a null string); the file can be opened with any copy of Biota. (If the User Password system has been activated, you must have a valid User Name and password to launch Biota, however.)

To activate the Data File Password Link, take these steps:

1. Launch Biota.

- If the User Password system has been activated, sign on as “Administrator” (or with the alternative User Name you have given the user with Super User privileges).
- If the Password screen does not appear when you launch Biota, the User Password system has not been activated. You are automatically signed on as Administrator.
- If you are already signed on as a different user, you need not quit Biota. Choose “Change Password” from the Special menu and sign on as Administrator without shutting down Biota. *Be sure to reenter the Administrator’s password correctly if you use this trick.*

NOTES:

- a. “Administrator” is the User Name assigned to the database Administrator when you first activate the User Password system. You can change the Administrator’s User Name (see “[Editing a User’s Password and Profile](#)” earlier in this chapter).
 - b. You need not activate the User Password system in order to activate the Data File Password Link. The two systems are functionally independent.
2. From the Special menu, choose “Edit Data File Password Link.”
- If the Data File Password Link has not been activated, this message appears:



Continue with the next step in this section.

- If the Data File Password Link has already been activated, this message appears instead:



Go to the next section of this chapter, “[Changing the Data File Password](#).”

3. Click the “OK” button in the message window. A password request window appears (illustrated in the next step).

4. **Enter the new Data File Password** (below) and click the “OK” button. The password can consist of up to 15 characters, including letters, numbers, and symbols.

You will need this password to open the Data File if you install a fresh copy or a new version of Biota, or if you need to change the Data File Password—don’t forget it!



Warning: Data File Passwords are case sensitive. If you create a Data File Password that includes uppercase and/or lowercase letters, you must always reproduce the case of each letter precisely.

Biota responds by requesting the new password a second time (illustrated in the next step).

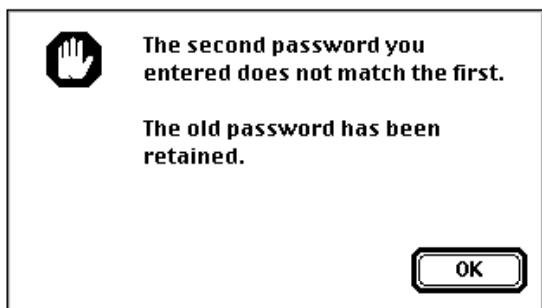
5. **Enter the same password again**, carefully repeating the case of each letter. Click the “OK” button.



- **If the two entries match**, Biota confirms the new password and warns you not to forget it.



- If the two entries do not match, Biota posts the message below. The Data File Password Link remains inactivated. To activate it, begin again with [Step 2](#), above in this section.



6. Click the “OK” button in the message window.

Changing the Data File Password

To change the password for the Data File Password Link, take these steps:

1. **Launch Biota.** If the User Password system has been activated, sign on as “Administrator” (or with the alternative User Name you have given the user with Super User privileges). See [Step 1](#) in the previous section “[Activating the Data File Password Link](#),” earlier in this chapter, for details.
2. **From the Special menu, choose “Edit Data File Password Link.”**
 - If the Data File Password Link has been activated, this message appears:



Continue with the next step in this section.

- If the Data File Password Link has not been activated, this message appears instead:



Go to the previous section of this chapter, “[Activating the Data File Password Link](#).”

3. Click the “OK” button in the message window. A password window appears, requesting the *current* Data File Password.



4. Enter the current Data File Password and click the “OK” button.

WARNING: Data File Passwords are case sensitive. If the Data File Password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely.

- If you enter the correct password, Biota requests the new Data File Password.



See [Step 4](#) in the section “[Activating the Data File Password Link](#),” earlier in this chapter, for instructions on completing the process of entering the new password.

- If you do not enter the correct password, Biota posts this message:



Deactivating the Data File Password Link

To deactivate the Data File Password Link, take these steps:

1. Follow Steps 1 through 4 in the previous section, “[Changing the Data File Password](#).”
2. When Biota requests the new Data File Password, enter nothing at all and click the “OK” button.



Biota responds by requesting the new “password” a second time (illustrated in the next step).

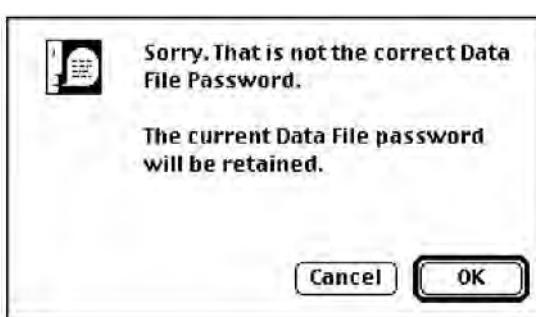
3. Again, enter nothing at all and click the “OK” button.



- If the two null entries match, Biota confirms the deactivation of the Data File Password Link.



- If you made a mistake, Biota posts the message to the right. The old Data File Password is still in force and the Data File Password Link is still activated. To deactivate the link, begin again with [Step 1](#), above in this section.



Opening a Password-Protected Data File with a New Copy or New Version of Biota

To open a password-protected Data File with a new copy or a new version of Biota, take these steps.

1. **Launch the new copy or new version of Biota**, finding and opening the existing Data File as detailed in the section “[Opening a Biota Data File When Launching Biota](#)” in Chapter 3.

If the Data File is protected by a Data File Password Link, the following request will appear near the end of the startup process:



2. **Enter the Data File Password** and click the “OK” button.



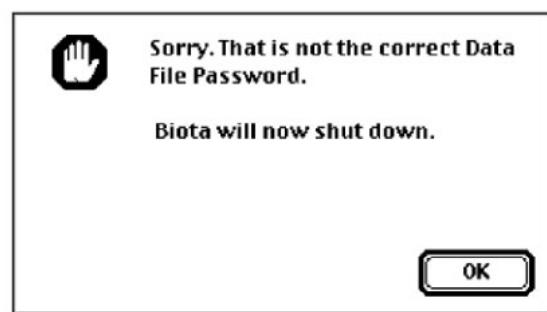
WARNING: Data File Passwords are case sensitive. If the Data File Password includes uppercase and/or lowercase letters, you must reproduce the case of each letter precisely.

You have three chances to enter the correct Data File Password.

- **If you enter the correct password**, Biota completes the startup process.

This copy of Biota is now authorized to open this particular Data File in the future, without requesting the Data File Password.

- **If you do not enter the correct password** in three attempts, Biota posts the message on the right and shuts down.



Using the Data File Password Link with Backup Files

One motivation for implementing a Data File Password Link is to guard against well-intended but mistaken use of the wrong Data File. Backup copies of Data Files are particularly easy to confuse with the active copy of the same file.

Of course you should always make regular backups of any actively used Biota Data File, using a clear naming convention for the backup files (see Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#)”).

If you decide to use the Data File Password Link, consider changing the Data File Password (see “[Changing the Data File Password](#)” earlier in this chapter) in each backup, using the same naming convention for the Data File Password that you use for the file name, so you can open the backups later if necessary. With this strategy, the Data File Password for the *active* Data File remains constant and each backup has a distinct Data File Password that you can remember easily, should it ever be needed.

If You Need High Security

The User Password system and Data File Password Link features of Biota are designed to prevent accidental damage to your database through carelessness, ignorance, or foolishness. A clever hacker can break into any file to which he or she has direct access, including Biota Data Files. Of course, a hacker with direct access to the machine that holds your database can find a way to copy any file in its entirety anyway.

If your database requires the highest level of security (if it includes collection or incidence localities for endangered species of commercial value, for example), you should not rely on software tools, alone, for security. Instead, run Biota4D under 4D Server (Appendix E) in a physically secure room, and allow access to your database only through 4D Client on remote machines, with the User Password system enabled. All authentication of passwords is done by Biota4D on the Server, and the Data File itself resides only on the Server. There is no data caching on Client machines between Biota sessions. This is not an inexpensive solution, but good security is rarely cheap.

PART

7

Exporting and Importing Data

Chapter 27 Exporting Data

Any database that cannot easily export any required set of fields and records in digital form is likely to become a La Brea tarpit of extinct information. Biota has been designed for maximum longevity for your data. There is nothing you can put into a Biota Data File that you cannot later export to files that can be opened, read, and edited by text processors, spreadsheet applications, database management applications, or image processing applications.

- **General purpose export tools described in this chapter**
 - ◊ **Biota's Export Editor** (see "[Exporting Data by Tables and Fields](#)" later in this chapter) makes it easy to control the scope and format of any text data you need to export from individual Biota tables to plain text flatfiles. (A *flatfile* is a row-by-column table of records and fields.)
 - ◊ **The Quick Report Editor** (a 4th Dimension utility) offers an alternative way to create your own, custom export format, by using fields from several tables at once (see "[Exporting Custom Flatfiles](#)" later in this chapter). With the Quick Report Editor, you can save the format, as well as exported text files, to disk.
- **Special purpose export tools described in this chapter**
 - ◊ **Tools for exporting Notes.** See "[Exporting Notes](#)" later in this chapter.
 - ◊ **A tool for exporting Taxonomic Flatfiles** that show the taxonomic classification for any selection of taxa. See "[Exporting Taxonomic Flatfiles](#)" later in this chapter).
 - ◊ **A tool for exporting Specimen-based flatfiles**, including virtually any field in any Biota table. See "[Exporting Specimen Flatfiles](#)" later in this chapter.
 - ◊ **A tool for exporting formatted text for "Specimens Examined"** (or "Exsiccatae") sections of taxonomic monographs. See "[Exporting Specimens Examined Lists for Publications](#)" later in this chapter.
 - ◊ **A tool for exporting incidence or abundance matrices** for input to ordination and other statistical procedures. See "[Exporting Place- by-Taxon Incidence or Abundance Tables](#)" later in this chapter.
- **Special purpose export tools described in other chapters**
 - ◊ **Tools for exporting Images** in individual or batch mode. See "[Exporting and Importing Images](#)" in Chapter 19.

- ◊ **Tools for exporting Auxiliary Fields.** See “[Exporting Auxiliary Field Values](#)” in Chapter 16.
- ◊ **Tools for exporting References.** See “[Exporting References](#)” in Chapter 20.
- ◊ **A tool for exporting NEXUS matrices** (created in Biota Auxiliary Fields) for input to MacClade, PAUP, or other applications See “[Exporting Auxiliary Fields in the NEXUS Format](#)” in Chapter 16.
- ◊ **A tool for exporting hyperlinked static Web pages** for any selection of records and taxonomic scope, including Images and host-guest links. See Chapter 33, “[Exporting Static Web Pages](#).”

NOTE: Exporting data from a Biota Data File has no effect on the records in the file. A copy of the data is exported to a text file, leaving the records themselves unaltered.

Exporting Data by Tables and Fields

Biota’s Export Editor (“Export by Tables and Fields,” from the Im/Export menu), can export data to disk files from any Biota table, one table at a time (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). If you need to combine fields from several Biota tables in an export file, use a different export tool (see the overview of export tools at the beginning of this chapter).

The Export Editor creates free-format, delimited text (ASCII) files, such as the column-by-row, plain text files you can read and create with a spreadsheet application (e.g., Microsoft Excel), or import as text flatfiles to database management applications (e.g., SQL Server, Access, FileMaker, or 4th Dimension) or Geographic Information Systems (GIS) applications.

Text files created by the Export Editor can be read in unaltered form by Biota’s Import Editor (see Chapter 28, “[Importing Data](#)”), making it easy to move records from one Biota Data File to another (see Appendix G, “[Merging Two Biota Data Files](#)”).

The Export Editor is designed to make exporting data flexible and easy. You choose a Biota table to export from, and then choose which of its fields you want to export and which records to export. You have complete control over the number and order of fields in text files you create by exporting data, which need not match the number or order of fields in the Biota source table. You can specify your choice of field and record delimiters for the text file. If you wish, Biota can create column headings for the text file, based on Biota field names.

NOTE: Although you may assign any character you wish as a record delimiter (see “[Exporting by Tables and Fields: Step by Step](#)” later in this chapter), this section assumes that you are exporting *tab-delimited* text files (using a line end character or characters: ASCII Character 13 for Macintosh, ASCII 13 + 10 for Windows), so that Biota records become table rows, and Biota fields become table columns in the exported text file.

Key Fields

Most of the tables in Biota's structure (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) have a Key field (Record Code, taxon name, etc.; see “[Key Fields](#)” in Chapter 3) that contains a unique value for each record. The exceptions are the Notes tables and the Determination History table, which do not require a unique Key (the “Record Code” fields in these child tables are “foreign keys” that need not be unique), and the Auxiliary Field Value and Reference Links tables, which have a two-field (composite) Key.

Generally speaking, you will need to include the Key field, if there is one, among the fields to be exported, so you can tell records apart in the text file that may be otherwise identical. The Key field *must* be included (for any table that has one) if you intend later to use the Import Editor to import text files into another Biota Data File (see Chapter 28, “[Importing Data](#)”).

Field Types and Field Lengths

Appendix A (“[Biota Tables, Fields, and Relational Links](#)”) shows the field type and field length (maximum number of characters) for each field in the Biota data structure. When you export data from a Biota field, the exported data will reflect the type (and length) of the Biota field it represents, as detailed below.

- **Alphanumeric fields.** A value exported from an alphanumeric field may include any ASCII characters. Biota exports only what it finds in an alphanumeric field without adding trailing space characters. (In other words, Biota exports free-format fields, not fixed-length fields.) For a particular alphanumeric field, the number of characters exported will vary from none (if there was no entry in that field for a particular record) to the maximum indicated for the field in [Appendix A](#). If a field to be exported is blank in a record, Biota nonetheless exports the field delimiter character, so that columns in the exported file will be correctly aligned.
- **Date fields.** Before exporting dates, please read or review the “[Dates](#)” in Chapter 9. Whenever you select a Date field, using the Export Editor, Biota offers you a choice of three standard date formats for the export.

If you want exported dates in some other format, you must convert them after export. Spreadsheet applications (e.g., Microsoft Excel) can easily convert columns of dates from the International or U.S. date output formats to any other format, by applying format commands for date columns in the spreadsheet.



- **Partial Dates: Date Flag fields.** As explained in full in “[Importing and Exporting Partial Dates](#)” in Chapter 9, for some date fields, Biota can display and print partial dates: Month-Year dates and Year-only dates. These fields are [Collection] Date Collected, [Collection] Date Coll End, [Specimen] Date Prepared, and [Specimen] Date Determined. Each of these *Date fields* is paired with an integer *Date Flag field* (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

If you are exporting complete dates only, you need not export any values for Date Flag fields, which have the value 0 (zero) for complete dates.

If you need to export partial dates, you should include the corresponding Date Flag field along with the Date field in the list of fields to be exported. In the text file produced by the Export Editor, you can then decode partial dates, as follows:

- ◊ **Month-year dates.** For a month-year date (e.g., May 1975), the Date field itself will be exported as a complete date. The corresponding Date Flag field will contain a “1,” the code for a month-year date. The value of the Day element in the Date field of month-year dates is arbitrary. If the records were created in Biota, however, Biota’s own convention will have been applied: the first day of the month (e.g., May 1, 1975 for May 1975).
- ◊ **Year-only dates.** For year-only dates (e.g., 1975), the Date field itself will be exported as a complete date. The corresponding Date Flag field will contain a “2,” the code for a year-only date. The values of the Day and Month elements in the Date field of year-only dates are arbitrary. If Biota created the records, however, Biota’s own convention will have been applied: the last day of the year (December 31, 1975 for 1975).
- **Latitude and Longitude fields.** These two fields in the Locality table are of type Real. Regardless of the coordinate display setting in the Preferences screen (see “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#)” in Chapter 9), Latitude and Longitude are exported by the Export Editor in decimal degrees, the standard for GIS, using the GIS conventions for hemispheres:
 - ◊ **North and East** are positive values.
 - ◊ **South and West** are negative values.

After export, you can convert decimal degrees to traditional Degree-Minute-Second coordinates or to Degrees and Decimal Minutes (used by some GPS devices) by the formulas detailed in the section “[Conversion Formulas for Latitude and Longitude Unit Systems](#)” in Chapter 9.

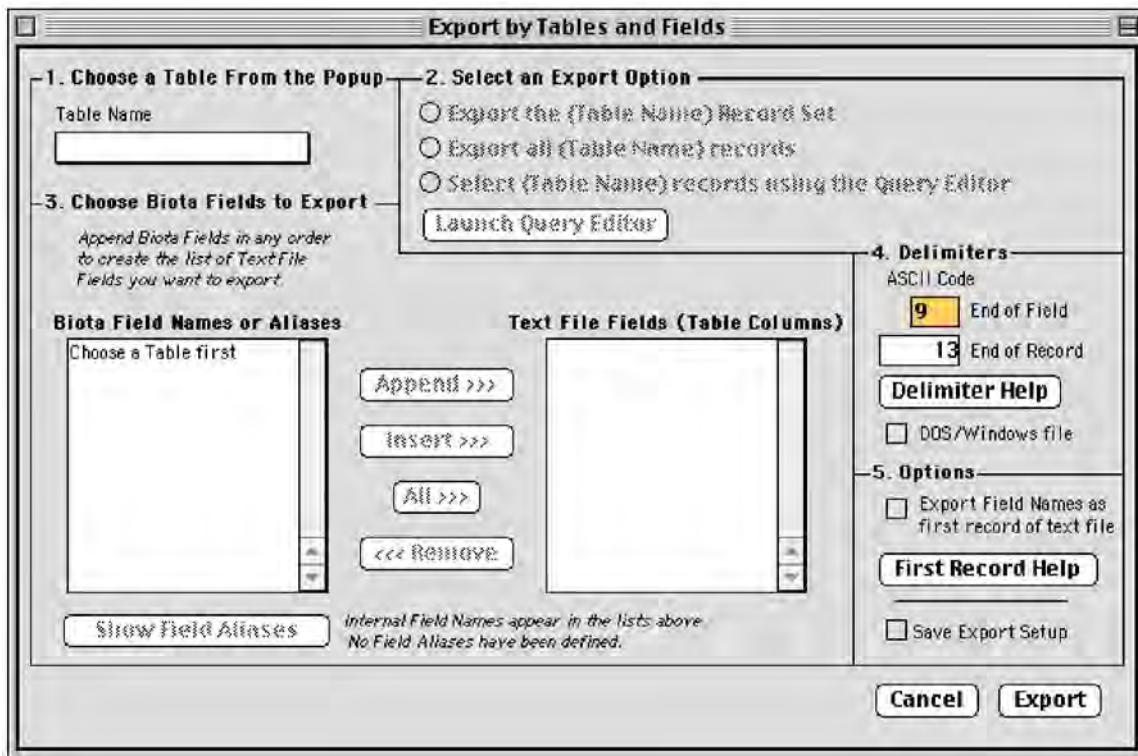
- **Text fields.** Biota uses text fields for the “Locality Name” field in the Locality table, for the “Note” and “Heading” fields of the Project table, for several fields in the Reference table, for the “Notes” field in the Personnel table, for the “Description” field of the Loans table, and for the “Note Text” fields of Notes tables. A text field may contain up to 32,000 characters.
- **Boolean fields.** Boolean fields have one of two values: True or False. In an exported text file, a Boolean field will have either a zero (for False) or a 1 (for True). There are only 3 Boolean fields in Biota:
 - ◊ **The “Group” field in the Personnel table** which, when True, identifies a Personnel record as a Group Name record, rather than an Individual record. The Group field has the value False for an individual (see “[Entering Personnel Data: The ‘Group’ Tab](#)” in Chapter 11).
 - ◊ **The “Project” field in the Personnel table** which, when True, identifies a Personnel record as a Project-Linked record, rather than an Individual record. (See “[Personnel Input](#)” in Chapter 11).
 - ◊ **The “Active” field in the Project table** which, when True, identifies a Project record as the Active Project record (there is only one Active Project at any given time). See “[Project Input](#)” in Chapter 16.
- **Picture field.** You cannot export the “Picture” (Image) field in the Image Archive table using the Export Editor (although you can use it to export the alphanumeric

fields in the Image Archive table). Images can be exported to disk files using other Biota tools. See “[Exporting and Importing Images](#)” in Chapter 19.

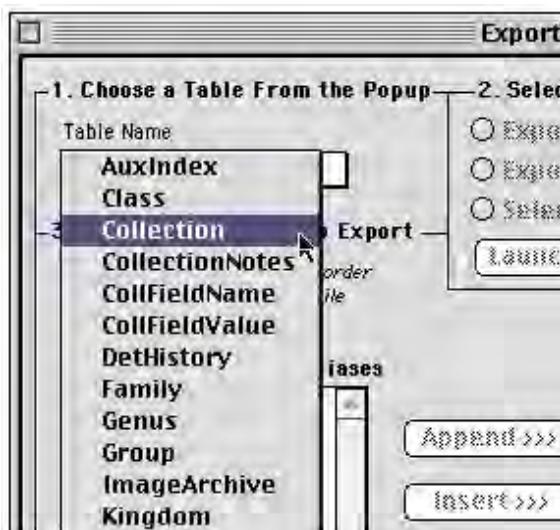
Exporting by Tables and Fields: Step by Step

Follow these steps to export records from a Biota Data File using the Export Editor. This tool exports the fields and records you choose, for one Biota table at a time.

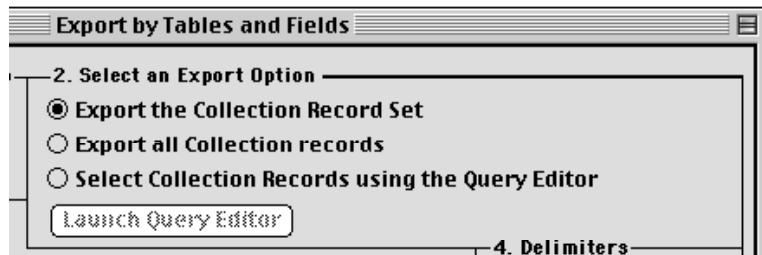
1. Choose **Export by Tables and Fields** from the Im/Export menu. The Export Editor appears.



2. Select a table. From the “Table Name” popup list at the upper left, select the name of the Biota table from which you want to export records (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).



- 3. Select the records for export.** The three option buttons in the upper-right panel define your options for selecting records for export. Once you choose a table from the popup list, the words *Table Name* in the button text are replaced by the name of the table you selected (“Collection” in this example).



- **Export the [Table Name] Record Set.** This option is *enabled* if the table you choose is a Core table (see “[Core Tables](#)” in Chapter 3) or the Determination History table (see Chapter 22, “[Determination Histories](#)”), and you have previously defined a current Record Set for the table (see “[Record Sets](#)” in Chapter 3).

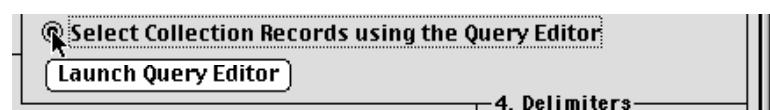
If you choose this option (when it is enabled), values for the fields you choose (field choice is described in a later step in this section) will be exported for each record in the current Record Set when you launch the export.

The button is *disabled* under two circumstances:

- ◊ If you select a Peripheral table other than Det History.
- ◊ If you select a Core table or the Determination History table, but the current Record Set for the table is empty. In this case, Biota posts the message illustrated below.



- **Export all [Table Name] records.** This option is available for all tables. If you click this button, values for the fields you choose (in a later step in this section) will be exported for *all* records in the table when you launch the export.
- **Select [Table Name] records using the Query Editor.** This option is available for all tables except for the Lists table, from which all records must be exported (see “[Transferring Choice Lists to a Different Biota Data File](#)” in Chapter 17). If you choose this button, the “Launch Query Editor” button is activated.



When you click the “Launch Query Editor” button (above), the Query Editor appears, set to search among all records for the table you selected. (See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12, for help using the Query Editor.) If you use this method to select records, Biota will inform you how many records it found, before you continue with the rest of the Export procedure. When you launch the export, the fields you select will be exported for the records you found using the Query Editor, as detailed below.

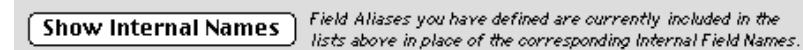
- 4. Using the “Field Name/Alias” button.** The button below the “Biota Field Names or Aliases” panel controls whether Biota lists strictly Internal Field Names (as given in Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) or substitutes a Field Alias for the corresponding Internal Field Name for each field you have given an Alias. (See Chapter 18, “[Re-naming Fields](#),” to learn about Field Aliases.)

- **If no Aliases have been defined,** the button is disabled and reads: “Show Field Aliases.” The caption to the right of the button reads: “Internal Field Names appear

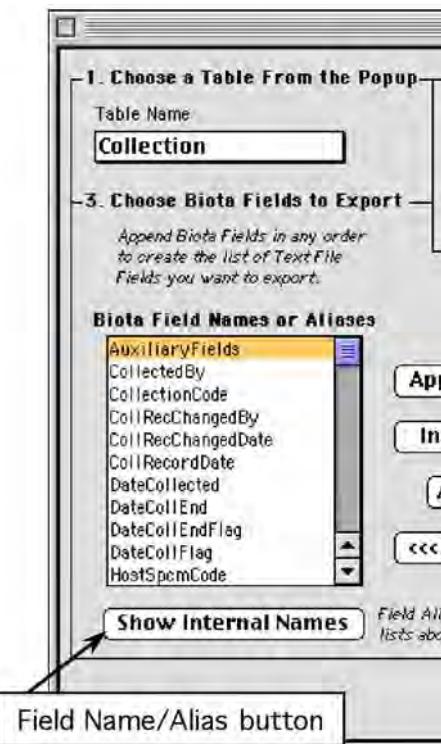


in the lists above. No Field Aliases have been defined.”

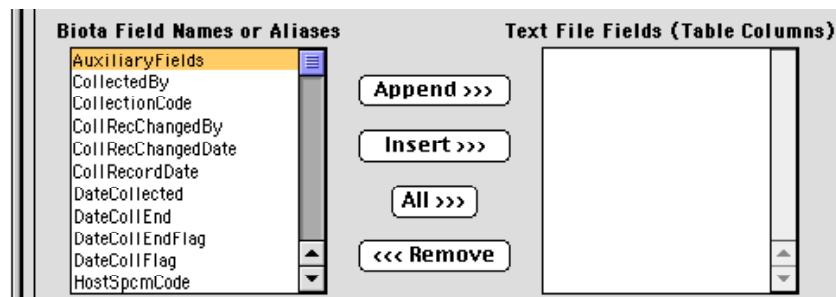
- **If any Aliases have been defined,** when you first open the Export Editor the button is enabled and reads: “Show Internal Names.” The caption to the right of the button reads: “Field Aliases you have defined are currently included in the lists above in place of the corresponding Internal Field Names.”



- **If you click the “Show Internal Names” button,** the button text changes to “Show Field Aliases” and the caption reads: “Internal Field Names appear in the lists above. Click the button to the left to include the Field Aliases you have defined.”



- 5. Choose the fields to export.** The Biota Field Names or Aliases panel is simply a source of field names. The panel labeled Text File Fields (Table Columns), at the right, is the list Biota will consult in exporting data from your Biota Data File to a text file.



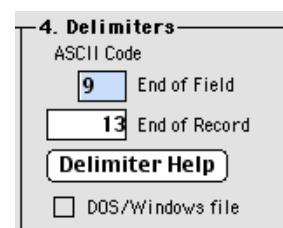
6. Use the buttons

between the two lower panels in the Export Editor to create the list of fields in the “Text File Fields” panel. The list of fields you create can include any or all of the field names or aliases from the list available, in any order. You can even repeat fields if you want.

- **“Append” button.** Click a field in the “Biota Field Name” panel to select it, then click the “Append” button. The field name is added to the end of the list in the “Text File Fields” panel.
- **“Insert” button.** Click a field already listed in the “Text File Fields” panel to select it. Then click the field in the “Biota Field Name” panel that you want to insert. When you click the “Insert” button, the new field is inserted just *above* the selected field in the “Text File Fields” panel.
- **“All” button.** The “All” Button is a toggle. When the button text reads “All>>>,” it means “Append All.” If you click the button, all fields in the “Biota Field Name” panel are entered in the “Text File Fields” panel (in the order listed in the Field Name Panel), *replacing* any fields already listed in the “Text File Fields” panel. The button text then changes to read “<<<All,” meaning “Remove All.” If you click the button again, the “Text File Fields” panel is cleared and the button text changes back to “All>>>.”
- **“Remove” button.** To remove a single field already entered in the “Text File Fields” panel, select the field by clicking it in the list, then click the “Remove” button.



- 7. Set the Field and Record Delimiters.** In the “Delimiters” panel of the Export Editor, you specify the characters Biota will insert between fields (columns) and at the end of records (rows) in the exported text file. You may use any characters in the standard ASCII set (Characters 33–126), but, of course, they must make sense in the context of other applications you intend to use in working with the text file. The “Delimiter Help” button presents a list of common options.



- **Windows:** The default delimiters are TAB (ASCII Character 9) for the field delimiter and RETURN + LINE FEED (ASCII Characters 13 + 10), for the record delimiter—the characters that Windows spreadsheet applications use for “TAB-separated values” text files.

If you are exporting data to a Macintosh text file, using a Windows machine, click the “DOS/Windows File” checkbox to *uncheck* it. The “End of Record” box will then read “13.”

- **Macintosh:** The default delimiters are TAB (ASCII Character 9) for the field delimiter and RETURN (ASCII Character 13) for the record delimiter—the characters that Macintosh spreadsheet applications use for “TAB-separated values” text files.

If you are using a Mac OS machine to export data to a PC (DOS or Windows) text file that uses the standard PC line termination (RETURN + LINE FEED, ASCII Characters 13 + 10), click the “DOS/Windows File” checkbox to set the check mark. The “End of Record” box will then read “1310.”

8. **Set the Options.** There are two checkboxes in the “Options” panel. Both are unchecked, by default.

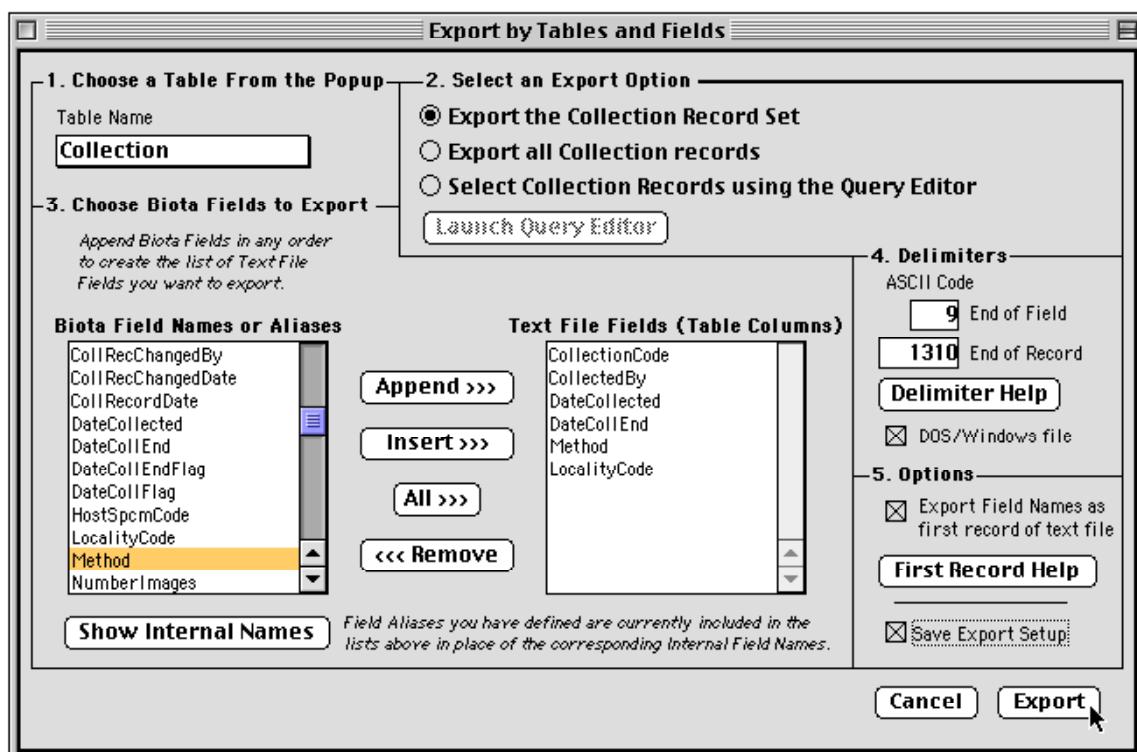
- **“Export Field Names...” Checkbox.** If you want the first row (record) of the exported text file to consist of column headings, you should check this option. Biota will use the Internal Field Names to create column headings. If you have included any Aliases in the list of fields to be exported, however, Biota will instead create headings from Aliases, where appropriate.



You can click the “First Record Help” button to review these instructions in context.

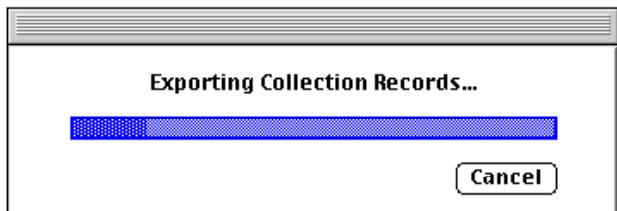
- **“Save Export Setup” Checkbox.** If you check this option, Biota will remember the way you have set up the Export Editor, even if you Cancel without attempting to export, for the duration of the current Biota session, or until you make changes in the setup.

9. **Launch the export.** When the list of “Text File Fields” and the settings are ready, click the “Export” button to launch the export process.

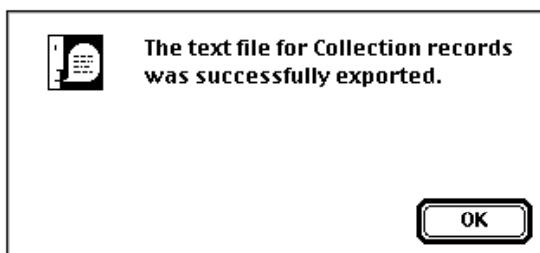


The standard “Save File” window for your operating system appears.

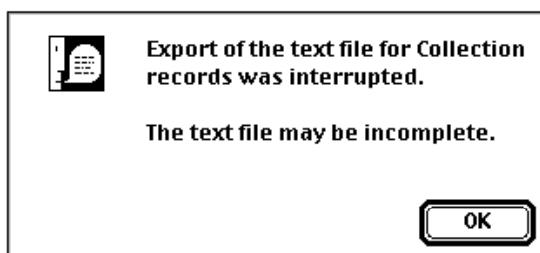
10. **Name the text file.** Find the folder or directory where you want to create the text file, name the file, and click the “OK” button (Windows) or the “Save” button (Macintosh). The progress indicator appears.



When the export is complete, a message informs you.



11. **To halt the export,** click the “Cancel” button in the progress window. Biota posts a warning that the text file may be incomplete.



NOTE: You can carry out other tasks with Biota or other applications while the export is in progress.

Exporting Notes

For five Biota Core tables—Specimen, Species, Collection, Locality, and Loans—you can create as many Notes as you want for each Core table record. Each Note is actually a separate (child) record in a Notes table, linked to a parent record in the Core table (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

Biota provides two tools for exporting Notes records, the Export Editor and the Export Notes tool from the Im/Export menu. The Export Editor produces text files containing fields you select from Notes tables *only*. In contrast, the Export Notes tool exports certain fields from each parent record, along with full records for each selected Note.

Exporting Notes with the Export Editor

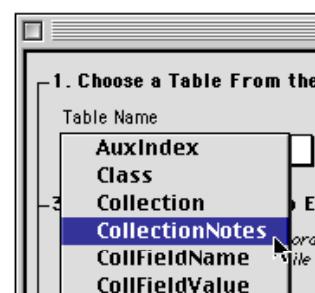
The Export Editor is discussed in detail earlier in this chapter (see “[Exporting Data by Tables and Fields](#)”). Using the Export Editor, you can export any of the following:

- All Notes records that are linked to any record in the current Record Set for the parent table (see the next section of this chapter, “[Exporting Notes Records Linked to Records in the Current Parent-Table Record Set](#)”).
- All Notes records for a particular Notes table (see “[Exporting All Notes Records for a Notes Table](#)” later in this chapter).
- Notes records you find using the Query Editor (from the Export Editor itself), based on content of the Notes records themselves, or on the content of parent records (see “[Exporting Notes Records Based on Their Own Content](#)” or “[Exporting Notes Records Based on the Content of Parent Records](#)” later in this chapter).

Exporting Notes Records Linked to Records in the Current Parent-Table Record Set

To illustrate, suppose you want to export all *Collection* Notes for a particular group of Collection records. Although Collection Notes will be used as an example, *the technique is the same for any Core table with Notes* (Species, Specimen, Locality, and Loans, as well as Collection).

1. **Display the group of Collection records for which you want to export Notes**, using any technique from the Find menu (see Chapter 12, “[Finding and Updating Records](#)”).
2. **Designate these records as the current Collection Record Set** (see “[Record Sets](#)” in Chapter 3).
3. **From the Im/Export menu, select “Export by Tables and Fields”** to open the Export Editor.
4. **Select the “Collection Notes” table** from the “Table Name” popup list.
5. **Click the first option button**, which will be activated and will read: “Export CollectionNotes records for the Collection Rec Set.”



2. Select an Export Option
<input checked="" type="radio"/> Export CollectionNotes records for the Collection Rec Set <input type="radio"/> Export all CollectionNotes records <input type="radio"/> Select CollectionNotes Records using the Query Editor <input type="button" value="Launch Query Editor"/>
4. Delimiters

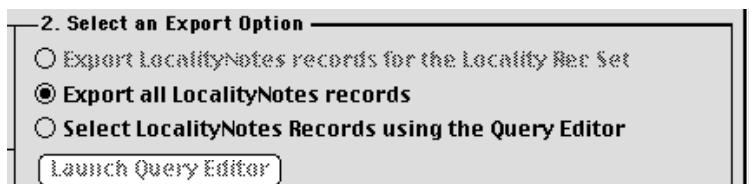
If the Collection Record Set is currently empty, this option is disabled (dimmed).

6. Complete the export Editor setup and launch the export by following the instructions in [Steps 4–11](#) of the section “[Exporting by Tables and Fields: Step by Step](#)” earlier in this chapter.

Exporting All Notes Records for a Notes Table

To illustrate, suppose you want to export all *Locality* Notes from a Biota Data File. Although Locality Notes will be used as an example, *the technique is the same for any Core table with Notes* (Species, Specimen, Collection, and Loans, as well as Locality).

1. From the Im/Export menu, select “Export by Tables and Fields” to open the Export Editor.
2. Select the “Locality Notes” table from the “Table Name” popup list.
3. Click the second option button, labeled “Export All LocalityNotes records.” (If the Locality Record Set is empty, this will be the default option and the first option will be disabled—dimmed, as illustrated below.)

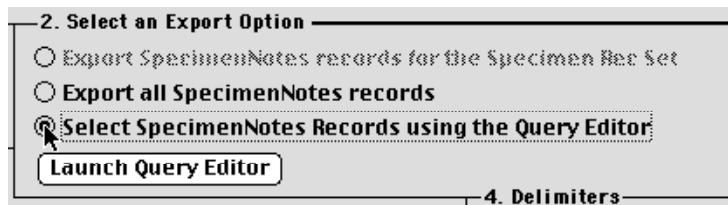


4. Complete the export Editor setup and launch the export by following the instructions in [Steps 4–11](#) of the section “[Exporting by Tables and Fields: Step by Step](#)” earlier in this chapter.

Exporting Notes Records Based on Their Own Content

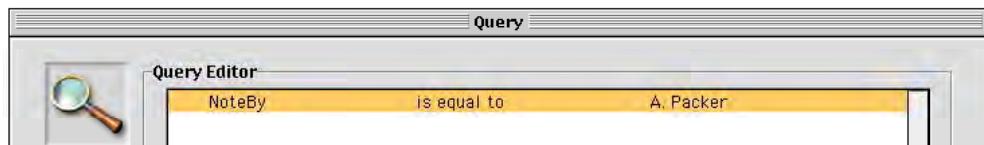
To illustrate, suppose you want to export all *Specimen* Notes written by “A. Packer.” Although Specimen Notes will be used as an example, *the technique is the same for any Core table with Notes* (Species, Collection, Locality, and Loans, as well as Specimen).

1. From the Im/Export menu, select “Export by Tables and Fields” to open the Export Editor.
2. Select the “Specimen Notes” table from the “Table Name” popup list.
3. Click the third option button, labeled “Select Specimen Notes Records using the Query Editor.”



4. Click the “Launch Query Editor” button. The Query Editor appears.

5. In the Query Editor, set up the query, for example: “Note By *is equal to* A. Packer” and launch the search. (See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12 for detailed instructions on using the Query Editor.)



NOTE: The Query Editor looks for precise matches when you use the “is equal to” operator. For this example it might be wiser to use the “contains” operator instead, so that notes by “A. Packer” as well as “Adolph Packer,” “A. L. Packer,” “A Packer,” and “APacker” would all be found.

6. Complete the export Editor setup and launch the export by following the instructions in [Steps 4–11](#) of the section “[Exporting Data by Tables and Fields](#)” earlier in this chapter.

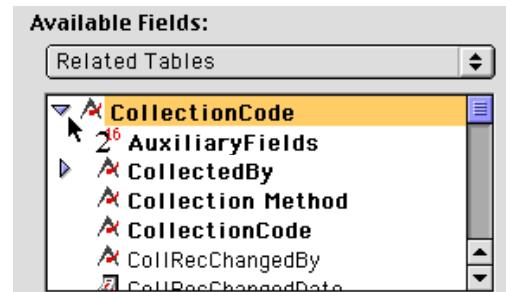
Exporting Notes Records Based on the Content of Parent Records

To illustrate, suppose you want to export to a text file all *Collection Notes* for *collections made by* (not for all notes written by) “A. Packer.” Although Collection Notes will be used as an example, *the technique is the same for any Core table with Notes* (Species, Specimen, Locality, and Loans, as well as Collection).

1. From the Im/Export menu, select “Export Table and Fields” to open the Export Editor.
2. Select the “Collection Notes” table from the “Table Name” popup list.
3. Click the third option button, labeled “Select Collection Notes Records using the Query Editor” (see the previous section for an illustration).
4. Click the “Launch Query Editor” button. The Query Editor appears.
5. In the Query Editor, display the fields for the Collection table (*not* the Collection Notes table) in the “Biota Field Names” panel.

Example: Click on the triangle next to “Collection Code” to expand the field list for the Collection table, then select “CollectedBy.” Set up the search criterion “Collected By *is equal to* A. Packer” and launch the search.

(See the note at [Step 5](#) of the previous section of this chapter, “[Exporting Notes Records Based on Their Own Content](#),” for a suggestion regarding variations in personal names. See “[The Query Editor, a General-Purpose Tool for Finding Records Based on Content](#)” in Chapter 12 for detailed instructions on using the Query Editor.)



6. Complete the export Editor setup and launch the export by following the instructions in [Steps 4–11](#) of the section “[Exporting Data by Tables and Fields](#)” earlier in this chapter.

Note: In addition to using parent record content to select Notes records for export, you can also use the content of *any related table farther up the same hierarchy* to select Notes records, using the Query Editor directly from the Export Editor, as illustrated above. For example, you could select and export all Specimen Notes for a Family, or all Collection Notes for Localities in Peru.

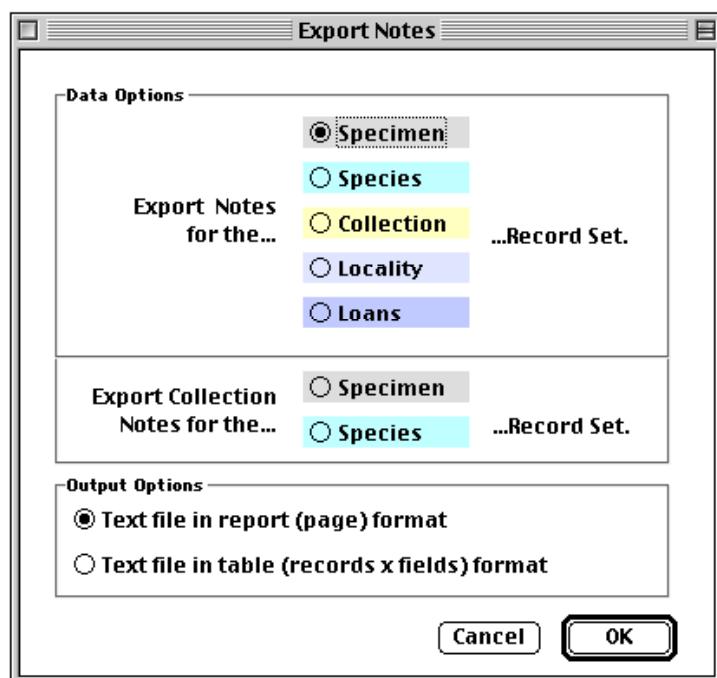
Exporting Notes Records Using the Export Notes Tool

The Export Editor produces text files containing fields only from Notes tables themselves. In contrast, the “Export Notes” tool exports not only the full record for each attached Note, but also certain fields from each parent record in a Record Set, as well as important fields from other linked Core tables, where appropriate.

For example, if you print Specimen Notes using the “Export Notes” tool, Biota exports, for each Specimen record in the current Specimen Record Set: Specimen Code, Specimen Record Date, Genus, Specific Name, Collected By, Date Collected, Locality Name, and all fields (Note Date, Note By, and Note Text) for each Note associated with the Specimen Record (see the example below).

Here is the procedure for using the Export Notes tool.

1. Find the Species, Specimen, Collection, Locality, or Loans records whose Notes you want to export (or the Specimen or Species records for which you want to export linked Collection Notes).
2. Establish the records as the current Record Set for the table. (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
3. From the Im/Export menu, select “Export Notes.” The Export Notes option screen appears.



4. **Select a Data Option from the upper panel** in the Export Notes screen.
 - **The top pane of the “Data Options” panel** offers export of Notes records and information from their parent records (and other related records, as appropriate) for each of the five Core tables that support Notes.
 - **The bottom pane of the “Data Options” panel** permits you to export Collection Notes based on the current Specimen or Species Record Set. Each Collection Note is printed only once, even if several Specimen or Species records are linked to the Note’s parent Collection Record.
5. **Select an Output Option** from the lower panel in the Export Notes screen.
 - **Either:** “Text file in report (page) format.”
 - **Or:** “Text file in table (records X fields) format.”

Output examples based on these options appears below.
6. **Click the “OK” button** in the Export Notes screen. Biota presents an option screen with a choice of Data format, then the standard Save File window for your operating system appears.
7. **Name the text file.** Find the folder or directory where you want to create the text file, name it, and click the “OK” button (Windows) “Save” button (Macintosh). The progress indicator appears. You can click the “Cancel” button in the progress indicator window at any time to halt the export.

Sample output from the Export Notes tool is illustrated below, for the Specimen table. Notice that the first Specimen record has two notes. Biota exports all notes for each parent record in the parent table Record Set. Notice, also, that information from related Core tables (Species and Collection) is included for each Specimen record.

Text file in report (page) format:

```
*****
SPECIMEN CODE: HMSB001; RECORD DATE: 21 May 1996; GENUS: Geospiza;
SPECIES: fortis; COLLECTED BY: C. Darwin; DATE COLLECTED: 19 Sep 1932;
LOCALITY NAME: San Cristóbal Island
NOTE DATE: 9 Oct 1832; NOTE BY: C. Darwin
NOTE TEXT: Time of collection 7:20 in the morning.
NOTE DATE: 2 Jun 1939; NOTE BY: D. Lack
NOTE TEXT: Bill exceptionally wide for this species.
*****
```

```
SPECIMEN CODE: HSB002; RECORD DATE: 14 May 1996; GENUS: Geospiza;
SPECIES: fortis; COLLECTED BY: R. Fitzroy; DATE COLLECTED: 18 Sep 1832;
LOCALITY NAME: San Cristóbal Island
NOTE DATE: 14 Sep 1832; NOTE BY: R. Fitzroy
NOTE TEXT: Collected 350 rods inland from the landing.
*****
```

```
SPECIMEN CODE: HSB003; RECORD DATE: 14 May 1996; GENUS: Geospiza;
SPECIES: fuliginosa; COLLECTED BY: R. Fitzroy; DATE COLLECTED: 18 Sep 1832;
LOCALITY NAME: San Cristóbal Island
NOTE DATE: 21 Jun 1955; NOTE BY: D. Lack
NOTE TEXT: Specimen typical of this species for this island.
```

Text file in table (records X fields) format

SPECIMEN CODE	SPCM RECORD DATE	GENUS	SPECIES	COLLECTED BY	DATE COLLECTED	LOCALITY NAME	NOTE DATE	NOTE BY	NOTE TEXT
HMSB001	21 May 1996	Geospiza	fortis	C. Darwin	19 Sep 1932	San Cristóbal Island	9 Oct 1832	C. Darwin	Time of collection 7:20 in the morning.
HMSB001	21 May 1996	Geospiza	fortis	C. Darwin	19 Sep 1932	San Cristóbal Island	2 Jun 1939	D. Lack	Bill exceptionally wide for this species.
HMSB002	14 May 1996	Geospiza	fortis	R. Fitzroy	18 Sep 1832	San Cristóbal Island	14 Sep 1832	R. Fitzroy	Collected 350 rods inland from the landing.
HMSB003	14 May 1996	Geospiza	fuliginosa	R. Fitzroy	18 Sep 1832	San Cristóbal Island	21 Jun 1955	D. Lack	Specimen typical of this species for this island.

NOTE: If you want to create a Record Set for *all* parent (Core table) records that have Notes attached to them, for a particular Core table, you can use the following trick:

- a. From the Find menu, select “By Using Query Editor.”
- b. From the popup list of tables, select the *parent* table for the Notes (e.g., the Specimen table), then click the “Search” button.
- c. In the Query Editor, select the related *Notes* table (e.g., the Specimen Notes table) in the Fields panel (see “[Using Fields from Child Tables in the Query Editor](#)” in Chapter 12 for help switching to the Notes table in the Fields panel).
- d. Set up a query of this form: *SpecimenCode is not equal to !@#\$%^&**. In this query, *be sure to use the Record Code field from the Notes table, not the parent table*. For the text string to search for, you can use any garbage you like instead of *!@#\$%^&**, just as long as it cannot possibly be a real Record Code in your Data File.
- e. When the Core table records (Specimen records, in this example) are found, click the “Done” button and create a Record Set for them. Then use the Export Notes tool (explained in this section) to export the related Notes.

Exporting Taxonomic Flatfiles

A common way of organizing lists of taxa is a *taxonomic flatfile*, with taxa of a lower taxonomic level (rank) as rows and information on the higher classification of those taxa in columns. In the example below, the rows are plant species, and the columns show the specific name, genus, and family for each of these plant species.

Family	Genus	Specific Name
Campanulaceae	<i>Centropogon</i>	<i>caoutchouc</i>
Campanulaceae	<i>Centropogon</i>	<i>erianthus</i>
Campanulaceae	<i>Lobelia</i>	<i>laxiflora</i>
Campanulaceae	<i>Lobelia</i>	<i>salicifolia</i>
Campanulaceae	<i>Siphocampylus</i>	<i>ecuadorensis</i>
Campanulaceae	<i>Siphocampylus</i>	<i>sanguineus</i>
Campanulaceae	<i>Siphocampylus</i>	<i>scandens</i>
Ericaceae	<i>Anthopterus</i>	<i>verticillatus</i>
Ericaceae	<i>Cavendishia</i>	<i>forreroi</i>
Ericaceae	<i>Cavendishia</i>	<i>gilgiana</i>
Ericaceae	<i>Cavendishia</i>	<i>leucantha</i>
Ericaceae	<i>Cavendishia</i>	<i>lindauiana</i>
Ericaceae	<i>Cavendishia</i>	<i>tenella</i>
Ericaceae	<i>Ceratostema</i>	<i>nodosum</i>
Ericaceae	<i>Ceratostema</i>	<i>peruvianum</i>
Ericaceae	<i>Ceratostema</i>	<i>reginaldi</i>
Ericaceae	<i>Macleania</i>	<i>bullata</i>
Ericaceae	<i>Macleania</i>	<i>cf. ericae</i>
Ericaceae	<i>Macleania</i>	<i>coccoboides</i>
Ericaceae	<i>Macleania</i>	<i>glabra</i>
Ericaceae	<i>Macleania</i>	<i>loeserneriana</i>

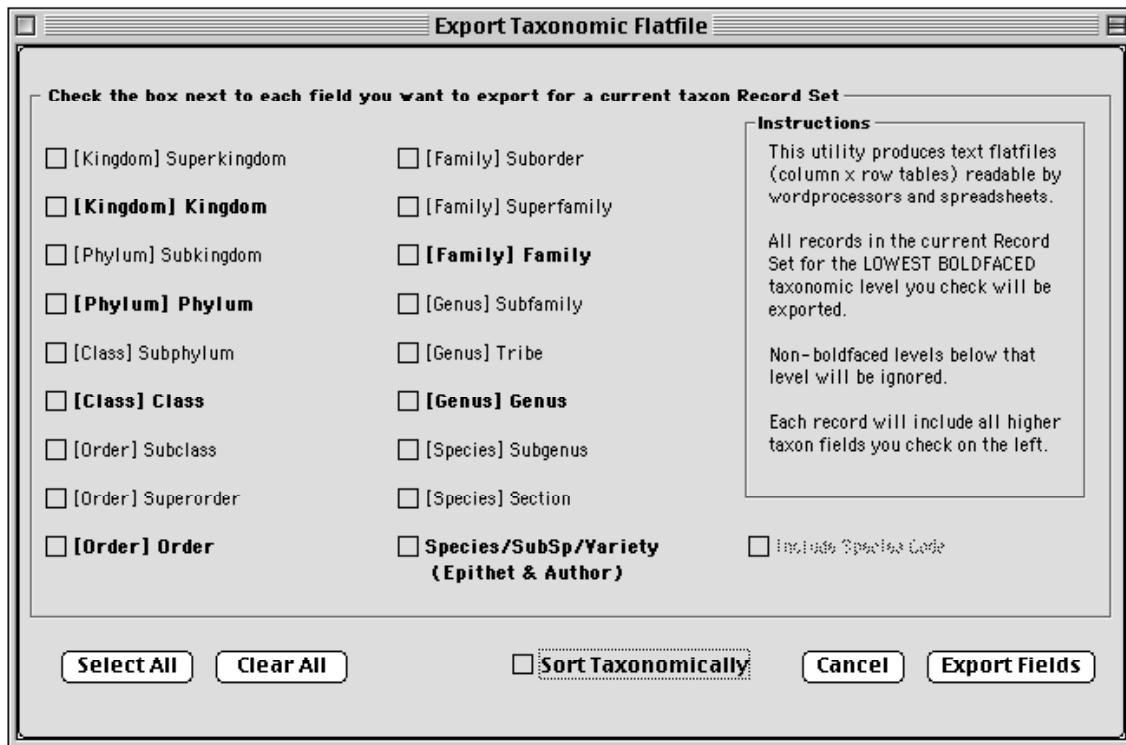
The Export Taxonomic Flatfile tool creates text files organized in this way, based on whatever range of taxonomic levels (ranks) that you specify, building from the current Record Set for the lowest level (rank) in the specified scope of taxonomic levels.

Using the Export Taxonomic Flatfile Tool: Step by Step

NOTE: The text files created by this tool use the TAB character as a field delimiter.

1. **Decide which taxonomic level will form the base of the flatfile to be exported.** In the illustration above, the rank of Species is the base level. Records of the base level become the rows of the flatfile.
2. **Find the records, at the base level, for which you want to export a taxonomic flatfile.** You can use any of the tools of the Find menu (or the Series menu, for Specimen records) to gather the records you want (see Chapter 12, “[Finding and Updating Records](#),” and Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”).

3. Establish these records as the current Record Set for the base level table. (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
4. From the Im/Export menu, select “Export Taxonomic Flatfile.” The Export Taxonomic Flatfile setup screen appears.



5. Click the checkbox for the base level, which will form the rows of the flatfile to be exported. *The base level must be one of the obligatory taxonomic levels (in boldface type).* If the current Record Set for the base level is empty, Biota posts an error message.
6. Click the checkboxes for the columns you want in the flatfile. *The base level must be the lowest rank checked.*

NOTE: The Species Author field is exported automatically if Species is checked. You can delete the Author column from the flatfile later if you don't want it.

7. To order the base level taxa in the exported file according to the higher taxonomic levels checked, click the “Sort taxonomically?” checkbox at the bottom of the screen. Within taxa, subtaxa will be ordered alphabetically, as in the table of plant species at the beginning of this section.



8. When the setup is ready, click the “Export Fields” button in the setup screen. The standard Save File window for your operating system appears.
9. Name and save the text file.
10. To halt the export, click the “Cancel” button in the progress indicator window. If you stop the export before it is done, the exported file may be incomplete.

NOTE: You can carry out other tasks with Biota or other applications while the export is in progress.

Exporting Specimen Flatfiles

Using the Export Specimen Flatfile tool, you can export any or all of 102 fields from ten Biota tables, for each record in the current *Specimen Record Set*. Because the Specimen table lies at the base of both the place (Collection/Locality) and taxonomic table hierarchies (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”), a Specimen-based flatfile may logically include any field from any table in either hierarchy. (In technical terms, the Specimen file has many-to-one relations, directly or through intermediate tables, with Collection, Locality, and all Taxon tables.)

The order of columns in exported Specimen flatfiles corresponds to the order of fields in the two Export Specimen Flatfile screens (see steps 2 and 4 below). You can easily rearrange the columns in the exported file using a spreadsheet application such as Excel.

Here is an example of a file exported using this tool.

Specimen Code	Date(s) Collected	State/Prov	Country	Latitude	Longitude	Genus	SpeciesName	Family
JLL5650	3 Apr 1978	Pichincha	Ecuador	0°0'0"N	0°0'0"E	Anthopterus	verticillatus	Ericaceae
JLL14691	15 Oct 1992	Napo	Ecuador	0°37'0"S	77°51'0"W	Ceratostema	nodosum	Ericaceae
JLL5657	5 Apr 1978	Napo-Pastaza	Ecuador	0°0'0"N	0°0'0"E	Ceratostema	peruvianum	Ericaceae
JLL14757	6 Nov 1992	Carchi	Ecuador	0°50'0"N	78°2'0"W	Macleania	loeserneriana	Ericaceae
JLL14789	17 Nov 1992	Pichincha	Ecuador	0°6'0"N	78°30'0"W	Macleania	cf. ericae	Ericaceae
JLL13382	22 Nov 1989	Pichincha	Ecuador	0°35'0"S	78°25'0"W	Macleania	loeserneriana	Ericaceae
JLL13330	7 Nov 1989	Pichincha	Ecuador	0°4'0"S	78°44'0"W	Macleania	bullata	Ericaceae
JLL8474	20 May 1982	Pichincha	Ecuador	0°15'0"S	78°45'0"W	Macleania	coccloboides	Ericaceae
JLL7269	19 Apr 1979	Chocó	Colombia	4°40'0"N	76°25'0"W	Cavendishia	tenella	Ericaceae
JLL5642	2 Apr 1978	Pichincha	Ecuador	0°0'0"N	0°0'0"E	Cavendishia	gilgiana	Ericaceae
JLL11106	19 Jan 1985	Cañar	Ecuador	2°35'0"S	78°49'0"W	Siphocampylus	scandens	Campanulaceae
JLL10953	10 Jan 1985	Carchi	Ecuador	0°45'0"N	77°40'0"W	Siphocampylus	ecuadoriensis	Campanulaceae
JLL11314	12 Feb 1985	Cajamarca	Peru	7°5'0"S	78°25'0"W	Siphocampylus	sanguineus	Campanulaceae
JLL11280	28 Jan 1985	Loja	Ecuador	3°58'0"S	79°20'0"W	Centropogon	erianthus	Campanulaceae
JLL11176	21 Jan 1985	Azuay	Ecuador	3°20'0"S	78°53'0"W	Centropogon	caoutchouc	Campanulaceae
JLL10573	15 May 1984	Chocó	Colombia	4°40'0"N	76°25'0"W	Cavendishia	forreroi	Ericaceae

NOTE: The text files created by this tool use the TAB character as a field delimiter.

Using the Export Specimen Flatfile Tool: Step by Step

- 1. Find the Specimen records for which you want to export the Specimen Flatfile.** You can use any of the tools of the Find menu or Series menu to gather the Specimen records you want (see Chapter 12, “[Finding and Updating Records](#),” and Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”).
- 2. Establish these records as the current Specimen Record Set.** (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
- 3. From the Im/Export menu, select “Export Specimen Flatfile.”** The first of three field export options screens appears. Notice that the [Specimen] Specimen Code field is already checked. This field is the only obligatory one.



- 4. In the first screen, click the checkbox for each field that you want to export.**



NOTE: Collection dates.

In the first screen of options, there are checkboxes for both “[Collection] Date(s) Collected (Start)” and “[Collection] Date(s) Collected (End)”.

- **If you check one of these boxes**, but not both, the checked field is exported without comment.
- **If you check both of these boxes**, Biota post the following option screen:

<input type="checkbox"/> [Collection] Collected By
<input checked="" type="checkbox"/> [Collection] Date Collected (Start)
<input checked="" type="checkbox"/> [Collection] Date Collected (End)
<input type="checkbox"/> [Collection] Site



The default option is to export the two Collection Date fields as separate fields. The second option combines information from the [Collection] Date Collected and [Collection] Date Coll End fields, formatted as described in the section “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9.

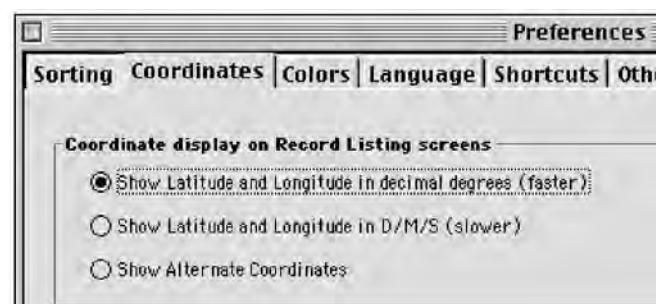
5. Click the “Second Screen of Fields” button to display the next set of options.

Second Screen of Fields...
Third Screen of Fields...

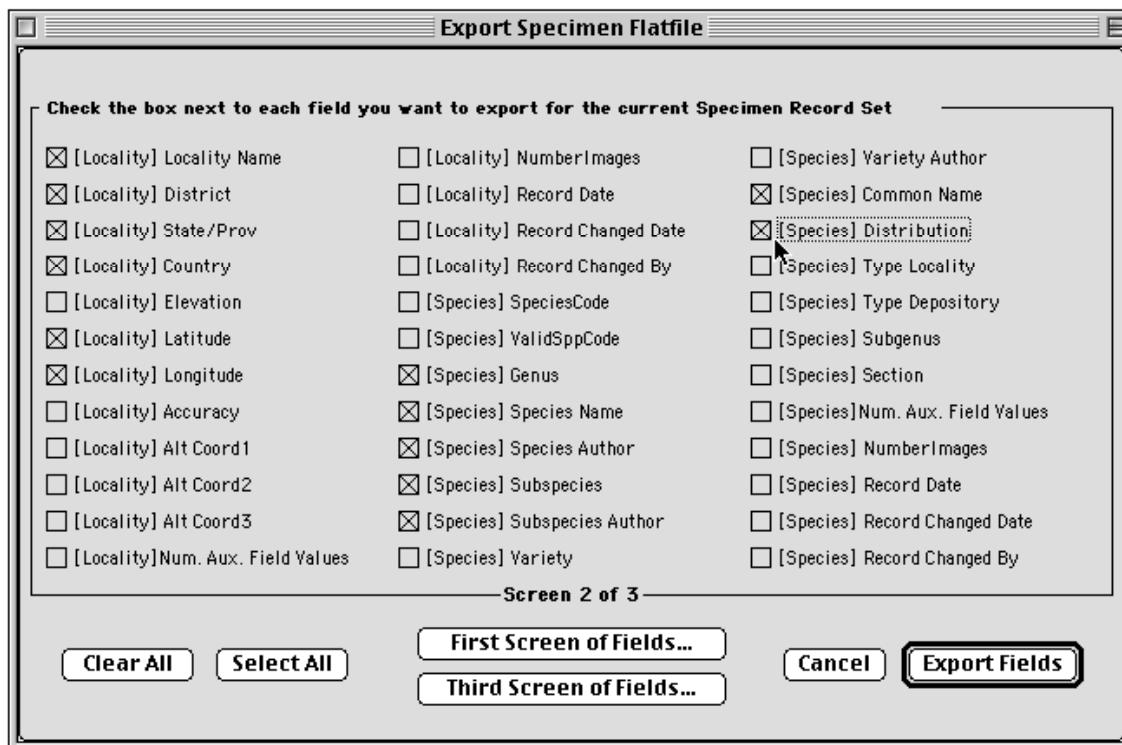
NOTE: Latitude and Longitude.

<input type="checkbox"/> [Locality] Elevation
<input checked="" type="checkbox"/> [Locality] Latitude
<input checked="" type="checkbox"/> [Locality] Longitude
<input type="checkbox"/> [Locality] Accuracy
<input type="checkbox"/> [Locality] Alt Coord1

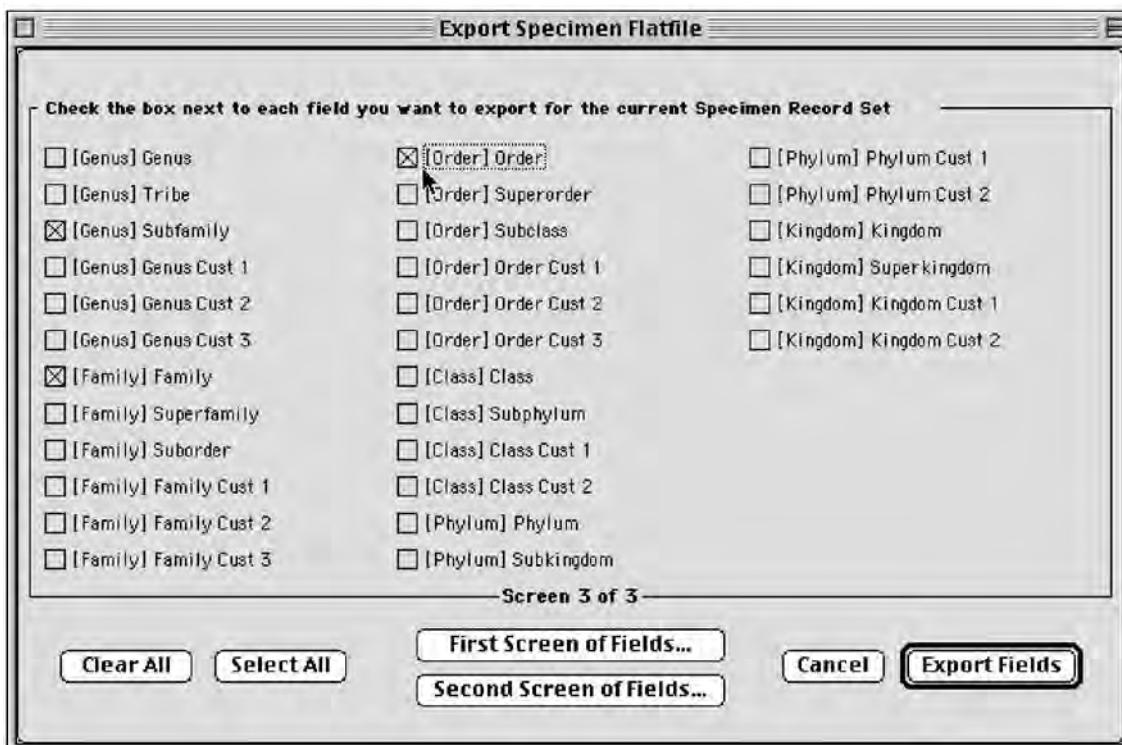
If you check “[Locality] Latitude” and/or “[Locality] Longitude” in the second screen of options, the format of the values exported is controlled by the current “Coordinate Display” setting in the “Coordinates” tab of the Preferences screen (Special menu). See “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#)” in Chapter 9.



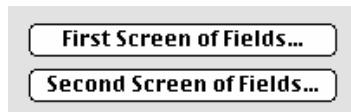
6. In the second screen, click the checkbox for each field that you want to export.



7. Click the “Third Screen of Fields” button to display the final set of options.



8. If you want to return to the first or second screen for any reason, click the appropriate button. (You can toggle back and forth as often as you wish without launching the export or losing the settings.)
9. To select all fields on **all three screens**, click the “Select All” button on **any** screen.
10. To clear the checkboxes for all fields on **all three screens**, click the “Clear All” button on **any** screen.
11. When the setup is ready, click the “Export Fields” button in the setup screen. The standard Save File window for your operating system appears.
12. Name and save the text file.
13. To halt the export, click the “Cancel” button in the progress indicator window. If you stop the export before it is done, the exported file may be incomplete.



NOTE: You can carry out other tasks with Biota or other applications while the export is in progress.

Exporting Custom Flatfiles

Using the “Export Custom Flatfile” tool from the Im/Export menu, you can use the Quick Report Editor to create, use, save, and reload your own custom formats for exporting Biota records and fields to disk files.

A Custom Flatfile export must be based on a Record Set from any of Biota’s Core tables (see “Core Tables” in Chapter 3 and Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). The flatfile exported automatically includes column headers based on Biota field names, and you may choose to create an “indented table” as an option (see the example in the section “[Examples of Custom Flatfiles Exported by Biota](#)” later in this chapter).

When to Use the Custom Flatfile Tool

In general, it is easier and more efficient to use other tools from the Im/Export menu when they are appropriate for your needs. But there are some things the Custom Flatfile tool can do that the others cannot.

- The Custom Flatfile tool differs from the Export Editor (see “[Exporting Data by Tables and Fields](#)” earlier in this chapter) in that the Custom Flatfile tool allows you to include Core fields from related parent tables (up to any level of “grandparent” records), whereas the Export Editor exports fields from one table at a time. For example, using the Custom Flatfile tool, you can design an export format based on Species records that includes the fields [Species] Genus, [Species] Species Name, [Species] Author, [Family] Family, and [Genus] Custom1. (On the other hand, you could *not* include any fields from Specimen, Collection, or Locality tables, or from Species Notes or Auxiliary Fields tables, since these are not parent or higher level tables to the Species table.)
- The Export Taxonomic Flatfile tool (see “[Exporting Taxonomic Flatfiles](#)” earlier in this chapter) can produce a file with the fields [Species] Genus, [Species] SpeciesName, [Species] Author, and [Family] Family, based on Species records, but has no provision for including any of the “Custom” fields in the higher taxon

tables, such as [Genus] Custom 1 (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”)—unlike the Custom Flatfile tool.

- **The Export Specimen Flatfile tool** (see “[Exporting Specimen Flatfiles](#)” earlier in this chapter) can export virtually any field from any Core table, but is based strictly on Specimen records. The Custom Flatfile tool can base the export on records from any Core table.

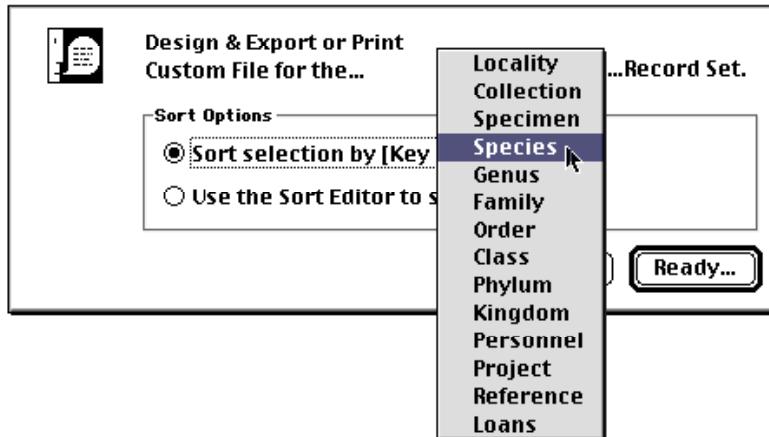
You cannot use the Custom Flatfile tool to export data in any useful way from any Peripheral table, including Notes, Images, and Auxiliary Fields. Use the Export Editor or the appropriate special tools discussed elsewhere in this chapter.

Using the Export Custom Flatfile Tool: Step by Step

1. **Decide which Core table level will form the *base*** of the Custom Flatfile to be exported.
2. **Find the records, at the base level, for which you want to export a Custom Flatfile.** You can use any of the tools of the Find menu (or the Series menu, for Specimen records) to gather the records you want (see Chapter 12, “[Finding and Updating Records](#),” and Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”).
3. **Establish these records as the current Record Set** for the base level Core table. (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
4. **From the Im/Export menu, select “Export Custom Flatfile.”** The Custom Flatfile option window appears.



5. **Select the base Core table** from the “Table Name” popup list in the option window.

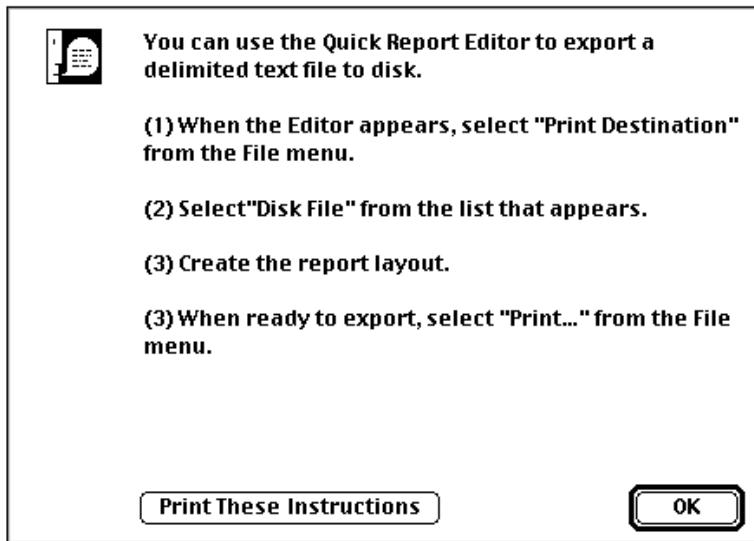


6. Choose a Sort Option in the option window:

- To sort the records by Key field (Record Code for Locality, Collection, Specimen, Species, or Loans; taxon for Genus or higher taxon tables), make sure the first option (the default) is selected.
- To use the Sort Editor to sort the records, click the second option. See “[Sorting Records in Record Listing Screens](#)” in Chapter 10 for help using the Sort Editor.

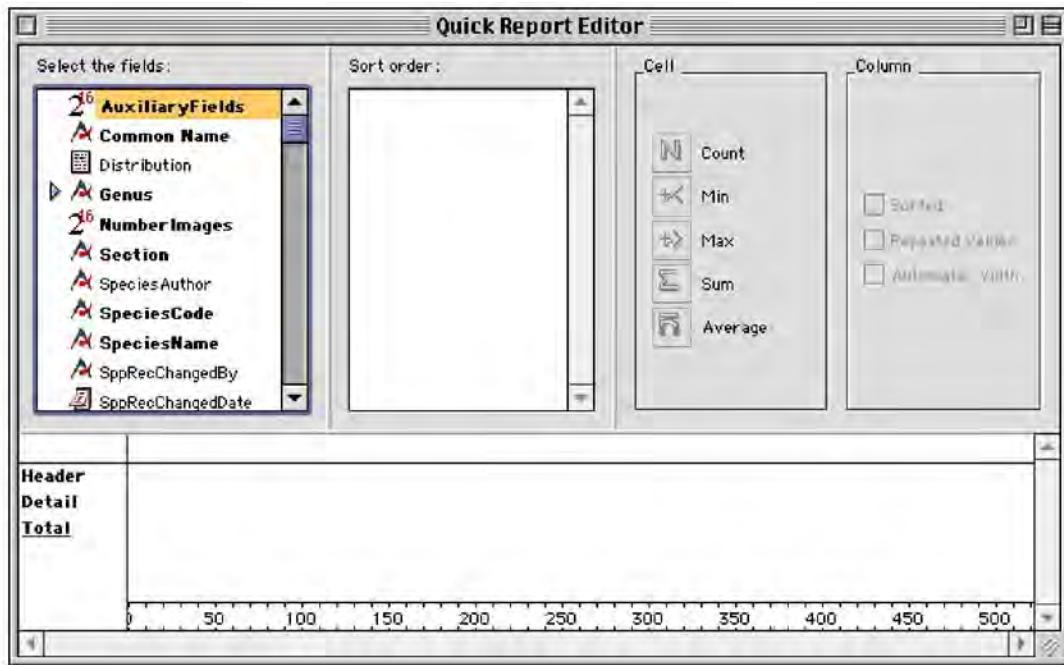
NOTE: You can use the Quick Report Editor’s own sorting capabilities (see Appendix E, “[The 4D Quick Report Editor](#)”) if you prefer. This will override either option in the Custom Flatfile option window. See [Step 8](#), below, and the section “[Examples of Custom Flatfiles Exported by Biota](#)” later in this chapter.

7. Click the “Ready” button in the options window. An instruction screen appears.



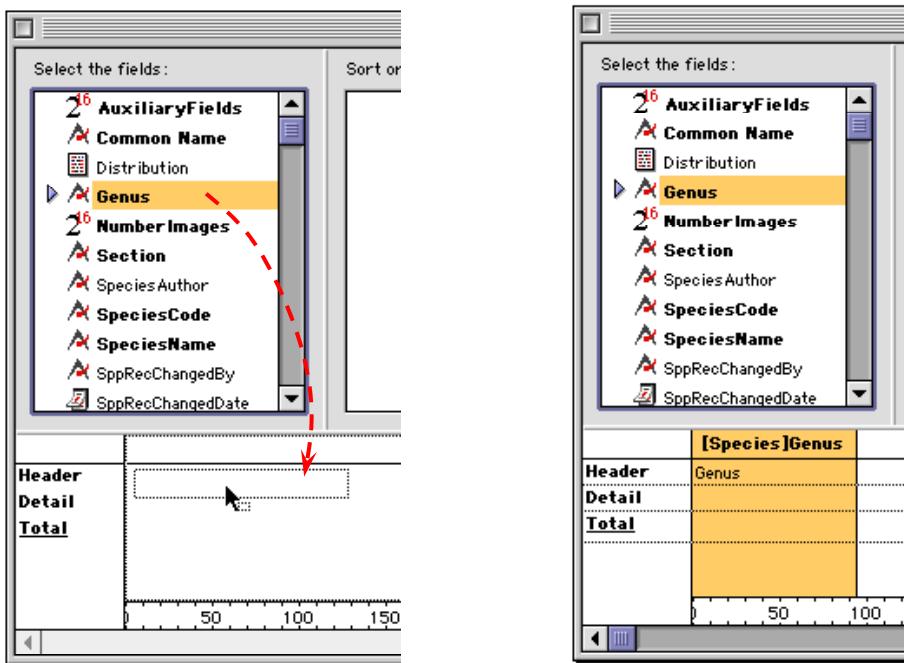
Biota provides these onscreen instructions (which you can print if you want, using the “Print These Instructions” button on the instruction screen) because of the complex interface that 4D provides for exporting files using the Quick Report Editor.

8. Click the “OK” button in the instruction screen to proceed. The Quick Report Editor appears (see the next page).

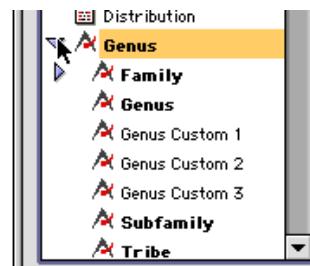


9. Set up the columns for the fields you want to export. For detailed help with the Quick Report Editor, see Appendix E, “[The 4D Quick Report Editor](#).”

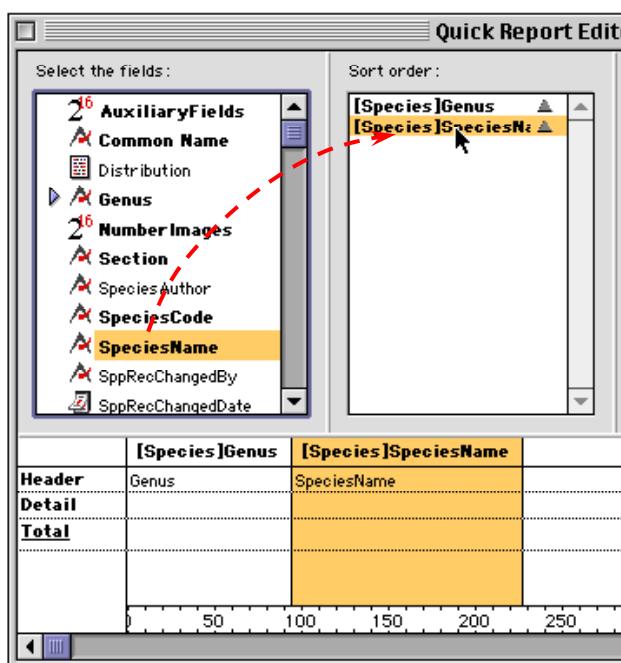
Briefly, drag field names from “Select the fields” panel on the upper left and drop them in the empty form below the list of fields, as shown here. (Use commands from the Quick Report Editor’s Edit menu to delete columns or insert intervening ones.)



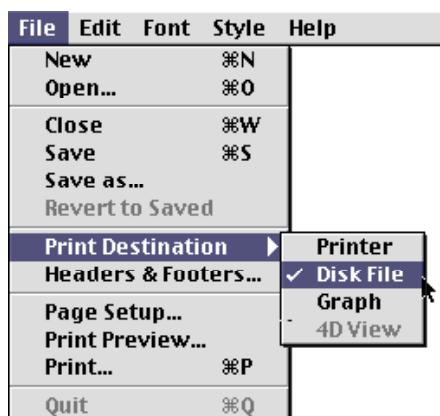
You can access fields from parent tables by clicking on the expansion icon (triangle) just to the left of any linking field.



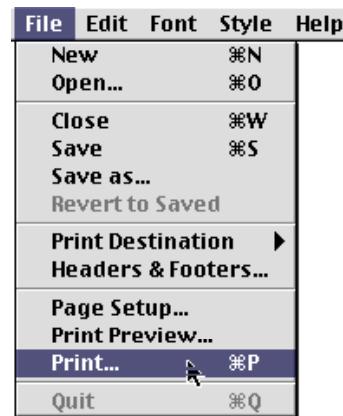
- To add sort criteria in the Quick Report Editor itself, which will produce an “indented table” effect (see “[Examples of Custom Flatfiles Exported by Biota](#)” later in this chapter), drag field names from the “Select the fields” panel on the left and drop them on the “Sort Order” panel to the right. The name of the column will be added to the Sort list in the panel. (Select Delete Last Sort from the Special menu to remove Sort levels.)



- To specify export to a text file on disk, instead of printing a report, select “Print Destination” from the Quick Report Editor File menu, then choose “Disk File” from the sub-menu. (The Quick Report Editor must be open.)



12. **To check the output before exporting**, select “Print Preview” from the File menu, while the Quick Report Editor is open.
13. **To export the text file**, select “Print” from the File menu, while the Quick Report Editor is open.
A Save File window appears, entitled “Save Report into.”
14. **To launch the export**, click the “Save” button in the “Save Report into” window.
15. **To save the Custom Flatfile format** you have created, select “Save As” from the Quick Report Editor File menu while the Quick Report Editor is still open.
16. **To load a Custom Flatfile format** that you have previously saved, use the “Open” command from the Quick Report Editor File menu while the Quick Report Editor is open.
17. **To dismiss the Quick Report Editor**, click the Close box in the Quick Report window or select “Close” from the File menu while the Quick Report Editor is open.



Examples of Custom Flatfiles Exported by Biota

Here are two examples of flatfiles exported using the Quick Report Editor, accessed through the Export Custom Flatfile tool. The same Species records form the basis for both examples.

Notice, in the second example, the “indented table” effect produced by adding sort criteria to the Quick Report Editor setup (no repeated values for Family and Genus).

- **Sorted on Family, Genus, and Species Name using the Sort Editor** (see [Step 6](#) in the previous section of this chapter, “[Using the Export Custom Flatfile Tool: Step by Step](#)”). No sort criteria were set in the Quick Report Editor:

Family	Genus	Species Name	Species Author	Species Code
Campanulaceae	Centropogon	caoutchouc	(H.B.K) Gleason	cencau
Campanulaceae	Centropogon	erianthus	(Benth.) Benth. & Hook. f.	ceneria
Campanulaceae	Siphocampylus	ecuadorensis	Wimmer	sipecua
Campanulaceae	Siphocampylus	sanguineus	A. Zahlbr.	sipsang
Campanulaceae	Siphocampylus	scandens	(HBK) G. Don	sipscan
Ericaceae	Cavendishia	forrestii	Luteyn	cavforr
Ericaceae	Cavendishia	lindauiana	Hoer.	cavlind
Ericaceae	Cavendishia	palustris	A.C. Smith	cavpalu
Ericaceae	Cavendishia	pseudospicata	Sleumer	cavpseud
Ericaceae	Cavendishia	tenella	A.C. Smith	cavtene

- **Sorted on Family, Genus, and Species Name within the Quick Report Editor** (see [Step 6](#) in the previous section of this chapter, “[Using the Export Custom Flatfile Tool: Step by Step](#)”). The Sort Editor not used.

Family	Genus	Species Name	Species Author	Species Code
Campanulaceae	Centropogon	caoutchouc erianthus	(H.B.K) Gleason (Benth.) Benth. & Hook. f. Wimmer	cencaou ceneria sipecua sipsang
	Siphocampylus	ecuadorensis sanguineus scandens forreroi lindauiana palustris pseudospicata tenella	A. Zahlbr. (HBK) G. Don Luteyn Hoer. A.C. Smith Sleumer A.C. Smith	sipscan cavforr cavlind cavpalu cavpseud cavtene
Ericaceae	Cavendishia			

Exporting “Specimens Examined” Lists for Publications

One of the most tedious tasks in preparing taxonomic or floristic/faunistic manuscripts is the compilation and formatting of lists of specimens examined for each species treated. Biota produces virtually journal-ready “Specimens Examined lists” for any Record Set of species you designate, exported to a text file in an easily edited format.

NOTE AND APOLOGY: Because this tool was developed originally for a publication in acarology¹, the formatting it produces is somewhat entomologically biased. Nevertheless, the work the tool does for you may still save time over manual equivalents, for formats in other taxonomic specialties, even with necessary post-export editing.

What the Specimens Examined Tool Exports

“Specimens Examined” or “Exsiccatae” sections of published works in systematics follow different traditional formats for different taxa—and vary among journals and among different authors within disciplines. Although Biota’s Specimens Examined tool provides some key format options, you will need to add the finishing touches using a text editor (e.g., Microsoft Word) to reflect specific styles for your field and to suit your own taste. Changes needed will almost certainly include punctuation and fonts, but perhaps also the ordering and repetition rules for certain fields. Even so, Biota does the hard part: collating and condensing the Collection and Locality data for the specimens of the species you designate.

The exported text file has the following format (see “[Examples of Specimens Examined Lists Exported by Biota](#),” later in this chapter, for actual examples):

¹ Naskrecki, P., and R. K. Colwell. 1998. Systematics and host plant affiliations of hummingbird flower mites of the genera *Tropicoseius* Baker and Yunker and *Rhinoseius* Baker and Yunker (Acari: Mesostigmata: Ascidae): Thomas Say Publications in Entomology: Monographs. Lanham, Maryland, Entomological Society of America.

1. To mark the beginning of the text section for each species, a line of asterisks is exported. You will want to remove this marker line in a text editor when you edit the file for format and details.
2. The phrase “Specimens examined for Genus species” follows the marker line (where “Genus species” is the name of a species in the Species Record Set). You will need to underline or italicize Latin binomials using a text editor.
3. The following Biota fields are exported—if neither repeated nor blank—for each Specimen record you choose to include, in this order (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”):
 - [Locality] Country. Set in uppercase characters. Not repeated if Country is the same as for the previous specimen.
 - [Locality] State/Province. Not repeated if State/Province is the same as for the previous specimen.
 - [Locality] District. Not repeated if District is the same as for the previous specimen.
 - [Locality] Locality Name. Not repeated if this Specimen record is linked to the same Locality record as the previous one.
 - [Locality] Latitude and [Locality] Longitude. Exported in Degree-Minute-Second format, *regardless* of the Lat/Long format setting in the Preferences screen (Special menu). Not repeated if this Specimen record is linked to the same Locality record as the previous one.
 - [Locality] Elevation. Not repeated if this Specimen record is linked to the same Locality record as the previous one.
 - [Collection] Site. Not repeated if this Site is the same as for the previous specimen.
 - Host Specimen information. If the [Collection] Host Spcm Code field is not blank in the Collection record (and is not the same for the previous Specimen), Biota exports the phrase “Ex Genus species” based on the [Species] Genus and [Species] Species Name fields for the Host Specimen that is linked to the Collection record (see Chapter 24, “[Host-Guest Relations](#)”).
 - Collection date(s) The collection date entry combines information from the [Collection] Date Collected and [Collection] Date Coll End fields, formatted using the [Collection] Date Coll Flag and [Collection] Date Coll End Flag fields, formatted as described in the section “[Collection Date Ranges on Labels and in Exported Text Files](#)” in Chapter 9. Not repeated if this Specimen record has precisely the same collection date(s) as the previous one.
 - [Collection] Collected By. Not repeated if this Specimen record is linked to the same Collection record as the previous one.
 - [Specimen] Specimen Code (optional). Including specimen codes (collector’s numbers or museum or herbarium accession numbers) in Specimens Examined lists is standard in some fields (e.g., botany), and with the advent of barcodes and specimen-level databases, may well become standard in others (e.g., entomology).

NOTE: In systematic botany, published “Specimens Examined” lists are traditionally based on collector’s numbers, further identified by appending the standard abbreviation for the herbarium holding individual specimens examined.

For example, “Smith 6557 (US, NY)” means that two specimens (herbarium sheets) from Smith’s collection number 6557 were examined, one held by the Smithsonian and one by the New York Botanical Garden.

To produce such lists with Biota, one strategy is to use the collector’s number followed by the herbarium abbreviation as the Specimen Code for individual sheets examined. If you use this format, the exported Specimens Examined list will need little modification in a text editor. (Lists of specimens with the same collector’s number will need to be condensed and details of the collection locality deleted, if you follow the usual tradition.)

- **[Specimen] Stage/Sex (optional).** Not repeated if this Specimen record has the same value for Stage/Sex and is linked to the same Collection record as the previous one.

NOTE: In an attempt to deal with plurals, if the number of specimens for a Stage/Sex category is greater than 1, an “s” is appended to the value for Stage/Sex: e.g., female becomes females. You will have to correct most irregular plurals in the text file with a global search and replace. The only exception is that Biota, revealing its entomological heritage, looks specifically for larva and pupa, and correctly renders the Latin plurals larvae and pupae.

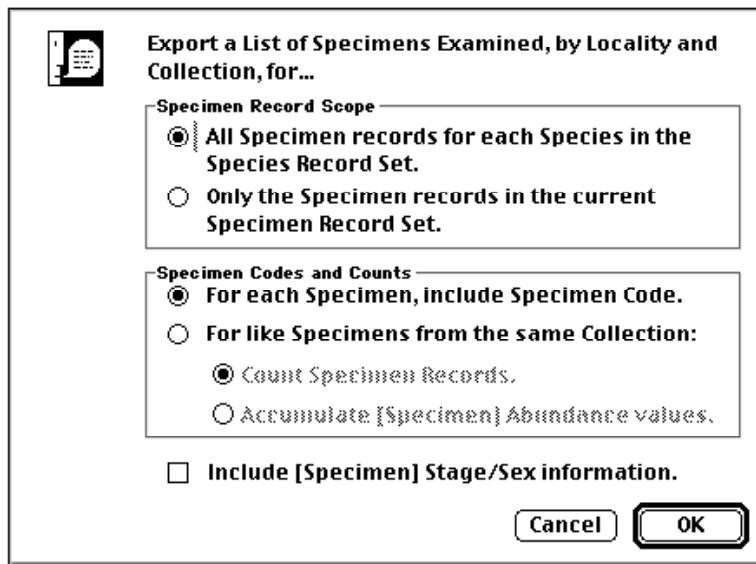
- **If individual Specimen Codes are not listed,** Biota totals the number of specimens examined for each Collection or for each Stage/Sex in each Collection. The number of specimens examined is computed in one of two ways, depending on the settings you establish for the export (see next section in this chapter).
 - ◊ **Option 1:** The number of specimens is simply the number of Specimen records (among those you choose to include in the export) that share the same value for Collection Code—or for Collection Code and Stage/Sex.
 - ◊ **Option 2:** The number of specimens is computed by accumulating the sum of values for the [Specimen] Abundance field, for Specimen records (among those you choose to include in the export) that share the same value for Collection Code—or for Collection Code and Stage/Sex.

Exporting a Specimens Examined List: Step by Step

1. **Find the Species records for which you want to export a “Specimens Examined” list.** You can use any of the tools of the Find menu to gather the Specimen records you want (see Chapter 12, “[Finding and Updating Records](#)”).
2. **Establish these records as the current Species Record.** (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
3. **Determine the scope for Specimen records:**
 - **If you want to include all Specimen records in the Data File** that are linked to records in the Species Record set, proceed directly to [Step 4](#), below.
 - **If you want to limit the export to certain Specimen records** for the species in the Species Record Set, you can do so by designating the Specimen records you want as the current Specimen Record Set.

NOTE: Here is one way to find the Specimen records you want to include. From the Find menu, select “Lower Taxa for Higher Taxa.” Set up the query “Find all Specimen Records for the Species Record Set” and click the “Find” button in the Lower Taxa for Higher Taxa screen. All Specimen records for the Species in the Species Record Set will be displayed. Find the ones you want and make them a Sub-selection, then click “Done” and make them the Specimen Record Set.

- From the Im/Export menu, select “Export Specimens Examined List.” An option window appears.



- Choose an option from the “Specimen Record Scope” panel.
 - To include **all Specimen records in the Data File** that are linked to records in the Species Record set (the default option), make sure the first option is selected in the “Specimen Record Scope” panel.
 - To limit the export to the **Specimen records** in the Specimen Record Set, choose the second option in the “Specimen Record Scope” panel.
- Choose options from the “Specimen Codes and Counts” panel.
 - To include the **Specimen Code for each Specimen record** in the exported Specimens Examined list (the default option), make sure the first option is selected in the “Specimen Codes & Counts” panel. If you choose this option, the lower pair of buttons remain disabled, since they concern counts of specimens.
 - To report **counts of specimens instead of Specimen Codes**, choose the second option in the “Specimen Codes & Counts” panel. If you choose this option, the lower two buttons in this panel are enabled and Biota offers another pair of options:

Specimen Codes and Counts
<input type="radio"/> For each Specimen, include Specimen Code. <input checked="" type="radio"/> For like Specimens from the same Collection: • Count Specimen Records. <input type="radio"/> Accumulate [Specimen] Abundance values.

- ◊ To report simple counts of specimens for each Collection, make sure the “Count Specimen Records” option (the default) is selected from the lower pair of buttons in the “Specimen Codes & Counts” panel.
 - ◊ To use the [Specimen] Abundance field to add up numbers of specimens examined, choose the “Accumulate [Specimen] Abundance value” option from the lower pair of buttons in the “Specimen Codes & Counts” panel. This is the option to choose if you have used each Specimen record for a “lot” (group) of conspecific specimens. For botanical specimens, you could select this option for duplicates that you have examined, if you choose not to list them individually.
7. To include information from the [Specimen] Stage/Sex field, click the checkbox at the bottom of the options screen.
- Include [Specimen] Stage/Sex information.
- If you chose to include Specimen Codes in Step 6, the Stage/Sex value is reported in parentheses after each Specimen Code—e.g., “USNMH362145 (female).” See the example below. (See Example 2 in “[Examples of Specimens Examined Lists Exported by Biota](#),” later in this chapter.)
 - If you chose to report counts in Step 6, counts of specimens for each value of Stage/Sex within each Collection are reported with the name of the stage or sex—e.g., “5 females.” (See Example 4 in “[Examples of Specimens Examined Lists Exported by Biota](#),” later in this chapter.)
8. Click the “OK” button in the options window to launch the export.
9. Name and save the text file. Biota displays a progress indicator.

WARNING: The progress indicator advances each time a Species is completed. If you include species with numerous Specimen records, the indicator will not change quickly. Be patient! Biota is working through hundreds of conditionals to save you from making all the same decisions yourself. You can do other tasks with Biota or with other applications while the export continues.

10. **Error messages during export.** Biota assumes that you do not want to list either a species with no specimens, or a specimen for which either Collection or Locality table data (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) are missing. If Biota finds incomplete information during the export, the export is aborted and you will see one of the following messages, with the genus and specific name substituted for *Genus species* in the messages:
- “No Specimen records found for *Genus species*.”
 - “No Collection records found for *Genus species*.”
 - “No Locality records found for *Genus species*.”

- 11. To halt the export for any reason**, click the ““Cancel” button in the progress indicator window. If you stop the export before it is done, the exported file may be incomplete.

Examples of Specimens Examined Lists Exported by Biota

Here are some examples of Specimens Examined lists, just as Biota exported them, to illustrate the effects of different sets of “Specimen Codes & Counts” and “Stage/Sex” options. The same specimens were used for all illustrations. (They are hummingbird flower mites collected from plant specimens, to illustrate the host specimen option.)

Example 1. With the option to include Specimen Codes selected, but not the Stage/Sex option:

```
*****
Specimens examined for Rhinoseius luteyni:
ECUADOR: Cotopaxi, Latacunga-Quevedo rd., 0°58'0"S, 78°56'0"W, 274-3350m, 3-14km E Pilaló, ex
Sphyrospermum buxifolium, 4 Apr 1992 (coll. J.L. Luteyn) — JLL14400:01, JLL14400:02, JLL14400:03,
JLL14400:04, JLL14400:05, JLL14400:06, JLL14400:07, JLL14400:08, JLL14400:09, JLL14400:10.
*****
```

```
*****
Specimens examined for Rhinoseius steini:
ECUADOR: Cañar, 7-9km NE Pindilíg tow. Rivera, 2°35'0"S, 78°49'0"W, 3000-3200m, None, ex
Siphocampylus scandens, 19 Jan 1985 (coll. J.L. Luteyn) — JLL11106:01, JLL11106:02, JLL11106:04,
JLL11106:05, JLL11106:06, JLL11106:07, JLL11106:08, JLL11106:09, JLL11106:10, JLL11106:13,
JLL11106:14;
Carchi, Tulcán-El Caramelo rd., 0°45'0"N, 77°40'0"W, 3300m, 27 km E Panam Hwy., ex Siphocampylus
ecuadorensis, 10 Jan 1985 (coll. J.L. Luteyn) — JLL10953:01, JLL10953:02, JLL10953:03,
JLL10953:05, JLL10953:06, JLL10953:07, JLL10953:08, JLL10953:09;
PERU: Amazonas, 19km SW Leimebamba, 6°45'0"S, 77°48'0"W, 3020m, along rd. to Balsas, ex
Vaccinium matthewsii, 13 Feb 1985 (coll. J.L. Luteyn) — JLL11382:01, JLL11382:02, JLL11382:03,
JLL11382:04, JLL11382:05, JLL11382:06, JLL11382:07, JLL11382:10.
```

Notice that each collection begins on a new line, to help you work with the text file in a text editor when you add the finishing touches.

In the remaining examples, only the first species (*Rhinoseius luteyni*), will be illustrated.

Example 2. With “Specimen Code” and “Stage/Sex” options selected:

```
*****
Specimens examined for Rhinoseius luteyni:
ECUADOR: Cotopaxi, Latacunga-Quevedo rd., 0°58'0"S, 78°56'0"W, 274-3350m, 3-14km E Pilaló, ex
Sphyrospermum buxifolium, 4 Apr 1992 (coll. J.L. Luteyn) — JLL14400:09 (Adult female), JLL14400:05
(Adult male), JLL14400:03 (Deutonymph), JLL14400:01 (Larva), JLL14400:04 (Larva), JLL14400:06
(Larva), JLL14400:08 (Larva), JLL14400:10 (Larva), JLL14400:02 (Protonymph), JLL14400:07
(Protonymph).
```

Example 3. With the “Count Specimen Records” option selected, but not the “Stage/Sex” option:

Specimens examined for *Rhinoseius luteyni*:
 ECUADOR: Cotopaxi, Latacunga-Quevedo rd., 0°58'0"S, 78°56'0"W, 274-3350m, 3-14km E Pilaló, ex *Sphyrospermum buxifolium*, 4 Apr 1992 (coll. J.L. Lutelyn) — 10 specimens,

Example 4. With the “Count Specimen Records” and “Stage/Sex” options selected:

Specimens examined for *Rhinoseius luteyni*:
 ECUADOR: Cotopaxi, Latacunga-Quevedo rd., 0°58'0"S, 78°56'0"W, 274-3350m, 3-14km E Pilaló, ex *Sphyrospermum buxifolium*, 4 Apr 1992 (coll. J.L. Lutelyn) — 1 adult female, 1 adult male, 1 deutonymph, 5 larvae, 2 protonymphs.

Exporting Place-by-Taxon Incidence or Abundance Tables

Biogeographers and conservation biologists often need to generate lists of taxa for particular sets of sites, and, conversely, lists of sites from which a taxon or group of taxa has been recorded.

In ecology, quantitative biodiversity data is of interest in its own right. In biodiversity inventories, data on frequencies of taxa in samples or collections are essential for statistical estimates of inventory progress or approach to completion.

Spatial statistics, ordination, and other multivariate statistical tools in ecology all begin with taxon-by-sample matrices of abundances, or with presence/absence (incidence) matrices.

Biota can export “Place-by-Taxon” (“Localities-by-Taxon” or “Collections-by-Taxon”) tables of either incidence data (presence/absence) or abundance data (number of individuals) based on:

- **A Taxon Record Set** (a general term for a Species, Genus, Family, Order, Class, Phylum, or Kingdom Record Set) and the Specimen, Collection, or (for “Localities-by-Taxon” tables) Locality records linked to the Taxon Records Set. Use this option if you want an incidence or abundance table of the Locality or Collection records (“Place” records) in which a Taxon or group of Taxa has been recorded.
- **A Specimen Record Set** and the Taxon (at a selected Taxon level) and Collection or Locality records linked to it. Use this option if you need to produce a “Localities-by-Taxon” or “Collections-by-Taxon” table for a subset of the Specimen records linked to a particular set of Taxa and Locality or Collection records. For example, in a vegetation study, one Biota user used this option to produce separate tables for seedlings, saplings, and mature trees, all representing the same set of Species from the same set of Collections (quadrats).
- **A Locality or Collection Record Set** and the Taxon records linked to it (at a selected Taxon level). Use this option if you want an incidence or abundance table of the Taxa recorded for a particular set of Locality or Collection records.
- **The Specimen records linked to both a Locality or Collection Record Set** and a Taxon Record Set (at a selected Taxon level). Use this option if you want an incidence or abundance table for *all* Specimens that are linked to *both* a chosen set of Place (Locality or Collection) records *and* to a chosen set of Taxon records.

In general, these four options produce *different* results, since the Locality or Collection records for a particular group of Taxa may well be linked to other Species as well. Likewise, the Taxa (at a selected Taxon level) linked to a chosen set of Locality or Collection records may well include Specimens are linked to other Locality or Collection records.

NOTE: The text files created by this tool use the TAB character as a field delimiter.

Exporting Place-by-Taxon Tables: Step by Step

1. **Find the Locality, Collection, Specimen, Species, or higher Taxon records** on which you want to base a Place-by-Taxon table. You can use any of the tools of the Find menu (or the Series menu, for Specimen records) to gather the records you want (see Chapter 12, “[Finding and Updating Records](#),” and Chapter 13, “[Creating, Finding, and Updating Specimen Series](#)”).
2. **Establish these records as the current Record Set** for table. (See “[Record Sets](#)” in Chapter 3 for help if necessary.)
3. **From the Im/Export menu, choose “Export Colls x Taxon Table” or “Export Locs x Taxon Table.”**

The corresponding option window appears (both are illustrated below).



Export Collections by... ...Table for...

The Collection Record Set.
 The Specimen Record Set.
 The Species Record Set.
 The Species & Collection Record Sets.

Data Options

Use incidence (presence/absence) data.
 Use abundance data (number of individuals per species per collection).
 Interrupt to flag zero Abundances.

Format Options

Export in EstimateS format.
 Export in Cornell Condensed Format.

Other Options

Interrupt to flag orphan Specimens.
 Include Collections with no Specimens.
 Include Species with no Specimens.

Export Localities by... ...Table for...

The Locality Record Set.
 The Collection Record Set.
 The Specimen Record Set.
 The Species Record Set.
 The Species & Locality Record Sets.

Data Options

Use incidence (presence/absence) data.
 Use abundance data (number of individuals per species per locality).
 Interrupt to flag zero Abundances.

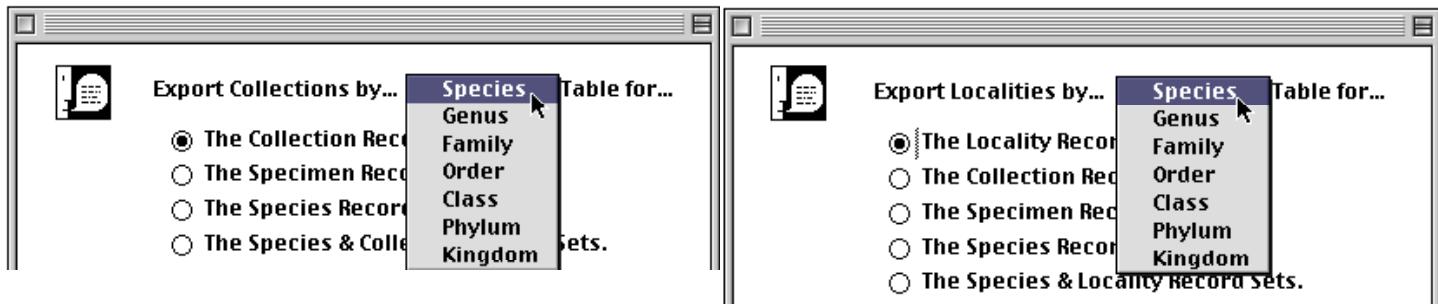
Format Options

Export in EstimateS format.
 Export in Cornell Condensed Format.

Other Options

Interrupt to flag orphan Specimens.
 Include Localities with no Specimens.
 Include Species with no Specimens.

4. Select a Taxon level from the popup list at the top of the options window.



5. From the upper set of 4 (Collection) or 5 (Locality) option buttons, choose the Record Set(s) on which you will base the analysis. This is the Record Set (or Sets) you set up in Step 1. See the introduction to this section (“[Exporting Place-by-Taxon Incidence or Abundance Tables](#),” earlier in this chapter) for help if you need it.



NOTE: Once you select a Taxon above the Species level from the Taxon popup in Step 4, above, the text in the last two buttons illustrated in each list above changes accordingly.

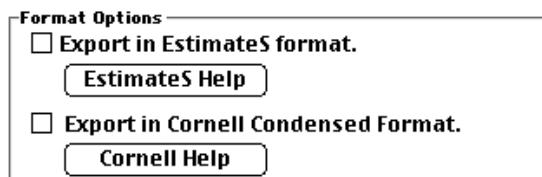
6. Choose a Data Option.



- If you choose the incidence (presence/absence) option (the default), Biota records a “1” for each Taxon (each Species, for example) that occurs in a particular Locality or Collection—regardless the number of Specimens—and records a zero otherwise.
- If you choose the abundance option (the lower button in the Data Options panel), Biota records *the sum of the [Specimen] Abundance field values* for the Specimen records for each Taxon (each Species, for example) in each Locality

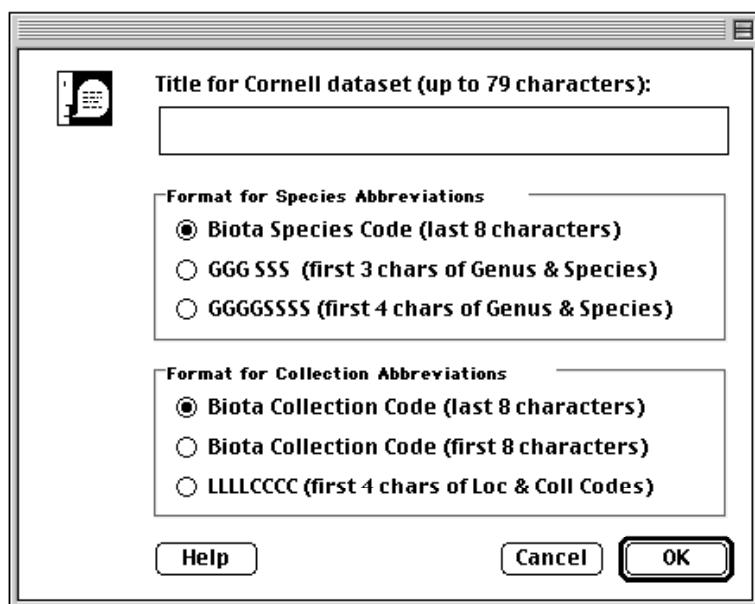
or Collection in the analysis. (If the Abundance value is 1 for each Specimen record—entered as the default when you create a Specimen record, the sum exported will be the number of Specimen records.)

7. Consider a Format Option (optional).



- **Export in EstimateS format.** If you check this option, the exported text files can be directly read by EstimateS, a freeware application (© Robert K. Colwell, author of Biota) for the statistical estimation of species richness and shared species from specimen-based sampling data. You can learn more about EstimateS and download a free copy of the software and User's Guide from <http://viceroy.eeb.uconn.edu/estimates>. (Click the “EstimateS Help” button below the checkbox for details on the export format.)
- **Export in Cornell Condensed Format.** If you check this option, the text file is exported in Cornell Condensed Format—the required input format for statistical programs such as CANOCO and DECORANA, widely used for ordination. (Click the “Cornell Help” button below the checkbox for details on the export format.)

When the Cornell option is checked and you click the “OK” button, Biota presents a second screen requesting a data set title (optional) and offering options for creating the species and sample abbreviations required for the Cornell format. Click the “Help” button in the option screen for details.



8. To interrupt the export for problem data warnings, consider setting the checkbox(es) at the bottom on the options window (optional).

Other Options <input type="checkbox"/> Interrupt to flag orphan Specimens. <input type="checkbox"/> Include Collections with no Specimens. <input type="checkbox"/> Include Species with no Specimens.	Other Options <input type="checkbox"/> Interrupt to flag orphan Specimens. <input type="checkbox"/> Include Localities with no Specimens. <input type="checkbox"/> Include Species with no Specimens.
--	---

Four kinds of errors (or potential errors) are flagged:

- **Specimen records not linked to any Species record** (“Interrupt to flag orphan Specimens.”) If you check this checkbox, Biota interrupts the import with a message, each time an orphan Specimen is encountered.
- **Collection or Locality records not linked to any Specimen record.** (“Include [Collections or Localities] with no Specimens.”) (For Locality records, either the Locality record or a linked Collection record may be childless). The default is to exclude such records. Check the checkbox if you want to *include* them in the export.
- **Taxon records not linked to any Specimen record.** (“Include [Taxa] with no Specimens.”) (For higher taxon records, either the Species record or a higher Taxon record may be childless). The default is to *exclude* such records. Check the checkbox if you want to *include* them in the export.

NOTE: The name of the Taxon in this option matches the Taxon level you chose from the popup in [Step 4](#), above.

- **Specimen records with zero in the [Specimen] Abundance field.** Such records are flagged if you choose the “Abundance” option in [Step 6](#), above. (If you checked the “Incidence” option, instead, Biota allows zeros in the Abundance field so that Specimen records can be used to link Taxon records and Collection or Locality records when no physical specimen exists; see “[Site-Based Species Lists with No Specimens](#)” in Chapter 5.

If Biota finds one of the errors you have asked it to flag during the export, a warning message like the one below is displayed. (Messages for other error types are analogous). If you click the “OK” button in the warning message, the export will proceed by excluding the problem record. If you click the “Cancel” button in the warning message window, the export is aborted.



NOTE: If you want to check for childless (empty) records beforehand, use the “Childless Records” tool from the Find menu. To find orphan Specimens, select “Orphan Records” from the Find menu. See “[Finding Childless and Orphan Records](#)” in Chapter 12 for help.

9. When the setup is ready, click the “OK” button in the setup screen. The standard Save File window for your operating system appears.
10. Name and save the text file.
11. To halt the export, click the “Cancel” button in the progress indicator window. If you stop the export before it is done, the exported file may be incomplete.

NOTE: You can carry out other tasks with Biota or other applications while the export is in progress.

An Example of a Collections-by-Species Table Exported by Biota

The table below shows the abundance of several species of hummingbird flower mites (the columns) in a set of host plant collections (the rows). The corresponding incidence table would have a “1” substituted for each non-zero cell value.

SP. CODE:	antio	lute	rhinhaplo	rhinrich	stein
GENUS:	Rhinoseius	Rhinoseius	Rhinoseius	Rhinoseius	Tropicoseius
SPECIES:	antioquensis	luteyni	haplophaedia	richardsoni	steini
SUBGENUS:	Gr. richardsoni	Gr. rafinskii	Gr. richardsoni	Gr. richardsoni	Gr. chiriquensis
JLL14587H	1	0	0	0	0
JLL11382H	0	0	0	0	8
JLL14400H	0	9	0	0	0
JLL12327H	0	0	0	1	0
JLL12329H	0	0	0	4	0
JLL12414H	0	0	0	7	0
JLL13339H	0	0	3	0	0
JLL11314H	0	0	0	2	27

NOTE: Biota includes 4 rows of Species identifiers: Species Code, Genus, Species (specific) Name, and Subgenus. If you need to code species for some special purpose, consider using the Subgenus field for this information. You can re-name the field with an alias if you want (see Chapter 18, “[Re-naming Fields](#)”) and the alias appears in place of “SUBGENUS” in the exported table. For example, a plant ecologist using Biota might rename the Subgenus field “Life Form” and use the information to sort columns of the text file into herbs, shrubs, and trees for data analysis.

Chapter 28

Importing Data

Biota's Import Editor ("Import by Tables and Fields," in the Im/Export menu), can import data into any Biota table from free-format, delimited text (ASCII) files, such as the column-by-row text files you can create with a spreadsheet application (e.g., Microsoft Excel), or export as text flatfiles from database management applications (e.g., 4th Dimension, Access, dBase, Paradox, or FileMaker).

Biota's Import Editor has three related functions.

- **Importing new records** to the Biota Data File. With this approach, *every* record in the text (donor) file must contain a record for which the Key field (see "[Key Fields](#)" in Chapter 3) is new to the Data File.
- **Updating fields** in records that are already in a Biota Data File. With this option, *every* record in the text (donor) file must contain a record for which the Key field matches a record already in the Data File, so Biota can find the record to update. (You cannot update a Key field.)
- **"Merging" new records** into a Biota Data File. With this option, you can import records from a text file that include a mixture of new records and records already in the Data File. Biota *imports* any record for which the Key field is *new* to the Data File, but *ignores* any record for which the Key field *matches* a record already in the Data File.

The Import Editor is designed to make importing data as pain-free and flexible as possible.

- **Columns in the text file can be in any order.**
- **Columns in the text file can be skipped.**
- **The text file can have column headings, or not.**
- **Any field and record delimiters can be used.**

The Import Editor does extensive error checking, and you can undo imports that run into trouble. When Biota finds an error in the text file, it displays the offending record and tells you what went wrong.

Nonetheless, importing ("migrating") data into any relational structure, however powerful the import tools, takes planning and effort. Expect some frustration.

Import Step 1: Match Fields

The first step is to compare the fields (columns) in the "donor" text file with the fields in Biota's data structure (see Appendix A, "[Biota Tables, Fields, and Relational Links](#)"). If you are importing data from another relational data structure, you will need to consider tables and relational links as well.

Almost inevitably, there will be fields that don't match. Remember that:

- **Many fields in Biota can be renamed** (choose "Core Field Aliases" from the Special menu to see the list).

- If you need more fields than Biota offers in its Core tables, you can create your own Auxiliary Fields to accommodate them (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).
- If you need longer fields than Biota offers, some kinds of data may work well as Notes (see “[Notes Input](#)” in Chapter 11).

If there are too many fields in your data file that have no natural or adoptive home in the Biota structure, however, you are probably better off not trying to use Biota for those data...or not using Biota at all for a particular dataset.

Import Step 2: Prepare the Text Files

You will need to prepare a separate text file for each Biota table that will receive data.

The *rows* in the text file will become Biota *records*, if you are importing new records, or will match Biota records, if you are updating existing records. The only potential exception is the first row of the text file, which you can use for column headings if you wish; see the next section of this chapter, “[The Column Heading Row Option](#).”

The *columns* in the text file correspond to *fields* in a Biota table. The columns can be in any order within a text file, and the file can include columns (even blank ones) that you do not want to import.

If you intend to import records from an existing text flatfile (a columns-by-rows table) that includes columns destined for fields in several different, linked Biota tables (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)” for tables and fields), you may wish to follow the suggestions in “[A Strategy for Importing Text Files Into Hierarchically Linked Tables](#)” (later in this chapter), after reading the sections below in this chapter on “[The Column Heading Row Option](#),” “[Key Fields and the Importing Process](#),” and “[Field Types and Field Lengths](#).”

The Column Heading Row Option

If you are working from a table in an existing text file from which you intend to import, chances are that the first row of the table consists of descriptive column headings, rather than data. Likewise, for a newly created text file, you will probably find it much easier to keep track of what you are doing if you use column headings.

Biota does not use the column headings from your text file to match up text file columns with Biota fields; the Import Editor has a much more flexible way to do that. But you can tell Biota’s Import Editor to *ignore* the first row of the text table so that you can leave your existing headings in the text file, or create new ones.

Because column headings are ignored during import (if you tell Biota to ignore them), it does not matter whether they are exactly the same as the names of the Biota fields they are destined to fill, or not. On the other hand, you may find it easier to keep track of what you are doing if column headings in the text file match or at least approximate Biota field names.

Automatic Stripping of Initial and Terminal Space Characters

In preparing text files for import, it is easy to start a field entry with a space character accidentally, and even easier to inadvertently append one or more spaces at the end of a field entry. These initial and terminal space characters wreak havoc in relating fields and make sorts and searches behave unintelligibly in any field (until you finally figure out what is wrong!).

To eliminate this problem for imported data, the Import Editor automatically strips off all initial and terminal space characters (ASCII Character 32). No error comments are issued.

“Internal” spaces—those with some other character both before and after—are not removed and are imported as text as part of the character string.

NOTE: Biota automatically strips terminal space characters and flags initial space characters in all Key and relating fields during input using Biota’s record input screens.

Key Fields and the Importing Process

Most of the tables in Biota’s structure (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) have a Key field (Record Code, taxon name, etc.; see “[Key Fields](#)” in Chapter 3) that requires a unique value for each record in a Biota Data File. The exceptions are the Notes tables and the Determination History table, which do not require a unique Key (the “Record Code” fields in these child tables are “foreign keys” that need not be unique), and the Auxiliary Field Value and Reference Links tables, which have a two-field (composite) Key. These exceptions are discussed later in this chapter (see “[Importing Data to Notes Tables or to the Determination History Table](#)” and “[Importing New Records and Updating Existing Records in Auxiliary Fields Tables](#)”).

Biota checks Key fields carefully during the import or update process. However, the way Key fields are handled depends entirely on whether you have indicated that you are importing new records, updating existing ones, or merging records.

If you are *importing new records*, and a unique value in the Key field is required, Biota halts the import and posts an error message if it encounters a record with any of the following:

- **A blank Key field.**
- **A Key field value that duplicates a value already imported.**
- **A Key field value that duplicates a value that was already in the Data File** when you started the import.

In contrast, if you are *updating existing records*, and a unique value in the Key field is required, Biota halts the import and posts an error message if it encounters a record with either of the following:

- **A blank Key field.**
- **A Key field value that does not match any value already in the Data File** when you started the import. Biota cannot tell which record to update if there is no match.

Finally, if you are *merging new records* (importing records from a text file that includes a mixture of new records and records already in the Data File), Biota *imports* any record for which the Key field is *new* to the Data File, and *ignores* any record for which the Key field *matches* a record already in the Data File. Biota halts the import and posts an error message if it encounters a record with a blank Key field.

Import error messages are discussed in detail later in this chapter (see “[Displays and Error Messages During Record Importing or Updating](#)”).

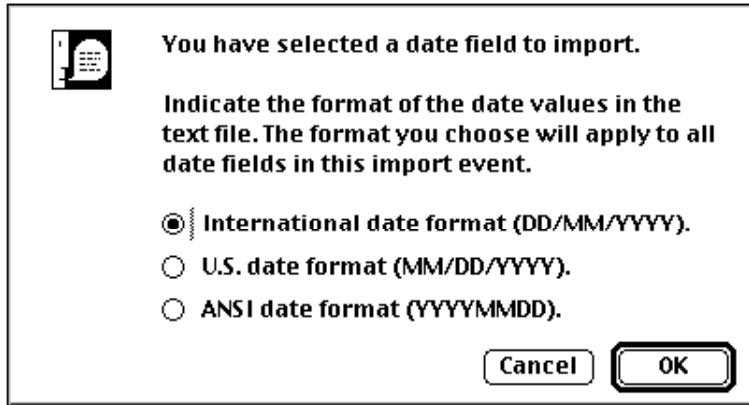
If you are importing new records, it is likely that you will need to create Record Codes for records in one or more of the Specimen, Species, Collection, Locality, or Reference

tables. Read or review Chapter 8, “[Record Codes](#)” before assigning codes. Once you decide on a system, you can use spreadsheet tools (e.g., the “Series” command in Microsoft Excel) to assign Record Codes in a column of your text file, by using an alphanumeric prefix with a consecutive integer counter, e.g., ABC001, ABC002, ABC003, etc. (see “[A Strategy for Importing Text Files Into Hierarchically Linked Tables](#),” later in this chapter).

Field Types and Field Lengths

Appendix A, “[Biota Tables, Fields, and Relational Links](#),” shows the field type and field length (maximum number of characters) for each field in the Biota data structure. The fields in the text file from which you import data should match the type and length of the Biota fields they will fill, although Biota allows as much flexibility as possible, as explained for each field type, below.

- **Alphanumeric fields.** An alphanumeric field accepts all characters. You can import a number or a date into an alphanumeric field, but the characters are treated as text, not numbers or dates. The number of characters that can be imported ranges from zero (a blank value) to the maximum indicated in [Appendix A](#) for each field. If you try to import a longer value, Biota issues a warning, giving you the option to accept a truncated value or abort the import (see “[Displays and Error Messages During Record Importing or Updating](#),” later in this chapter).
- **Date fields.** Before importing dates, please read or review the sections on “Dates” in Chapter 9. Whenever you select a Date field, using the Import Editor, Biota offers you a choice of three standard date formats for the import.



NOTES:

- a. The choice screen above appears only for the *first* date field you choose to import in setting up the Import Editor for each import session. Any additional Date fields in the same import session must be in the same, chosen format.
 - b. You can import Dates in *different* formats in different import sessions, to the *same* Data File. Biota converts all dates to a uniform internal format, but displays (in International or U.S. format) according to the current setting in your operating system. You can export dates in any of the same 3 fields permitted for import (International, U.S., or ANSI).
-

If you want exported dates in some other format, you must convert them to one of these three (International, U.S., or ANSI) before export. Spreadsheet applications (e.g., Microsoft Excel) can easily convert columns of dates among formats.

Biota checks all imported dates for Gregorian calendar validity as well as format. Month cannot exceed 12 and Day cannot exceed the maximum number of days in the month, given the year. (February 29 is allowed only in years divisible by 4 and only in centennial years divisible by 400.) If a format error is encountered in a date, or an invalid date is found, Biota posts an error message (see “Displays and Error Messages During Record Importing or Updating,” later in this chapter).

- **Partial Dates: Date Flag fields.** As explained in full in the Chapter 9 (see the section on “[Dates](#)”), for some date fields, Biota can display and print partial dates: Month-Year dates and Year-only dates. These fields are [Collection] Date Collected, [Collection] Date Coll End, [Specimen] Date Prepared, and [Specimen] Date Determined. Each of these fields is paired with an integer field for a Date Flag (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

If you are importing complete dates only, you need not import any values for Date Flag fields, which are initialized by default to zero, the code for complete dates.

If you are importing complete dates mixed with partial dates, you can either enter a zero in the Date Flag field for individual records that have complete dates, or leave the Date Flag field blank for full-date records.

When you import partial dates, follow these rules:

- ◊ **Month-year dates.** For a month-year date (e.g., May 1975), the Date field itself must be imported as a complete date. You must also import a 1 in the corresponding Date Flag field: the code for a month-year date. You can use any convention you like for the Day element of month-year dates in the Date field. If you want to be consistent, however, use Biota’s own convention: the first day of the month (May 1, 1975 for May 1975).
- ◊ **Year-only dates.** For year-only dates (e.g., 1975), the Date field itself must be imported as a complete date. You must also import a 2 in the corresponding Date Flag field: the code for a year-only date. You can use any convention you like for the Day and Month components of year-only dates in the Date field. Biota’s own convention is the last day of the year (December 31, 1975 for 1975).
- **Number Fields (Long Integer and Real).** Biota checks values imported into Long Integer fields for nonnumeric characters (besides the minus sign). If you import a real number into a Long Integer field, it is truncated to its integer part.

Values imported into Real number field are checked for nonnumeric characters (besides the minus sign and decimal point). (Scientific notation, e.g., “2.13E3,” is not supported in Biota.)

If an invalid character is found in a number field, Biota posts an error message (see “[Displays and Error Messages During Record Importing or Updating](#),” later in this chapter).

- **Latitude and Longitude fields.** These two fields in the Locality table are of type Real. Latitude and longitude must be imported in *decimal degrees*, using the standard GIS conventions for hemispheres:

- ◊ **North and East** are positive values.
- ◊ **South and West** are negative values.

See “[Latitude and Longitude \(Locality Table\)](#)” in Chapter 9 for full details on coordinate systems and displays.

You can convert Degree-Minute-Second (DMS) coordinates to decimal degrees (in a spreadsheet, for example) for import, by the formula:

$$\text{Decimal Degrees} = \text{Degrees} + (\text{Minutes}/60) + (\text{Seconds}/3600)$$

You can convert Integer-Degrees-Decimal-Minutes coordinates to decimal degrees by the formula:

$$\text{Decimal Degrees} = \text{Int}(\text{Integer-Degrees-Decimal-Minutes})$$

$$+ \text{Frac}(\text{Integer-Degrees-Decimal-Minutes})/60$$

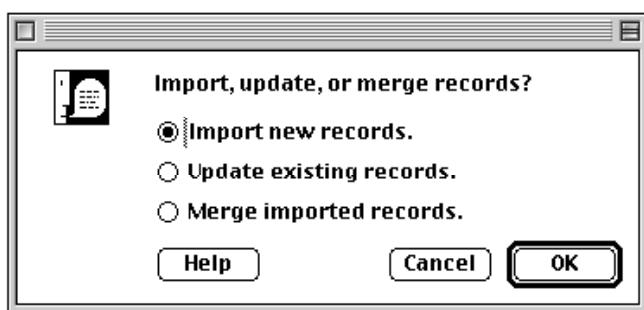
where *Int* means the integer part of a real number and *Frac* means the fractional part.

- **Text fields.** Biota uses text fields for the “Locality Name” field in the Locality table, for the “Note” and “Heading” fields of the Project table, for several fields in the Reference table, for the “Notes” field in the Personnel table, for the “Description” field of the Loans table, and for the “Note Text” fields of Notes tables. A text field may contain up to 32,000 characters (but they take up only as much memory in the Data File as required).
- **Boolean fields.** Boolean fields have one of two values: *True* or *False*. In a text file to be imported, a Boolean field must have either a zero (for False) or the number 1 (for True). There are only 3 Boolean fields in Biota.
 - ◊ **The “Group” field in the Personnel table** which, when True, identifies a Personnel record as a Group Name record, rather than an Individual record. The Group field has the value False for an individual (see “[Entering Personnel Data: The ‘Group’ Tab](#)” in Chapter 11).
 - ◊ **The “Project” field in the Personnel table** which, when True, identifies a Personnel record as a Project-Linked record, rather than an Individual record. (See “[Personnel Input](#)” in Chapter 11).
 - ◊ **The “Active” field in the Project table** which, when True, identifies a Project record as the Active Project record (there is only one Active Project at any given time). See “[Project Input](#)” in Chapter 16.
- **Picture (Image) fields.** You cannot import or update the [ImageArchive]Image field using the Import Editor. Images can be imported from disk files to the Data File either singly or in batch mode, using special import tools described in the section “[Exporting and Importing Images](#)” in Chapter 19.

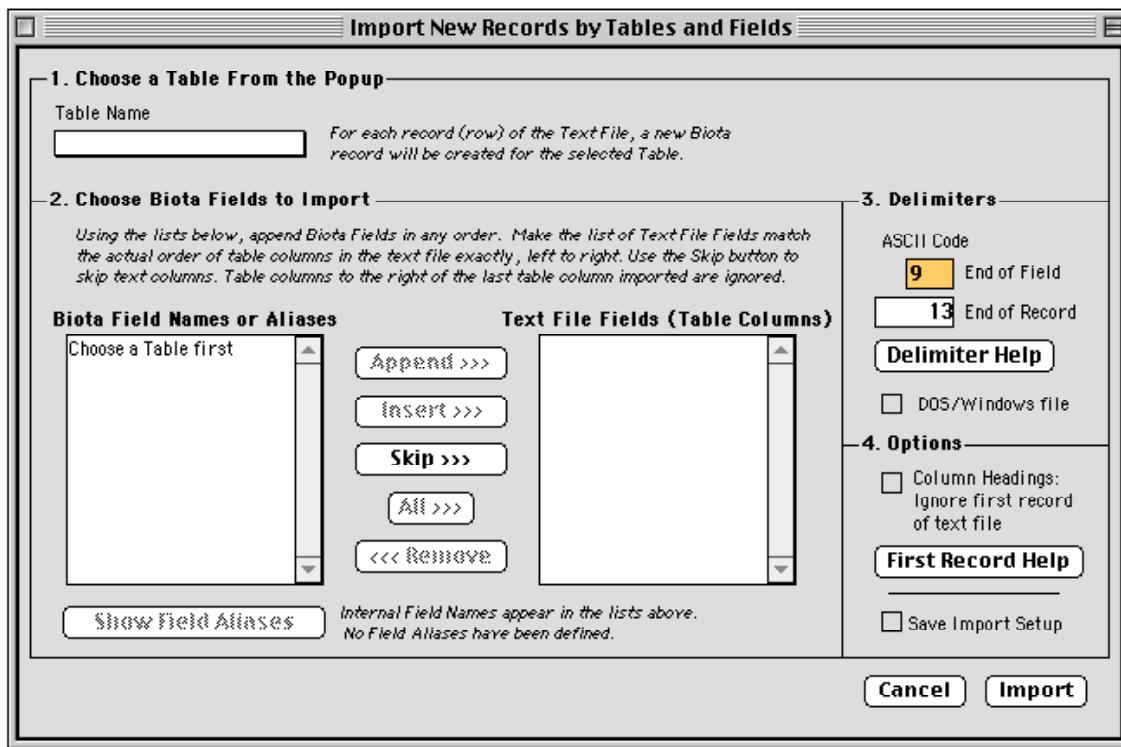
Import Step 3: Set Up and Launch the Import, Update, or Merge

When you have a text file ready to import, follow these steps to launch the Import Editor.

1. Choose “Import by Tables and Fields” from the Im/Export menu. An option screen appears, offering three options.
 - **“Import new records.”** With this approach, every record in the text (donor) file must contain a record for which the Key field (see “[Key Fields](#)” in Chapter 3) is new to the Data File.



- “**Update existing records.**” With this option, every record in the text (donor) file must contain a record for which the Key field *matches* a record already in the Data File, so Biota can find the record to update.
 - “**Merging imported records.**” With this option, you can import records from a text file that includes a mixture of new records and records already in the Data File. Biota *imports* any record for which the Key field is new to the Data File, and *ignores* any record for which the Key field *matches* a record already in the Data File.
2. Select the function you want and click the “OK” button. The Import Editor appears.



- If you selected the “New records” option, the Import Editor appears in a window with the title “Import New Records by Tables and Fields.”
- If you selected the “Update” option, the Import Editor appears in a window with the title “Import Fields to Update Existing Records.”
- If you selected the “Merge” option, the Import Editor appears in a window with the title “Merge Imported Records by Tables and Fields.”

NOTE: In the illustrations in this section, the window title will specify the new record option, but all aspects of setting up the Import Editor are the same for all three options.

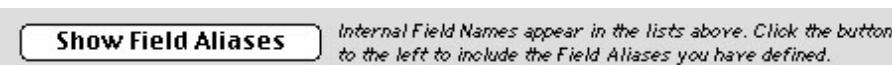
3. **Select a table.** From the “Table Name” popup list at the upper left, select the name of the table from which you want to export records (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”).

In the “Biota Field Names or Aliases” panel at the lower left, Biota displays all fields for the table you selected, listed alphabetically.

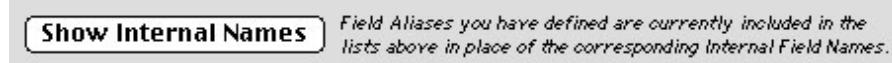
The image consists of two side-by-side screenshots of the Biota Import Editor. Both screenshots show the 'Import New Record' dialog with the 'Collection' table selected in the 'Table Name' dropdown. In the first screenshot, the 'Biota Field Names or Aliases' panel on the right shows a list of internal field names: AuxIndex, Class, Collection, CollectionNotes, CollFieldName, CollFieldValue, DetHistory, Family, Genus, Group, ImageArchive, Kingdom, and ListItems. In the second screenshot, the 'Biota Field Names or Aliases' panel shows the same list, but the 'Show Internal Names' button below it is highlighted with a red arrow, indicating it has been clicked. This highlights the difference between the state when no aliases are defined (disabled button) and when aliases are defined (enabled button).

4. **Using the “Field Name/Alias” button.** The button below the “Biota Field Names or Aliases” panel controls whether Biota lists strictly Internal Field Names (as given in Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) or substitutes a Field Alias for the corresponding Internal Field Name for each field you have given an Alias. (See Chapter 18, “[Re-naming Fields](#),” to learn about Field Aliases.)

- **If no Aliases have been defined,** the button is disabled and reads: “Show Field Aliases.” The caption to the right of the button reads: “Internal Field Names appear in the lists above. No Field Aliases have been defined.”



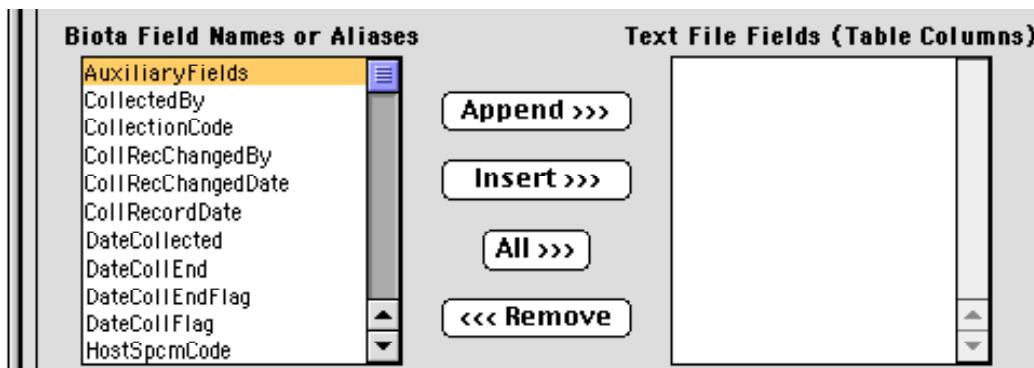
- **If any Aliases have been defined,** when you first open the Import Editor the button is enabled and reads: “Show Internal Names.” The caption to the right of the button reads: “Field Aliases you have defined are currently included in the lists above in place of the corresponding Internal Field Names.”



- If you click the “Show Internal Names” button, the button text changes to “Show Field Aliases” and the caption reads: “Internal Field Names appear in the lists above. Click the button to the left to include the Field Aliases you have defined.”



5. List the Biota fields that will receive data from the text file. The “Biota Field Names or Aliases” panel is simply a source of field names. The panel labeled “Text File Fields (Table Columns),” at the right, is the list Biota will consult in placing data from your text file into fields in your Biota Data File.



Usually, the number and order of field names (Internal Field Names or Aliases) in the list you create in the “Text File Fields” panel must match the number and order of columns in your text file. There are two exceptions to this rule:

- If you want to skip a column in the text file, click the “Skip” button to enter “[Skip a Text File Column]” in the Text File Fields panel (see [Step 6](#), below in this section).
- If there are columns in your text file to the right of the last column you list to import, Biota will ignore them. There is no need to list “[Skip a Text File Column]” entries for such columns (although it would do no harm).

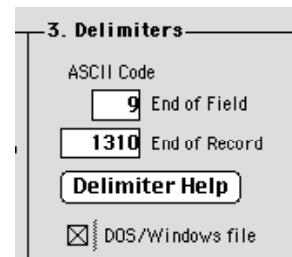
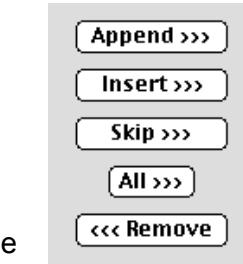
NOTE: If you have included column headings in your text file, the headings need not match the field names you list in the “Text File Fields” panel, since headings are ignored (see [The Column Heading Row Option](#), earlier in this chapter, and [“Column Headings’ checkbox](#), Step 8 below).

6. Use the buttons between the two lower panels in the Export Editor to create the list of fields in the “Text File Fields” panel. The list of fields you create can include any or all of the field names or aliases from the list available, in any order. You can even repeat fields if you want.
 - **“Append” button.** Click a field in the “Biota Field Name” panel to select it, then click the “Append” button. The field name is added to the end of the list in the “Text File Fields” panel.



- **“Insert” button.** Click a field already listed in the “Text File Fields” panel to select it. Then click the field in the “Biota Field Name” panel that you want to insert. When you click the “Insert” button, the new field is inserted just *above* the selected field in the “Text File Fields” panel.
- **“Skip” button.** If there is a column in your text file that you want Biota to ignore, click the “Skip” button to append or insert the phrase “[Skip a Text File Column]” in the “Text File Fields” panel. You must do this for each intervening column to be skipped. (Columns to the right of the last one listed are skipped automatically, however.)
- **“All” button.** The “All” Button is a toggle. When the button text reads “All>>>,” it means “Append All.” If you click the button, all fields in the “Biota Field Name” panel are entered in the “Text File Fields” panel (in the order listed in the Field Name Panel), *replacing* any fields already listed in the “Text File Fields” panel. The button text then changes to read “<<<All,” meaning “Remove All.” If you click the button again, the “Text File Fields” panel is cleared and the button text changes back to “All>>>.”
- **“Remove” button.** To remove a single field already entered in the “Text File Fields” panel, select the field by clicking it in the list, then click the “Remove” button.

7. **Set the Field and Record Delimiters.** In the “Delimiters” panel of the Import Editor, you specify the information that Biota needs in order to tell where one column (field) of your text file stops and the next begins, and where one record stops and the next begins. You may use any characters in the standard ASCII set (Characters 33–126), but, of course, they must make sense in the context of other applications you intend to use in working with the text file. The “Delimiter Help” button presents a list of common options.



- **Windows:** The default delimiters are TAB (ASCII Character 9) for the field delimiter and RETURN + LINE FEED (ASCII Characters 13 + 10), for the record delimiter—the characters that Windows spreadsheet applications use for “TAB-separated values” text files.

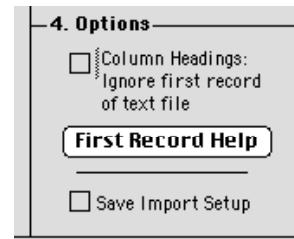
If you are importing data from a Macintosh text file, using a Windows machine, click the “DOS/Windows File” checkbox to uncheck it. The “End of Record” box will then read “13.”

- **Macintosh:** The default delimiters are TAB (ASCII Character 9) for the field delimiter and RETURN (ASCII Character 13) for the record delimiter—the characters that Macintosh spreadsheet applications use for “TAB-separated values” text files.

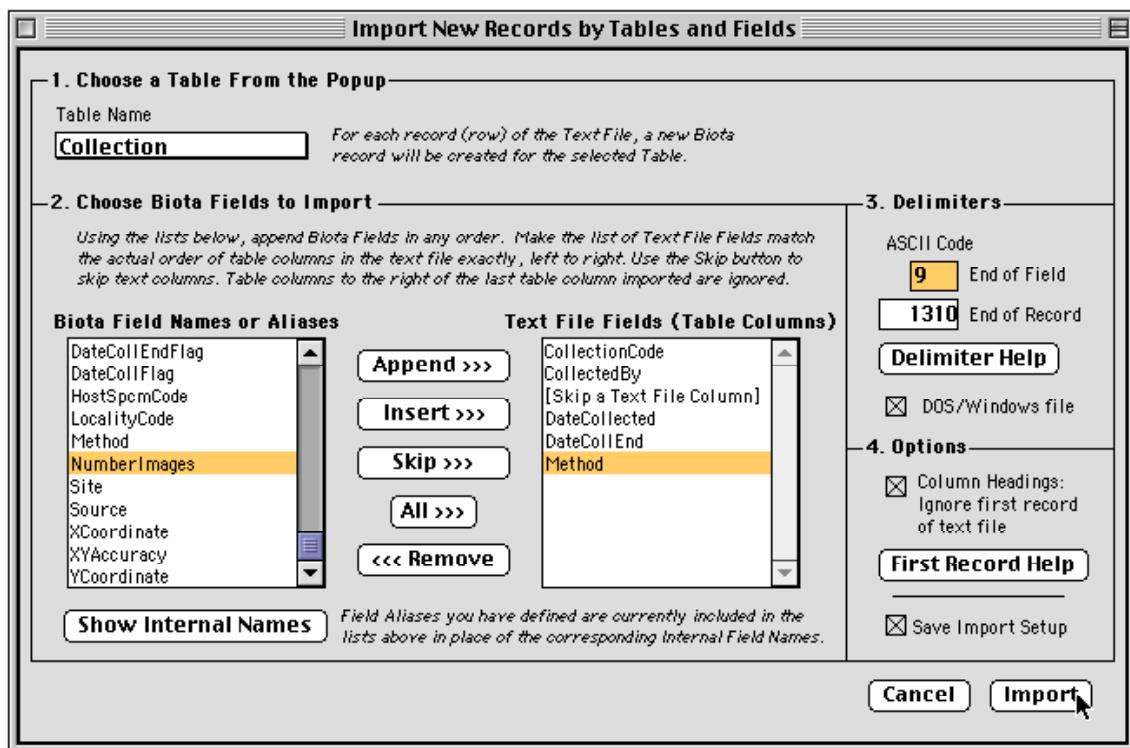
If you are using a Mac OS machine to import data from a PC (Windows) text file that uses the standard PC line termination (RETURN + LINE FEED, ASCII Characters 13 + 10), click the “DOS/Windows File” checkbox to set the check mark. The “End of Record” box will then read “1310.”

8. **Set the Options.** There are two checkboxes in the “Options” panel. Both are unchecked, by default.

- **“Column Headings” Checkbox.** If the first row (record) of your text file consists of column headings, you must check this option so that Biota will ignore the first row. Otherwise, Biota will import, or attempt to import, the headings as field values for a record. (See “[The Column Heading Row Option](#),” earlier in this chapter.)
You can click the “First Record Help” button to review these instructions in context.
- **“Save Import Setup” checkbox.** If you check this option, Biota remembers the way you have set up the Import Editor, even if you Cancel without attempting to import, for the duration of the current Biota session. If you have a problem while importing data, this option can save you time when you are ready to try again after you have made corrections in the text file.



9. **Click the “Import” button to launch the import process,** when the list of “Text File Fields” and the settings are ready.



Biota presents the standard Open File window for your operating system. Find the text file you have set up to import, then click the “Open” button.

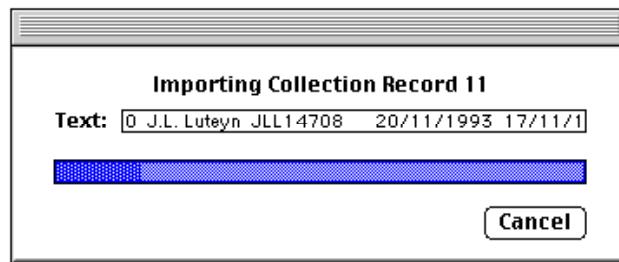
Displays and Error Messages During Record Importing or Updating

The Import Progress Indicator

Once the import or update begins, Biota displays a special progress indicator that shows the first few dozen characters of each record, as it is being imported from the text file. You can click the “Cancel” button in the progress indicator window at any time to halt the import.

If Biota encounters a problem, it posts an explanatory error message (discussed individually later in this section) and freezes the progress indicator with the first 50 characters or so of the offending record still displayed.

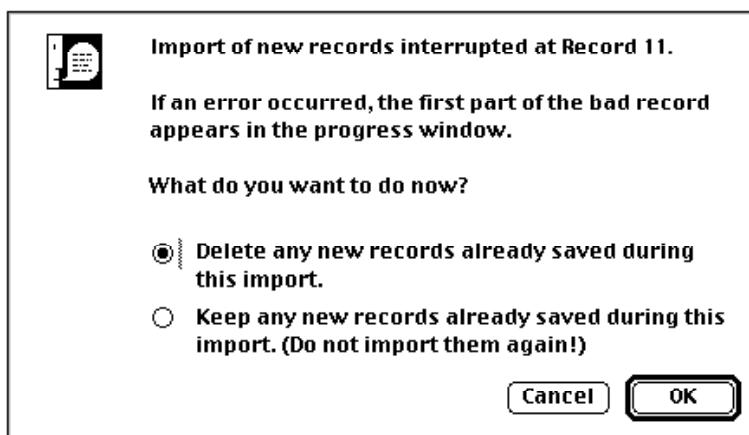
The progress indicator and all import and update error message windows (except for the “[Missing Key Error](#)” discussed later in this chapter) include the *Record Number* of the offending record (“Collection Record 3,” in the example above). The Record Number is *simply the position of the bad record in the text file*—not counting the column heading record, if any. (The Record Number specified in import error messages is *not* the Record Code or Key value for the bad record.)



Importing New Records: Undoing an Aborted Import

If Biota encounters an error while importing new records from a text file, an error message is displayed. (Errors are discussed individually later in this chapter.)

When you click the “OK” button on the error screen (or the “Cancel” button for a [Field Length Error](#), detailed later in this chapter), Biota presents the option screen below, to ask you how to proceed.



- If you choose the “Delete any new records...” option (the default), Biota will undo the entire import, deleting all records already imported in the current episode. While it may seem a pity to delete correctly imported records, this alternative is quite often the better one—unless the error occurs well into a very long import.
- If, instead, you choose the “Keep any new records already saved...” option, you will not have to import those records again, but you must delete them from your text file before you can import the remaining records (after correcting the bad record). Otherwise, you will get Duplicate Key errors.

The option screen above also appears if you interrupt the import by clicking Cancel in the progress indicator window. In this case, you will almost certainly want to delete all records imported before the interrupt, by selecting the first option in the screen above. You can use the Record Number to find out how far the import progressed in your text file before you canceled it, should you decide to keep the records already imported.

Updating Existing Records: Redoing an Aborted Import

If Biota encounters an error while updating existing records from a text file, an error message is displayed. (Errors are discussed individually later in this chapter.)

When you click the “OK” button on the error screen (or Cancel for “[Field Length Errors](#),” discussed later in this chapter), Biota presents the message on the right to inform you that any records correctly updated before the problem occurred remain in the Biota Data File in updated form.

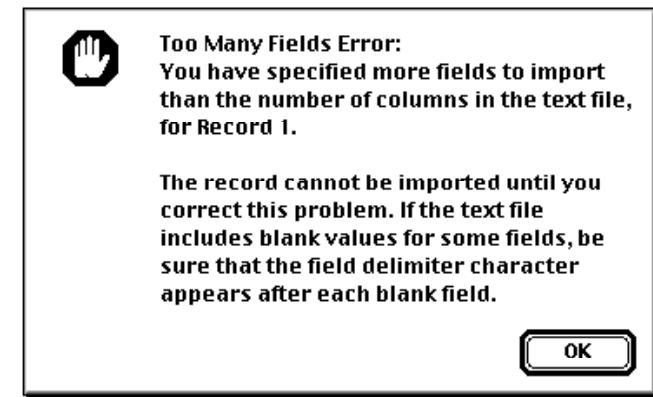
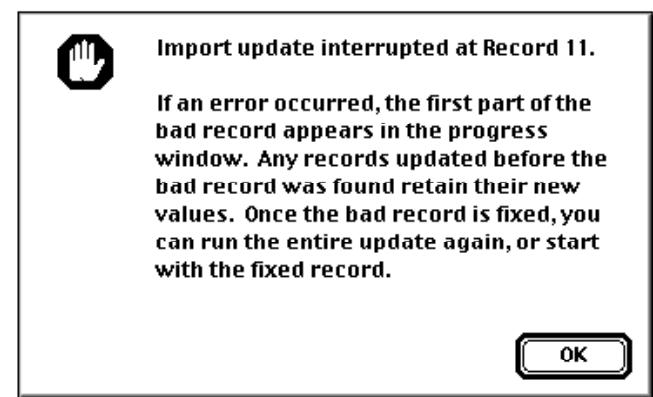
Once you correct the error in the text file, you can simply repeat the import if you wish. Records correctly updated before the error occurred will simply be “updated” again to the same values. If the import is a long one, however, you may wish to create a new text file containing only records not imported before—including the one that caused the problem, once it is fixed.

The screen above also appears if you interrupt the update by clicking Cancel in the progress indicator window.

Too Many Fields Error

In each record (row) in your text file, Biota looks for a field delimiter (see [Step 7](#) in the section “[Import Step 3: Set Up and Launch the Import, Update, or Merge](#)” earlier in this chapter) to match each field you have listed in the “Text File Fields” panel of the Import Editor. If Biota reaches the end of a record (the end of a row in the text file) before all fields in the list have been matched, you will see the message on the right.

If this message appears in response to the *first* record in your text file (as illustrated



above), chances are you truly listed more fields in the Import Editor than the number of columns in the text file, or you specified incorrect field or record delimiters. Open the text file (or better, a copy of it, so you can leave it open) in a spreadsheet application and check the number and order of columns against the number and order of fields in the “Text File Fields” panel of the Import Editor. There can be *fewer* fields (plus Skips) listed for import than the number of columns in the text file, but not *more*.

If the “Too Many Fields Error” screen appears after one or more records have been successfully imported or updated (the Record number cited in the error message is greater than 1), there is probably a missing field delimiter, or a missing delimiter and a missing field value in the offending record. As the message reminds you, if you have a blank field, you nevertheless must include the delimiter that separates the blank from the next field.

If you can’t find the problem using a spreadsheet application, as a last resort open the text file in a word processor (e.g., Microsoft Word), set to display TABS and RETURNS (paragraph marks), if those are the delimiters you have used. *If you make changes, be sure to save the file as Text.*

If you get the “Too Many Fields” error message on the *last* record of your text file, make sure the last line (record) in your text file ends with the record delimiter you have specified.

Missing Key Error: Importing New Records

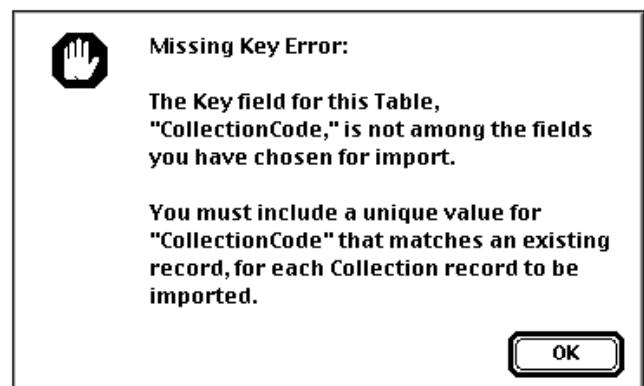
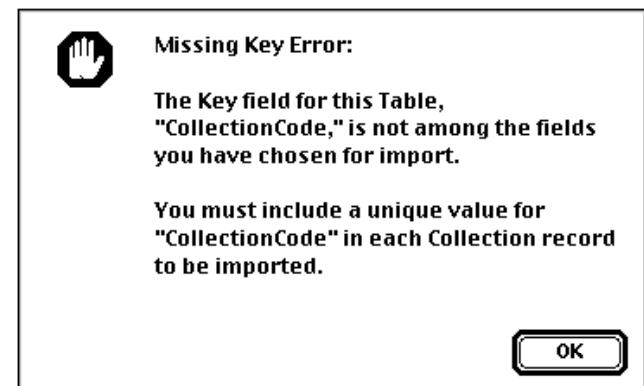
When you are importing new records into a Biota table that has a Key field (see “[Key Fields and the Importing Process](#)” earlier in this chapter), Biota issues a “Missing Key Error” message if you failed to include the Key field among those listed for import in the Text File Fields panel of the Import Editor.

Because Biota checks for this error *before* starting to import any data, a “Missing Key Error” simply aborts the import before it begins. If you get this message, you need to change the setup in the Import Editor to include the Key Field, make sure Key Field data exist in the correct column in the text file, and then launch the import again.

Missing Key Error: Updating Existing Records

If you are updating existing records in a Biota table that has a Key field (see “[Key Fields and the Importing Process](#)” earlier in this chapter), Biota issues a “Missing Key Error” message if you fail to include the Key field among those listed for import in the “Text File Fields” panel of the Import Editor.

Because Biota checks for this error *before* starting to import any data, a “Missing Key



Error” simply aborts the import before it begins. If you get this message, you need to change the setup in the Import Editor to include the Key Field, make sure Key Field data exist in the correct column in the text file, and then launch the import again.

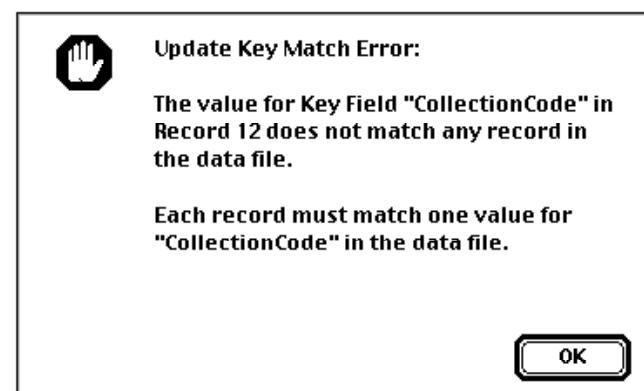
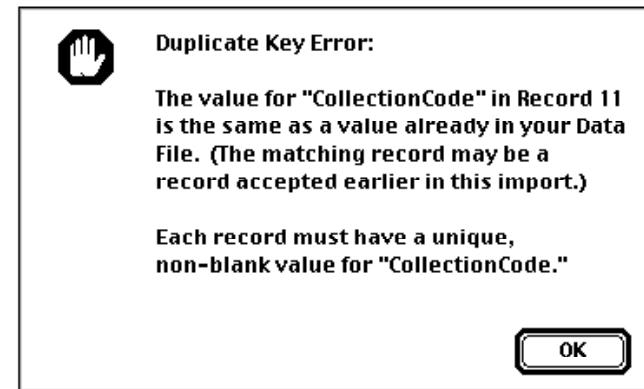
Duplicate Key Error: Importing New Records

If you are importing new records into a Biota table that has a Key field (see “[Key Fields and the Importing Process](#)” earlier in this chapter) that requires unique values, Biota posts a “Duplicate Key Error” message whenever it encounters a value for the Key field that is already in the Biota Data File.

Because each record is saved as it is imported, the duplication may be either between two records in the text file you are importing or between a record in the text file and a record that was already in the Biota Data File before the import began. You may have to check both possibilities—or you could simply change the Key field in the offending record.

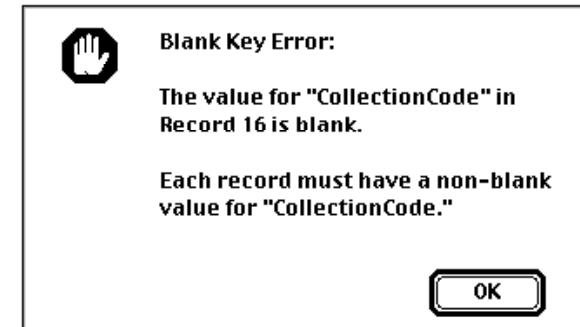
Update Key Match Error: Updating Existing Records

If you are updating existing records and Biota cannot match a Key field value (see “[Key Fields and the Importing Process](#)” earlier in this chapter) with any record already in your Biota Data File, Biota cannot tell which record to update and posts the “Update Key Match Error” message at the right.



Blank Key Error

If you are importing new records or updating records in a Biota table that has a Key field (see “[Key Fields and the Importing Process](#)” earlier in this chapter), Biota posts a “Blank Key Error” message whenever it encounters a blank value (no characters at all). A value entered as all space characters gives the same error, since initial spaces are automatically deleted.

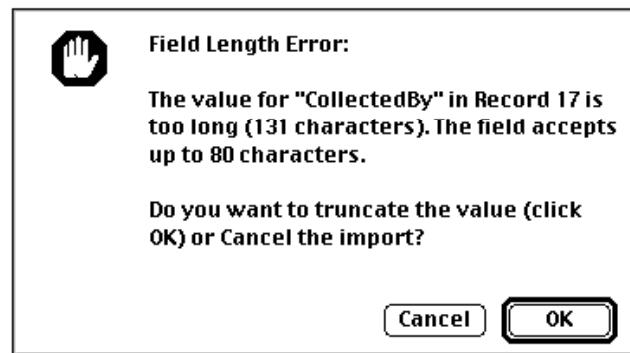


Field Length Error

Each alphanumeric field in the Biota structure has a maximum length, as specified in Appendix A, “[Biota Tables, Fields, and Relational Links.](#)”

If Biota encounters a value for a particular field that exceeds that field’s length limit, Biota posts the “Field Length Error” message.

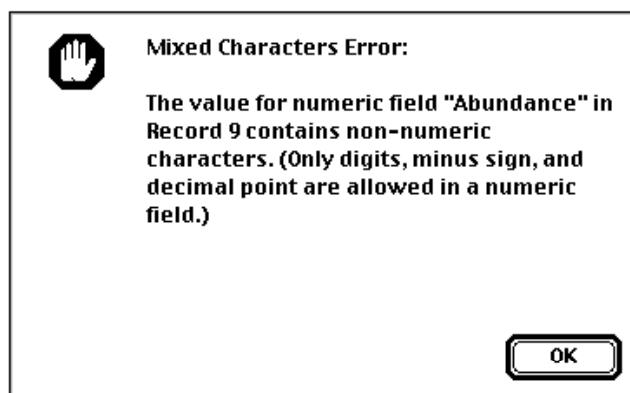
Unlike all other import error messages, the “Field Length Error” message allows you to continue with the import or the update if you choose—by accepting the problem value, truncated to fit the field. If you click the “Cancel” button, Biota posts the standard import or update error screen. In the case of new records, you can elect to delete records already imported or to keep them (see “[Importing New Records: Undoing an Aborted Import](#)” earlier in this chapter).



NOTE: If you get a Field Length Error message claiming a very long string, and/or the import progress indicator shows garbage, you have probably saved the text file in some format other than plain text (e.g., Microsoft Word document format, or Excel spreadsheet or workbook format). Open the file in the application and save it again as “Text.”

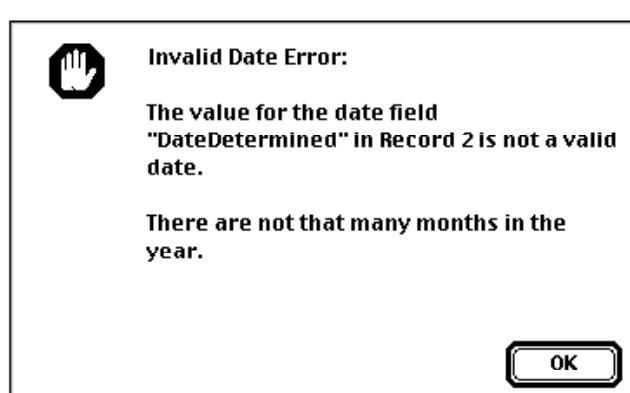
Mixed Characters Error

If you try to import alphabetic characters into a numeric field, Biota posts a “Mixed Characters Error” message. Fields of type Real allow digits, the decimal point, and the minus sign only. Integer and Long Integer fields allow only digits and the minus sign.



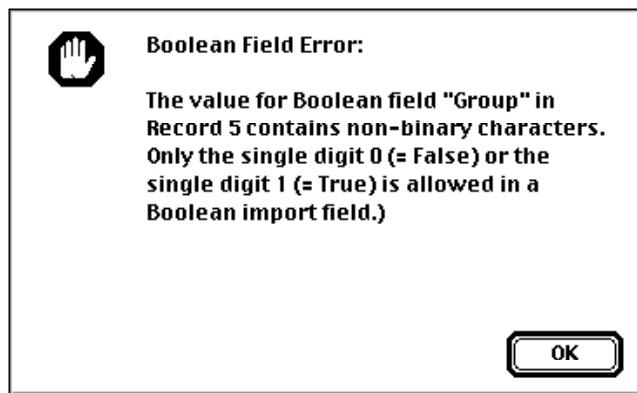
Invalid Date Error

If you attempt to import a date that is in the correct format, but violates the Gregorian calendar, Biota posts an “Invalid Date Error” message. See “[Field Types and Field Lengths](#)”, earlier in this chapter, for the conditions tested.



Boolean Field Error

In your text file, a Boolean field variable must take one of two values: a 1 if the variable is *True* and a 0 if the variable is *False*. See “[Field Types and Field Lengths](#),” earlier in this chapter, for more details.



Importing Data to Notes Tables or to the Determination History Table

Five Core tables in Biota’s structure—Species, Specimen, Collection, Locality, and Loans—are linked to Notes tables, with corresponding names (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). In each case, the Core table is the parent table and the Notes table the child table, so that many Notes records may be saved for each Core Table record. For example, for each Species record, you can create as many Species Notes as you wish (see “[Notes Input](#)” in Chapter 11). Each Species Notes record is linked to the parent Species record through the Species Code field.

The Determination History (“Det History”) table works in a similar manner. For each Specimen record, any number of Determination History records can be created, as determinations are updated over time.

Thus, you can import multiple Notes records with the same value in the Record Code field (the Notes may differ in author, date, and contents), without getting an error message. (The Record Code fields in the Notes tables are: [Species Notes] Species Code, [Specimen Notes] Specimen Code, [Collection Notes] Collection Code, [Locality Notes] Locality Code, and [Loans Notes] Loan Code.)

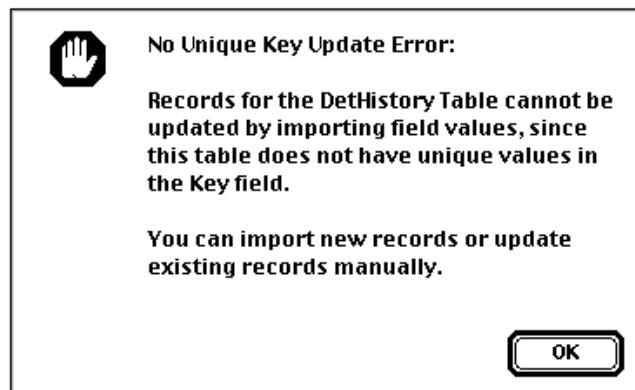
Likewise, you can import multiple Determination History records with the same [Det History] Specimen Code value.

You cannot update existing records in a Notes table or the Determination History table. Because the Key values for these tables are not unique, Biota would not know which record to update if there were any ambiguity.

Here are some special error comments you may receive in importing records to Notes tables or the Determination History table, in addition to general errors detailed in the previous sections of this chapter (see “[Displays and Error Messages During Record Importing or Updating](#)”).

No Unique Key Update Error

Because the Key value for Notes tables and the Determination History table are not unique, it is not possible to update existing records in a Notes table or the Determination History table. If you try to do so, Biota issues a “No Unique Key Update Error” message.

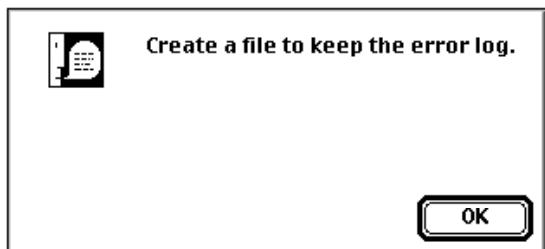
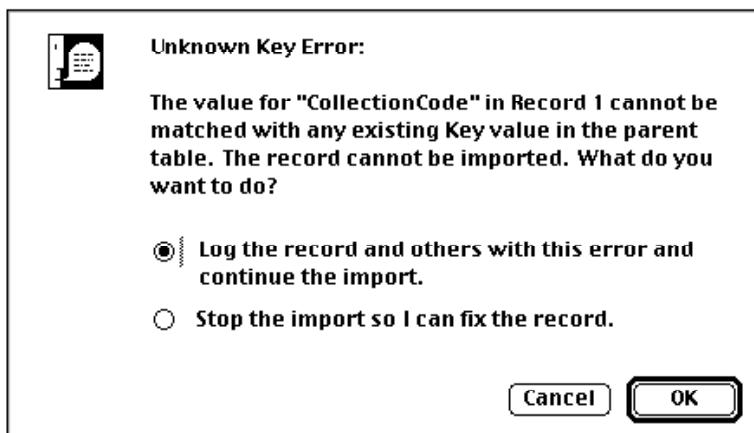


Unknown Key Error

For Biota to find and display a Notes record or Determination History record, it must be properly linked to a record in the corresponding parent table (see “[Linking Fields: Parent and Child Records](#)” in Chapter 3). If the Record Code value in a new Notes record or Determination History record you want to import does not match any record in the corresponding Core (parent) table, Biota issues an “Unknown Key” error message.

The message offers two options:

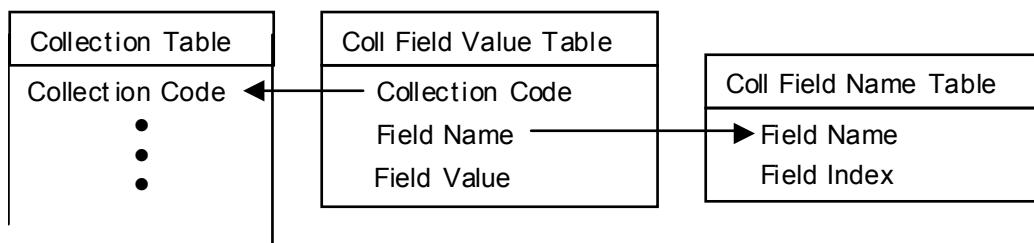
- **Either:** “**Log the record and others with this error and continue the import.**” If you choose this option, Biota presents the instruction screen on the right.
- After clicking the “OK” button in the instruction screen, name and place a text log file. You can use the log file to help you correct the errors in the input file. You can choose accept or delete any records correctly imported.
- **Or:** “**Stop the import so I can fix the record.**” With this option, the import stops, and you can accept or delete any records correctly imported.



Importing New Records and Updating Existing Records in Auxiliary Fields Tables

Before importing any data to Auxiliary Fields tables, it might be a good idea to read or review Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#),” although a brief outline follows here.

Biota supports user-defined Auxiliary Fields for four parent (Core) tables: Species, Specimen, Collection, and Locality. Linked to each parent table is a child table for Auxiliary Field Values (Appendix A, “[Biota Tables, Fields, and Relational Links](#)”). In the example below, a child table called “Coll Field Value” is linked to the Collection (parent) table.



As shown for the Coll Field Value table above, each *Field Value* table has just three fields: Record Code, Field Name, and Field Value (where “Record Code” is Species Code in the Spp Field Value table, Specimen Code in the Spcm Field Value table, Collection Code in the Coll Field Value table, or Locality Code in the Loc Field Value table).

A *Field Name* table is linked as a parent to each Field Value table, through Field Name fields. (The Coll Field Name table is illustrated above.) The Field Name tables keep track of the ordering of Auxiliary Field Names that you assign in the Field Name Editor (see “[Creating, Editing, and Ordering Auxiliary Field Names](#)” in Chapter 16) and speed up procedures that work with Auxiliary Fields. (The four Field Name tables are the Spp Field Name table, the Spcm Field Name table, the Coll Field Name table, and the Loc Field Name table.)

Importing or Updating Records in Field Name Tables

Importing new records from a text file to a Field Name table or updating existing Field Name records is straightforward. The Field Name field, which is the Key field for this table, requires unique values (within each FieldName table) for importing new records, or values that match existing ones for updating. (The previous section outlines the role of Field Name tables in managing Auxiliary Field data.)

The second and only other field, Field Index, is most logically assigned unique, consecutive integers, but in fact Biota will accept any integers or even blank fields (blanks are assigned a zero in the Field Index field). Fields are then ordered by Field Index value, with fields that share the same value in arbitrary order. You can easily correct such anomalies later using the Field Name Editor. (The “Sort” button in the Field Name Editor can renumber field names automatically, or you can do it manually, as shown in “[Creating, Editing, and Ordering Auxiliary Field Names](#)” in Chapter 16).

Importing or Updating Records in Field Value Tables

Biota imposes some special requirements for importing new records or updating records in Field Value tables. (The introductory paragraphs of this section, “[Importing New Records and Updating Existing Records in Auxiliary Fields Tables](#),” outline the role of Field Value tables in managing Auxiliary Field data.)

Field Value tables have a two-field (composite) Key. Each record must have a *unique combination* of values in the Record Code and Field Name fields (where “Record Code” is Species Code, Specimen Code, Collection Code, or Locality Code—depending on the table).

Furthermore, there is no point in importing or creating a record in a Field Value table with a blank in the Field Value *field*. (In fact, Biota does not even save such a record if you try to create one within Biota by using an Auxiliary Field input screen.)

For these reasons, the Import Editor does not accept any record for input to a Field Value table unless all three fields are present (Record Code, Field Name, and Field Value) and the two Key fields (Record Code and Field Name) contain a unique combination of values.

Note: In thinking about records in Field Value tables, you may find it helpful to visualize the Record Code value as a row index and the Field Name value as a column index for a columns-by-rows table with Field Values in the cells. Thus each combination of Record Code and Field Name points to a unique cell of the table. You import data only for the *nonempty* cells.

Auxiliary Field Setup Error

If you have set up the Import Editor to import data into a Field Value table (see “[Importing New Records and Updating Existing Records in Auxiliary Fields Tables](#)”) but you fail to include all three fields (Record Code, Field Name, and Field Value) in the list of fields destined to receive data from the text file, Biota does not allow you to proceed until you correct this problem.



Auxiliary Field Setup Error:

To Import Auxiliary Field Values for the CollFieldValue Table, you must list all three fields for this table in the Text File Fields panel of the Import Editor, and all three must be included in your text file.

OK

Auxiliary Field Blank Value Error

All three fields must be present in each record you import into a Field Value table (see above, “[Importing or Updating Records in Field Value Tables](#),” for the reasons). If one or more of the three values is blank, Biota posts the following error notice. (This is the message for an update error. For the same error while importing new records, the last sentence of the text begins: “To Import Auxiliary Field Values for....”)



Auxiliary Field Blank Value Error:

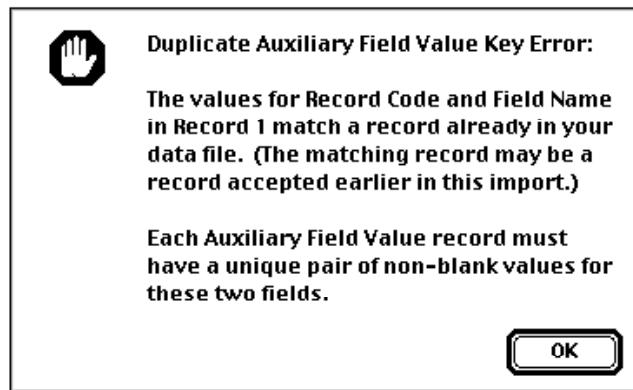
The value for "SpeciesCode" in Record 7 is blank.

To Update Auxiliary Field Values for the SppFieldValue Table, you must import non-blank values for all three fields for this table.

OK

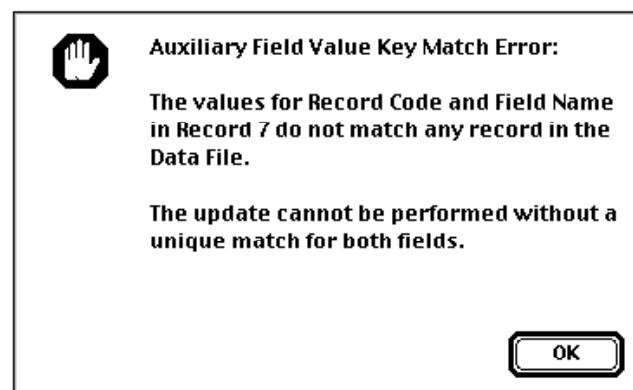
Duplicate Auxiliary Field Value Key Error: Importing New Records

If you attempt to import a Field Value record that duplicates an existing one in both the Record Code and Field Name fields, Biota aborts the import and posts the “Duplicate Auxiliary Field Value Key Error” message.



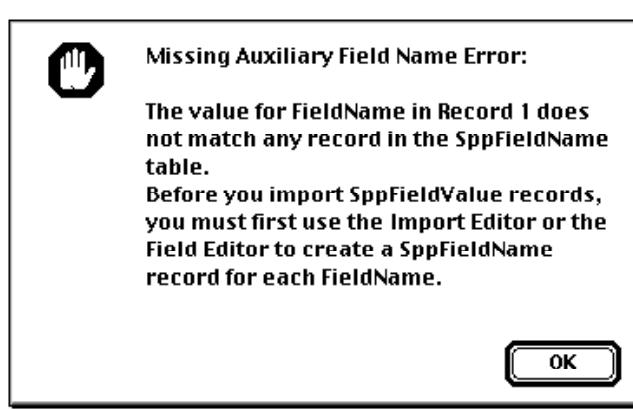
Auxiliary Field Value Key Match Error: Updating Existing Records

If you attempt to update a Field Value record that Biota cannot find a match for in both the Record Code and Field Name fields, Biota aborts the import and posts an “Auxiliary Field Value Key Match Error” message.



Missing Auxiliary Field Name Error: Importing New Field Value Records

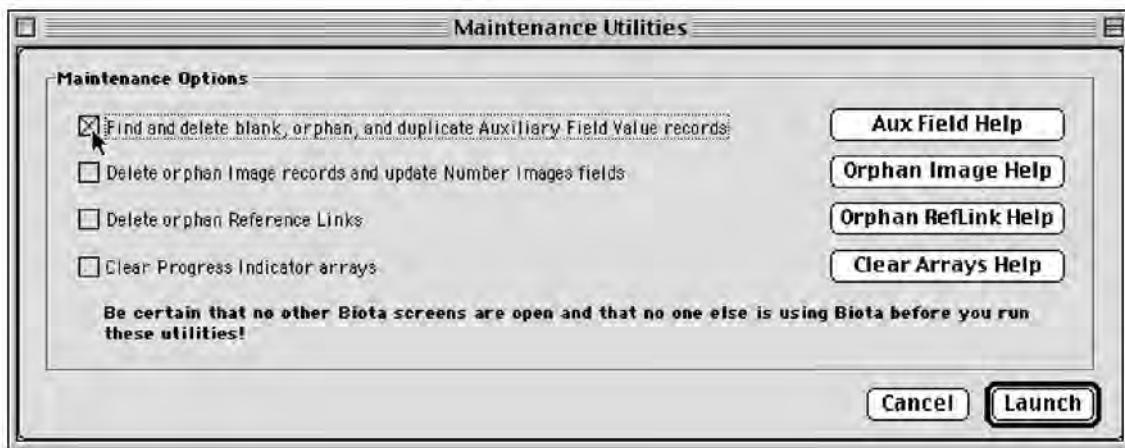
Biota refuses to import any new Auxiliary Field Value record for which the FieldName value does not match a FieldName in the corresponding FieldName table (see above, “[Importing or Updating Records in Field Value Tables](#),” for the reasons). If you are importing both FieldValue and FieldName records, you must import the FieldName records first or use the Field Editor to create the appropriate Auxiliary Field Name values (see “[Creating, Editing, and Ordering Auxiliary Field Names](#)” in Chapter 16).



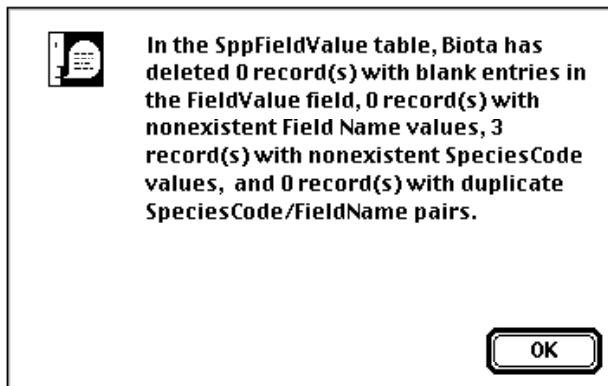
Checking and Repairing Auxiliary Fields After Importing

Despite all the error checking that Biota does during Auxiliary Field importing or updating, it is always a good idea to check that the resulting Auxiliary Fields and Field Values are just as you intended them in the database after import. In addition, it is a good idea to run the Auxiliary Fields option in the Maintenance Utilities (Special menu)

to “clean up” any orphan Field Value records and other anomalies. The option screen for this utility appears below.



Here is an example of a report from the Auxiliary Field Maintenance tool.



(See “[Maintaining and Repairing the Auxiliary Fields and Project Systems](#)” in Chapter 16 for more details on using this tool.)

Importing Records for the Lists and List Items Tables

The Lists table in Biota has two special purposes. It keeps track of Core Field Aliases you define (see Chapter 18, “[Re-naming Fields](#)”) and it enables or disables the Field Value Choice Lists you create (see “[Using Entry Choice Lists](#)” in Chapter 17). The Lists table has exactly three records, at all times.

The actual values that appear in Entry Choice Lists are represented by records in the List Items table.

Importing Records Into the Lists Table

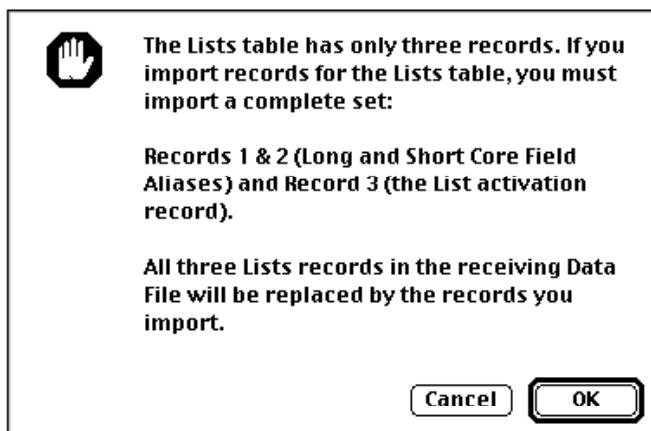
For most users, the only reason you will ever want to import records into the Lists table is to transfer Lists records from one Biota Data File to another (to a new, blank one, for example).

The procedure for exporting Lists records from one Biota Data File and importing them into another is detailed in Chapter 17, “[Transferring Choice Lists to a Different Biota Data File](#).”

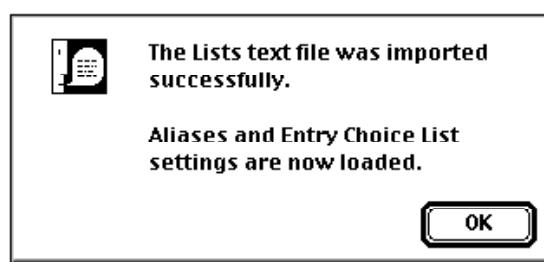
See Appendix A, “[Biota Tables, Fields, and Relational Links](#),” for details on the fields, default values, and required records for the Lists table. You should study Appendix A (“[Biota Tables, Fields, and Relational Links](#)”) if you intend to create the required records for import into the Lists table using another application (e.g., a spreadsheet application) or if you want to modify exported Lists records before importing them again.

The process of importing Lists records has three important special characteristics.

- When you import new Lists records, Biota *first deletes all three existing records* in the Lists table. The three new records you import replace all existing records.
- For this reason, *you cannot use the Import Editor to update existing Lists records*.
- If you import Lists records, Biota checks that all three required records are present. If not, you will see the following error message.



When Biota has completed the successful importation of a set of Lists records, the message below appears:



Importing Records Into the List Items Table

For instructions on importing List Items records, please read the sections “[Importing Choice List Data From a Text File](#)” and “[Transferring Choice Lists to a Different Biota Data File](#)” in Chapter 17.

A Strategy for Importing Text Files Into Hierarchically Linked Tables

If your raw text file is a flatfile (a columns-by-rows table) that includes columns destined for several hierarchically linked Biota tables, you may find it helpful to refer to this section, which outlines a strategy for creating the corresponding text files for import into Biota.

For example, you may have data in a taxonomic flatfile (see “[Exporting Taxonomic Flatfiles](#)” in Chapter 27), with rows for species (or some other taxonomic level) and columns for the higher taxonomic levels (genus, family, etc.) to which each species (or other taxon) belongs. Or, your text file may be a specimen flatfile (see “[Exporting Specimen Flatfiles](#)” in Chapter 27): one row per specimen, with fields for several levels in both the taxonomic and place hierarchies.

Strategy: Importing Hierarchically Linked Records from an Existing Text Flatfile

The two sections that follow this one describe, step by step, an efficient strategy for using your existing text file to create new text files in the format Biota requires for import. But before you begin, it would be a good idea to read or review “[Import Step 1: Match Fields](#)” and “[Import Step 2: Prepare the Text Files](#)” at the beginning of this chapter.

Don’t be intimidated by the number of steps. In fact, they simply fill in the details for a repeated cycle of a few steps, for a pair of linked tables (child and parent; see “[Linking Fields: Parent and Child Records](#)” in Chapter 3).

Step by Step: Importing Hierarchically Linked Records from an Existing Taxonomic Flatfile

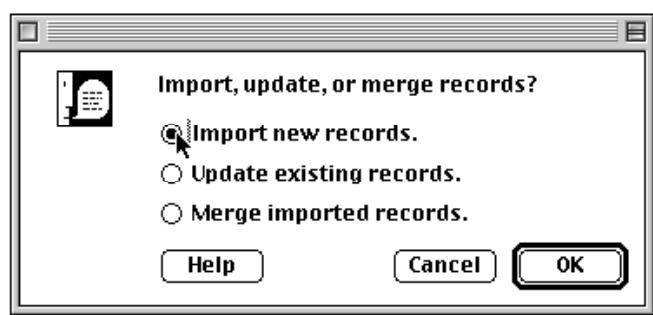
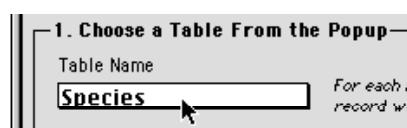
Suppose your raw text file looks something like the example for Galápagos finches and mockingbirds below (but probably with many more rows and columns).

Genus	Specific Name	Family	Order
Cactospiza	heliobates	Frinigillidae	Passeriformes
Cactospiza	pallida	Frinigillidae	Passeriformes
Camarhynchus	parvulus	Frinigillidae	Passeriformes
Camarhynchus	pauper	Frinigillidae	Passeriformes
Camarhynchus	psittacula	Frinigillidae	Passeriformes
Certhidea	olivacea	Frinigillidae	Passeriformes
Geospiza	conirostris	Frinigillidae	Passeriformes
Geospiza	difficilis	Frinigillidae	Passeriformes
Geospiza	fortis	Frinigillidae	Passeriformes
Geospiza	fuliginosa	Frinigillidae	Passeriformes
Geospiza	magnirostris	Frinigillidae	Passeriformes
Geospiza	scandens	Frinigillidae	Passeriformes
Pinaroloxias	inornata	Frinigillidae	Passeriformes
Platyspiza	crassirostris	Frinigillidae	Passeriformes
Nesomimus	parvulus	Mimidae	Passeriformes
Nesomimus	trifasciatus	Mimidae	Passeriformes

1. Open the text file in a spreadsheet application (e.g., Microsoft Excel).
2. Before making any changes, save the file with another name (let's call it "Taxon_Master" for purposes of illustration) and keep it open. This will act as a safeguard against making any changes to the original file, which you should keep as a backup.
3. In the "Taxon_Master" file, insert a column for Species Code and fill it with unique values (see "[Key Fields and the Importing Process](#)," earlier in this chapter, and "[Why Does Biota Require Species Codes?](#)" in Chapter 8, for background if necessary). Each Species Code value must be 30 characters or shorter.

Species Code	Genus	Specific Name	Family	Order
cactheli	Cactospiza	heliobates	Frinigillidae	Passeriformes
cactpall	Cactospiza	pallida	Frinigillidae	Passeriformes
camaparv	Camarhynchus	parvulus	Frinigillidae	Passeriformes
camapaup	Camarhynchus	pauper	Frinigillidae	Passeriformes
camapsit	Camarhynchus	psittacula	Frinigillidae	Passeriformes
certoliv	Certhidea	olivacea	Frinigillidae	Passeriformes
geosconi	Geospiza	conirostris	Frinigillidae	Passeriformes
geosdiff	Geospiza	difficilis	Frinigillidae	Passeriformes
geosfort	Geospiza	fortis	Frinigillidae	Passeriformes
geosfuli	Geospiza	fuliginosa	Frinigillidae	Passeriformes
geosmagn	Geospiza	magnirostris	Frinigillidae	Passeriformes
geosscan	Geospiza	scandens	Frinigillidae	Passeriformes
pinainor	Pinaroloxias	inornata	Frinigillidae	Passeriformes
platcras	Platyspiza	crassirostris	Frinigillidae	Passeriformes
nesoparv	Nesomimus	parvulus	Mimidae	Passeriformes
nesotrif	Nesomimus	trifasciatus	Mimidae	Passeriformes

4. Save the "Taxon_Master" file under a new name (e.g., "Taxon_Import"), as tab-delimited text, and close it.
5. Re-open the "Taxon_Master" file in Excel, leaving it open to use as a reference for field order. (Alternatively, you could write or print a list of the fields, in order, to use as a reference.)
6. In Biota, choose "Import by Tables and Fields" from the Im/Export menu.
7. Choose the "Import new records" option.
8. In the Import Editor, choose "Species" from the "Table Name" popup.



- Set up the Import Editor in Biota to import Species Code, Genus (the linking field to the Genus table), Specific Name, and any other Species fields (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) that you want to import from your “Taxon_Import” text file (e.g., SpeciesAuthor, SubSpecies, CommonNames, etc.). Do *not* try to import any fields destined for the Genus, Family, or higher taxon tables at this point.

Be sure to consult the open “Taxon_Master” file in Excel (or your written or printed list) for the order of fields in your “Taxon_Import” text file, and match it exactly in the “Text File Fields” panel of the Import Editor, using the “Skip” button if necessary. If

you need help setting up the Import Editor, see “[Import Step 3: Set Up and Launch the Import, Update, or Merge](#)” earlier in this chapter.

If you have a row of column headings in the “Taxon_Import” text file, be sure to check the “Column Headings” checkbox.

- Click the “Import” button in the Import Editor to launch the import.



- Find and open the “Taxon_Import” text file.

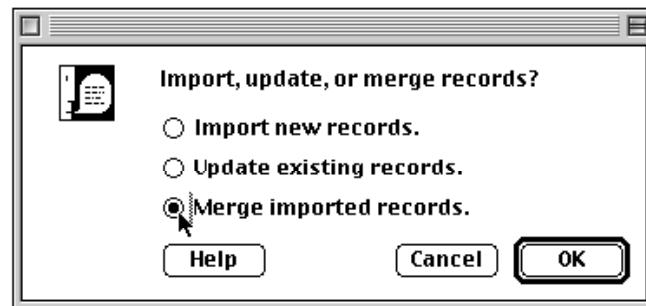
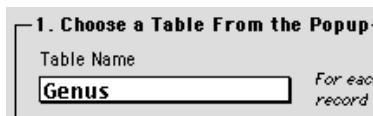
If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.

When the import is complete, it is time to import records to the Genus table.

- Again, choose “Import by Tables and Fields” from the Im/Export menu.

- This time, choose the “Merge imported records” option.

- In the Import Editor, choose “Genus” from the “Table Name” popup.



- Set up the Import Editor in Biota to import Genus, Family (the linking field to the Family table), and any other Genus table fields (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) that you want to import from your text file (e.g., Subfamily, Tribe, etc.).

- Click the “Import” button in the Import Editor to launch the import. If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.



- Find and open the “Taxon_Import” text file.

If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.

When the import is complete, it is time to import records to the Family table.

NOTE: Why use the “Merge imported records” option? Because there are many repeated values for Genus in the “Taxon_Import” table in the example (and no doubt in your own taxonomic flatfile). If you used the “Import new records” option instead, you would get a Duplicate Key Error for every subsequent copy of a name, after the first copy is imported. (See “[Duplicate Key Error: Importing New Records](#)” earlier in this chapter.) In contrast, in the case of the Species records earlier, each record must have a unique Key (Species Code), and you would want to know if any were *not* unique.

- 18. Repeat the process detailed in [Steps 12 through 17](#) for the Family, Order, and any additional ranks in the “Taxon_Import” text file.**

[This Chapter continues on the next page.]

Step by Step: Importing Hierarchically Linked Records from an Existing Specimen Flatfile

Suppose your raw text file looks something like Galápagos finch example below (but probably with many more rows and columns). (With apologies to Darwin and Fitzroy, these are made-up records, though with plausible dates and localities.)

Collected By	Date Collected	Locality Name	State/Prov	Country	Lat	Long	Genus	Specific Name
C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fuliginosa
C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	scandens
C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Geospiza	scandens
C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	psittacula
C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	pauper
C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	parvulus
R. Fitzroy	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Certhidea	olivacea
C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	magnirostris
C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	fortis
C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	difficilis
R. Fitzroy	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Cactospiza	heliobates
C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Cactospiza	pallida
C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Certhidea	olivacea
C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Geospiza	difficilis
C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Camarhynchus	parvulus

In Biota, each Specimen record needs to have a unique Specimen Code (see “[Key Fields and the Importing Process](#),” earlier in this chapter). Each Specimen record will be linked to a Species record through the linking field [Specimen]SpeciesCode and to a Collection record and through the linking field [Specimen]CollectionCode.

In turn each Collection Record will be linked to a Locality record through the linking field [Collection]LocalityCode.

Thus, we need to create four new columns in the Specimen flatfile: for SpecimenCode, SpeciesCode, CollectionCode, and LocalityCode, and fill them in appropriately. (It may well be that your flatfile already has columns that will do for some of these Record Codes.)

As detailed below, Specimen records can be imported from the text file, above, using the “Import new records” option in the Import Editor. Records for the Species table, any higher taxon tables, the Collection table, and the Locality table can be imported from the same text file using the “Merge imported records” option.

1. Open the text file in a spreadsheet application (e.g., Microsoft Excel).
2. Before making any changes, save the file with another name (let’s call it “Specimen_Master” for purposes of illustration) and keep it open. This will act as a safeguard against making any changes to the original file, which you should keep as a backup.

3. In the “Specimen_Master” file, insert and label blank columns for Specimen Code, Species Code, Collection Code, and Locality Code (unless you can use the data in existing columns instead; see the Note immediately below).

Note: Your flatfile may already include columns that will do for some of these Record Codes. For example, you may already have unique Locality names that are either short enough (30 characters or less) or could be shortened to become unique Locality Codes. Or, you may have “collection numbers” or “field numbers” for unique day/collector/site combinations (“collecting events”), which could become the Collection Code, etc.

It makes sense to take advantage of these existing data fields, if appropriate, instead of creating new columns and new Record Codes. We do this in [Step 5](#), below, for Locality Code, to illustrate.

4. Sort the rows (**Specimen records**), if you wish, into the order (if any) that you would like the Specimen Codes to represent.
5. Fill the Specimen Code column with unique values (see “[Key Fields and the Importing Process](#),” earlier in this Chapter, and Chapter 8, “[Record Codes](#),” for guidelines). Each Specimen Code value must be 30 characters or shorter.

Spcmn. Code	Spp Code	Coll Code	Collected By	Date Collected	Locality Name/Code	State/Prov	Country	Lat	Long	Genus	Specific Name
HMSB001			C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB002			R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB003			R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fuliginosa
HMSB004			C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	scandens
HMSB005			C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Geospiza	scandens
HMSB006			C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	psittacula
HMSB007			C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	pauper
HMSB008			C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	parvulus
HMSB009			R. Fitzroy	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Certhidea	olivacea
HMSB010			C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	magnirostris
HMSB011			C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	fortis
HMSB012			C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	difficilis
HMSB013			R. Fitzroy	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Cactospiza	heliobates
HMSB014			C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Cactospiza	pallida
HMSB015			C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Certhidea	olivacea
HMSB016			C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Geospiza	difficilis
HMSB017			C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Camarhynchus	parvulus

6. Sort the rows of the table by Genus, then Specific name so that all records of the same Species are together in the table.
7. Fill the Species Code column. Each Species must have a unique Species Code. Repeat the Species Code for each Specimen within a given Species.

Spcmn. Code	Species Code	Coll. Code	Collected By	Date Collected	Locality Name/Code	State /Prov	Country	Lat	Long	Genus	Specific Name
HMSB013	cactheli		R. Fitzroy	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Cactospiza	heliobates
HMSB014	cactpall		C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Cactospiza	pallida
HMSB008	camaparv		C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	parvulus
HMSB017	camaparv		C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Camarhynchus	parvulus
HMSB007	camapaup		C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	pauper
HMSB006	camapsit		C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	psittacula
HMSB009	certoliv		R. Fitzroy	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Certhidea	olivacea
HMSB015	certoliv		C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Certhidea	olivacea
HMSB012	geosdiff		C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	difficilis
HMSB016	geosdiff		C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Geospiza	difficilis
HMSB001	geosfort		C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB002	geosfort		R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB011	geosfort		C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	fortis
HMSB003	geosfuli		R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fuliginosa
HMSB010	geomagn		C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	magnirostris
HMSB004	geosscan		C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	scandens
HMSB005	geosscan		C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Geospiza	scandens

8. Sort the rows of the table by “Collected By,” then by “Date Collected,” then by “Locality Name” so that all records from the same collection event (same place, same day, same collector) are together in the table.
9. Fill the Collection Code column. Each Collection must have a unique Collection Code. Repeat the Collection Code for each Specimen within a given Collection.

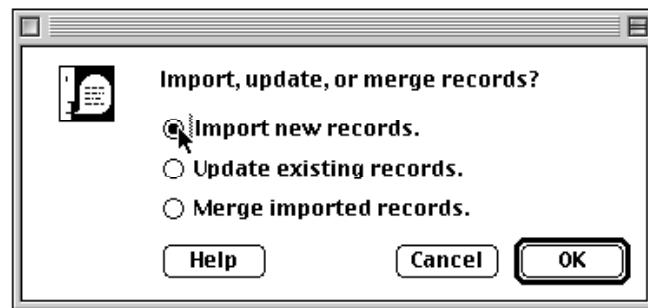
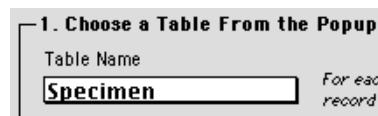
Spcmn. Code	Species Code	Coll. Code	Collected By	Date Collected	Locality Name/Code	State/ Prov	Country	Lat	Long	Genus	Specific Name
HMSB001	geosfort	CD001	C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB004	geosscan	CD001	C. Darwin	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	scandens
HMSB008	camaparv	CD002	C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	parvulus
HMSB007	camapaup	CD002	C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	pauper
HMSB006	camapsit	CD002	C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Camarhynchus	psittacula
HMSB005	geosscan	CD002	C. Darwin	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Geospiza	scandens
HMSB012	geosdiff	CD003	C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	difficilis
HMSB011	geosfort	CD003	C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	fortis
HMSB010	geomagn	CD003	C. Darwin	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Geospiza	magnirostris
HMSB014	cactpall	CD004	C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Cactospiza	pallida
HMSB017	camaparv	CD004	C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Camarhynchus	parvulus
HMSB015	certoliv	CD004	C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Certhidea	olivacea
HMSB016	geosdiff	CD004	C. Darwin	9 Oct 1832	Santiago I.	Galápagos	Ecuador	-0.23	-90.8	Geospiza	difficilis
HMSB002	geosfort	RF001	R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fortis
HMSB003	geosfuli	RF001	R. Fitzroy	18 Sep 1832	San Cristóbal I.	Galápagos	Ecuador	-0.83	-89.4	Geospiza	fuliginosa
HMSB009	certoliv	RF002	R. Fitzroy	24 Sep 1832	Floreana I.	Galápagos	Ecuador	-1.28	-90.4	Certhidea	olivacea
HMSB013	cactheli	RF003	R. Fitzroy	30 Sep 1832	Fernandina I.	Galápagos	Ecuador	-0.43	-91.5	Cactospiza	heliobates

10. Sort the rows of the table by “Country,” then “State/Prov,” then “District,” then “Locality Name,” so that all records from the same Locality are together in the table.
11. Fill the Locality Code column with values that are unique between Collections, repeated within Collections.

The text file is now ready for importing.

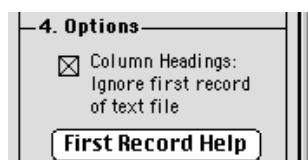
Note: Steps 10 and 11 are not illustrated here, since Locality Name doubled as Locality Code in the example.

12. Save the “Specimen_Master” file under a new name (e.g., “Specimen_Import”), as tab-delimited text, and close it.
13. Re-open the “Specimen_Master” file in Excel, and leave it open to use as a reference for field order. (Alternatively, you could write or print a list of the fields, in order, to use as a reference.)
14. In Biota, choose “Import by Tables and Fields” from the Im/Export menu.
15. Choose the “Import new records” option.
16. In the Import Editor, choose “Specimen” from the “Table Name” popup.



17. Set up the Import Editor in Biota to import Specimen Code, Species Code (the linking field to the Species table), Collection Code (the linking field to the Collection table), Specific Name, and any other Specimen fields (see Appendix A, [Biota Tables, Fields, and Relational Links](#)) that you want to import from your “Specimen_Import” text file (e.g., DeterminedBy, DateDetermined, Stage/Sex, Abundance, etc.). Do *not* try to import any fields destined for the Collection, Locality, Genus, Family, or higher taxon tables at this point.

Be sure to consult the open “Specimen_Master” file in Excel (or your written or printed list) for the order of fields in your “Specimen_Import” text file, and match it exactly in the “Text File Fields” panel of the Import Editor, using the “Skip” button if necessary. If you need help setting up the Import Editor, see [“Import Step 3: Set Up and Launch the Import, Update, or Merge”](#) earlier in this chapter.



If you have a row of column headings in the “Taxon_Import” text file, be sure to check the “Column Headings” checkbox.

18. Click the “Import” button in the Import Editor to launch the import.



19. Find and open the “Specimen_Import” text file.

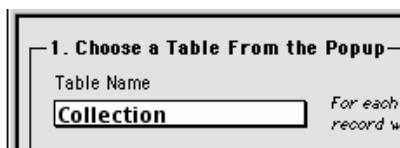
If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.

When the import is complete, it is time to import records to the Collection table.

20. Again, choose “Import by Tables and Fields” from the Im/Export menu.

21. This time, choose the “Merge imported records” option.

22. In the Import Editor, choose “Collection” from the “Table Name” popup.



23. Set up the Import Editor in Biota to import Collection Code, Locality Code (the linking field to the Family table), CollectedBy, DateCollected, and any other Collection table fields (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) that you want to import from your text file (e.g., Method, Site, Source, etc.).

24. Click the “Import” button in the Import Editor to launch the import. If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.



25. Find and open the “Specimen_Import” text file.

If you get error comments, consult “[Displays and Error Messages During Record Importing or Updating](#)” for troubleshooting help.

When the import is complete, it is time to import records to the Locality table.

Note: Why use the “Merge imported records” option? Because there are many repeated values for Collection Code in the “Specimen_Import” table in the example (and probably in your own taxonomic flatfile). If you used the “Import new records” option instead, you would get a Duplicate Key Error for every subsequent copy of a Collection Code, after the first copy is imported. (See “[Duplicate Key Error: Importing New Records](#)” earlier in this chapter.) In contrast, in the case of the Specimen records earlier, each record must have a unique Key (Specimen Code), and you would want to know if any were *not* unique.

26. Repeat the process detailed in [Steps 20 through 25 for the Locality, Species, Genus, and any additional taxonomic ranks](#) in the “Specimen_Import” text file.

- **For the Locality table,** in the example we have been following, you import the Locality Name/Code column into both the [Locality]LocalityCode field and into the [Locality]LocalityName field. Also import District, State/Province, Country, Latitude, and Longitude.
- **For the Species table,** import Species Code, Genus (the linking field to the Genus table), Specific Name, and any other Species fields (see Appendix A, “[Biota Tables, Fields, and Relational Links](#)”) that you want to import from your

- “Taxon_Import” text file (e.g., SpeciesAuthor, SubSpecies, CommonNames, etc.).
- **For the Genus table and any higher taxon rank tables**, follow the instructions in [Steps 12 through 18](#) of the previous section in this chapter, “[Step by Step: Importing Hierarchically Linked Records from an Existing Taxonomic Flatfile](#).”

Merging Two Biota Data Files or Moving All Records to a New Data File

Once in a while, you may need to merge all or part of the contents of one Biota Data File with another. You and a colleague or an assistant might work separately for a while, then merge records into a single Data File. Or you might decide to combine two Data Files of your own.

Or, as a last resort when a Data File is damaged and cannot be repaired with 4D Tools (see Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#)”) you might need to rescue all the data you can from the damaged file and import it into an empty, new one.

For full instructions on these operations, see Appendix G, “[Merging Two Biota Data Files](#).”

PART

8

Biota and the Internet

Chapter 29 Internet Strategies

Biota offers four distinct strategies for providing public or private access to your Biota Data Files over the Internet or a local network. All four offer access to images as well as text data. You can use the four modes in any combination, or simultaneously, to provide access to the same Data File. Each has its strengths and weaknesses, and they vary in cost.

The first two strategies rely on Biota's completely self-contained, onboard Web server (The Web server is an integrated component of Biota 2 but requires the purchase of a license to enable unlimited use. See "[Relative Costs of Internet Strategies](#)," below in this chapter.) With either of these two options, a remote user can access your Biota Data File directly and dynamically, using any Internet browser (such as Netscape or Microsoft Internet Explorer).

As Biota administrator, you have full control over who has Internet access to your Biota Data File, using Biota's Password System (see "[Security and Passwords with the Web Server](#)" in Chapter 30, and Chapter 26, "[Security: Passwords and Access Privileges](#)").

- **Onboard Web server in Web Browser Mode.** In this mode, Biota creates and serves Web pages dynamically in response to queries and links activated by the remote user. The user's Internet browser operates according to classic rules, including use of the browser's "Back" and "Forward" buttons. As Biota administrator, you have substantial control over which tables and fields are accessible to remote users, but only fairly simple queries, based on one table at a time, are supported. See Chapter 30, "[Biota's Onboard Web Server](#)" and Chapter 31, "[Web Browser Mode and the Web Assistant](#)."
- **Onboard Web server in Database Client Mode.** In this mode, Biota serves Web pages dynamically, but the user's Internet browser operates as a database client, maintaining "private" contact with the Biota Web server. This mode allows the user to take advantage of many of the same powerful query and browsing tools that Biota offers in desktop mode, including Taxa for Places and Places for Taxa. Necessarily, web site visitors must navigate strictly by using on-screen buttons; the Internet browser "Back" and "Forward" buttons cannot be used. See Chapter 30, "[Biota's Onboard Web Server](#)," and Chapter 32, "[Database Client Mode](#)."
- **Exported Web pages, posted on an external Web server.** In this mode, you export Web pages to static HTML files, using Biota's Export Web Pages tool, then post the pages on an external Web server. This may be your only option if your

institution has strict firewall rules. Your institution or Internet Service Provider can probably help you to create and maintain a Web site to post the Biota pages. With this approach, you have full control over which taxa and fields are included on the exported pages, which are organized by the taxonomic hierarchy. See Chapter 33, “[Exporting Static Web Pages](#).”

- **4D Server/Client.** If you use Biota4D under 4D Server to manage your Biota Data File, you can allow access to the Data File using 4D Client from anywhere on the Internet. See Appendix H, “[Using Biota4D with 4D Server or 4th Dimension](#).”

Relative Costs of Internet Strategies

NOTE: Information in this section is current as of January, 2004.

- **If you have access to a Web server,** the least expensive option is to post exported, static Web pages. Biota does not require a 4D Web Extension License to export static Web pages. See Chapter 33, “[Exporting Static Web Pages](#).”
- **Biota's Onboard Web server** runs for one hour (with unlimited connections) each time you launch Biota. To enable the Onboard Web server for unlimited (non-stop) service, you must buy a 4D "Web Extension License" from Sinauer Associates and install it on your computer.
 - ◊ **To place an order with Sinauer**, go to the [Biota Page at the Sinauer Website](#) (www.sinauer.com), telephone (413) 549-4300 (USA), or send a fax to (413) 549-1118 (USA).
 - ◊ **For 4D Web Extension License installation instructions**, see the section “[Installing a 4D Web Extension License](#)” in Chapter 30. If you move Biota to another computer, you can install the same number again.
- **Using Biota4D with 4D Server/4D Client** to provide access to your Biota Data File over the Internet is the most expensive option, but if you are using 4D Server anyway, there is no additional cost. It is not a practical way to provide access to more than a handful of collaborators, however, because 4D Server license fees (and Biota4D license fees) are based on the number of “seats” (simultaneous connections). The basic 4D Server license has 2 seats. Additional seat cost extra. For details on 4D Server, see Appendix H, “[Using Biota4D with 4D Server or 4th Dimension](#).”

Chapter 30

Biota's Onboard Web Server

Biota is based on the 4th Dimension (4D) application development environment. BiotaApp is driven internally by 4D Engine, and Biota4D runs under 4D Server. Both 4D Engine and 4D Server incorporate a fully integrated Web server, which Biota has been programmed to use. That means every copy of Biota is ready to use for publishing your data on the Internet or to give Internet access to selected colleagues through password authentication.

The only catch is that 4D, Inc. legally requires you to install a separate “Web Extension” license for 4D Engine (in BiotaApp) or 4D Server to enable the onboard Web server to run uninterrupted. However, you can use the Web server without the license, one hour at a time, to explore the options and help you decide whether to purchase a license. When the Web server times out, just restart Biota. See “[Relative Costs of Internet Strategies](#),” in Chapter 29, for details on license purchase, and “[Installing a 4D Web Extension License](#)” (below in this chapter) for instructions on installing it.

Web Server: Quick Start

Biota's onboard Web server is set up for generic use right after you install Biota. To see what it can do, here is a quick start procedure.

1. **Launch Biota** with your own Data File or with the BiotaDemo Data File that is installed with Biota.
2. **From the Special menu, choose Web Server.**
3. **Click the “Enable Web Assistant” box** on the Start/Stop tab.
4. **Click the “Start the Web Server” button.**
5. **Launch any Web browser** on another networked computer.
6. **Enter the Internet address of your Biota computer** (or its IP address). The generic Biota Gateway Home Page should appear. If it does not, work through the setup procedure in the next section, “[Web Server Settings and Controls](#).”
7. **Follow your inclinations.**

NOTE TO MAC OS X USERS: You need to re-set Biota's Web server port number. See “The Server Settings Tab” later in this chapter.

Web Server Settings and Controls

You display the Web Server Settings tools by choosing **Web Server** from the **Special** menu. All controls and settings for Biota's onboard Web server are accessible in this tabbed screen. Web settings are saved in your Biota Data File and in special settings files between Biota sessions, so you need not reset them between launches of Biota unless you want to change something.

The Start/Stop Tab



The first tab is devoted to the Start/Stop toggle for the Web server, a check box for enabling the Web Assistant (see Chapter 31, “[Web Browser Mode and the Web Assistant](#)”), and an option to start the Web server automatically when Biota is launched. Wait to start the Web server until you have verified the settings on the remaining tabs. You can change settings on the other tabs while the server is running, but not all options are implemented until you stop and restart the Web server.

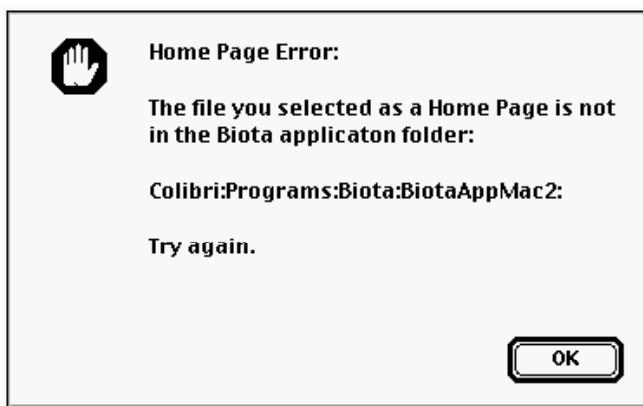
The Home Page Tab



You use the “Locate New Home Page” button on this tab to designate the static, HTML web page that serves as the Gateway Home Page for your Biota Web site. (In Web Browser Mode, Biota also generates a dynamic home page that lists the database tables available for search. See Chapter 31, “[Web Browser Mode and the Web Assistant](#).“)

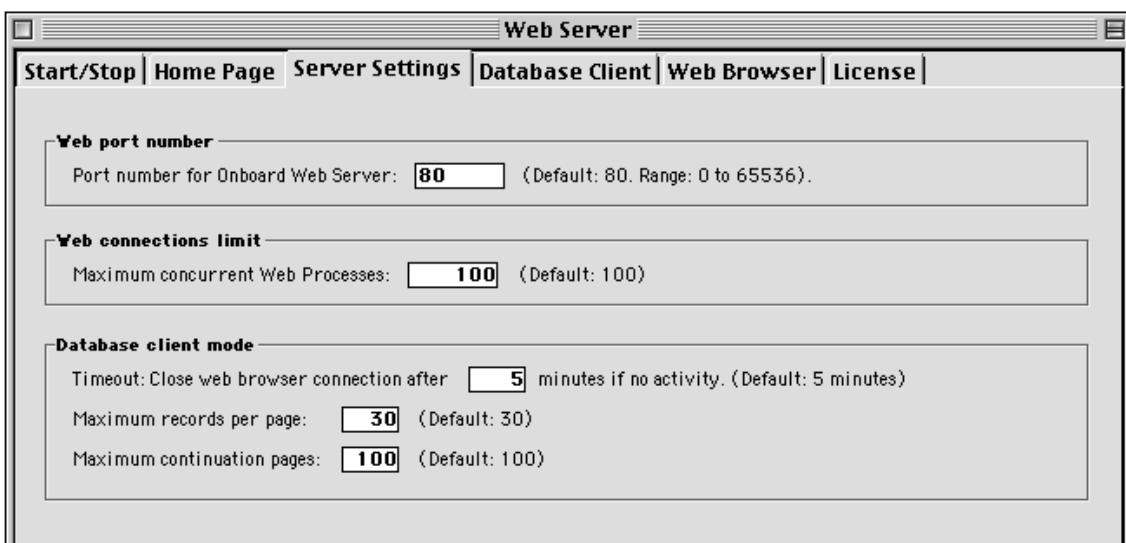
The Gateway Home Page must be an HTML document located in the same folder as the Biota application. When you first install Biota, the prototype home page “BiotaHomepage.html” is designated as the assigned Gateway Home Page. Biota saves the Gateway Home Page name indefinitely, so you need not use this tab unless you want to designate a different Gateway Home Page. Here’s how to make a change:

1. Click the “Locate New Home Page” button. A file navigation window appears.
2. Find and select the Gateway Home Page for your Biota Web site. The new Gateway Home Page must be an HTML document located inside the same folder as the Biota application.
3. Click the “OK” button in the file navigation window to select the Gateway Home Page. If you made a mistake and selected a file that is not located in the Biota application folder, this error message appears:



NOTE: You can name a Gateway Home Page anything you like, or have several different versions and switch among them using the button on the Home Page tab.

The Server Settings Tab



You use the settings on this tab to control how the Web server functions.

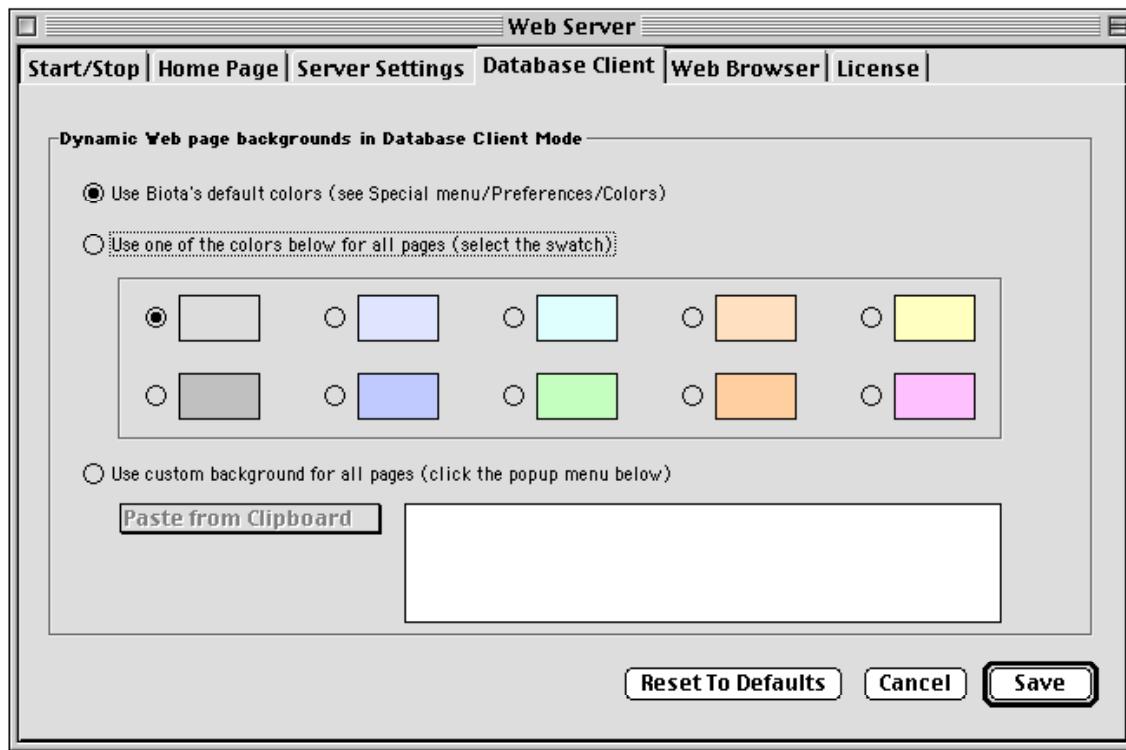
- **Web port number.** The default port that Web browsers look for is Port 80.
 - ◊ **Windows and Mac OS 9.** Unless you have another Web server using Port 80 on the computer you are using for Biota, leave the port number set to 80. If you need to use a different port, use a number above 2000 to avoid any possible conflicts. See the Note below.
 - ◊ **Mac OS X.** Under MacOS X, using TCP/IP Ports 0 through 1023 (including Port 80) for Web publishing requires specific access privileges: only the “Root” user of the machine can launch an application using these ports. If you try to launch Biota’s Web server on Port 80, you get an error message stating that “The Database cannot be published.” The easiest solution is to set Biota’s onboard Web server port to a number greater than 1023 (Port 2000 or Port 8080, for example.)

By default, the Root user is not enabled on a machine running MacOS X. If you prefer to use Port 80 under Mac OS X, you must first enable the Root user and then log in with this user name. You can enable the Root user by means of the NetInfo Manager utility (in the OS X Applications:Utilities folder). Once the utility has been launched, select the Security command in the Domain menu, choose Authenticate, then Root User, and follow the instructions. Close the NetInfo Manager and log in using the Root user name. You can then launch the Web server on port number 80. See the Mac OS X documentation if necessary.

NOTE: If you use a port number *other* than 80, visitors to your site must append the port number to the URL for your site, separated by a colon. For example, if your Web site address is "www.myhost.edu/mysite," and you are using port number 2000 for Biota, visitors must use the URL "www.myhost.edu/mysite:2000."

- **Maximum connections limit.** Each time a visitor clicks a link or a button on a static Web page (the home page or another file-based page) or on a page dynamically generated by Biota in Web Browser Mode (see Chapter 31, “[Web Browser Mode and the Web Assistant](#)”), a new “Web process” is initiated by the Web server. A single Web process is used by each connection in Database Client Mode (see Chapter 32, “[Database Client Mode](#)”). To control the load on the Web server, you can set a maximum number for concurrent Web processes.
- **Database Client Mode settings.**
 - ◊ **Timeout:** Each time a visitor initiates a connection in Database Client Mode (see Chapter 32, “[Database Client Mode](#)”), the connection is maintained until the user fails to click any further links or buttons for the period specified.
 - ◊ **Maximum records per page:** This setting limits the length of Web pages dynamically generated by the Web server for record listing pages in Database Client Mode.
 - ◊ **Maximum continuation pages:** In Database Client Mode, if there are more records in a selection than the maximum specified in the previous setting, Biota’s Web server posts links to continuation pages at the bottom of each page. This setting limits the number of links generated. If a record that a user is seeking is on a page beyond the number of links displayed, the user is forced to constrain the query to produce a smaller selection.

The Database Client Tab

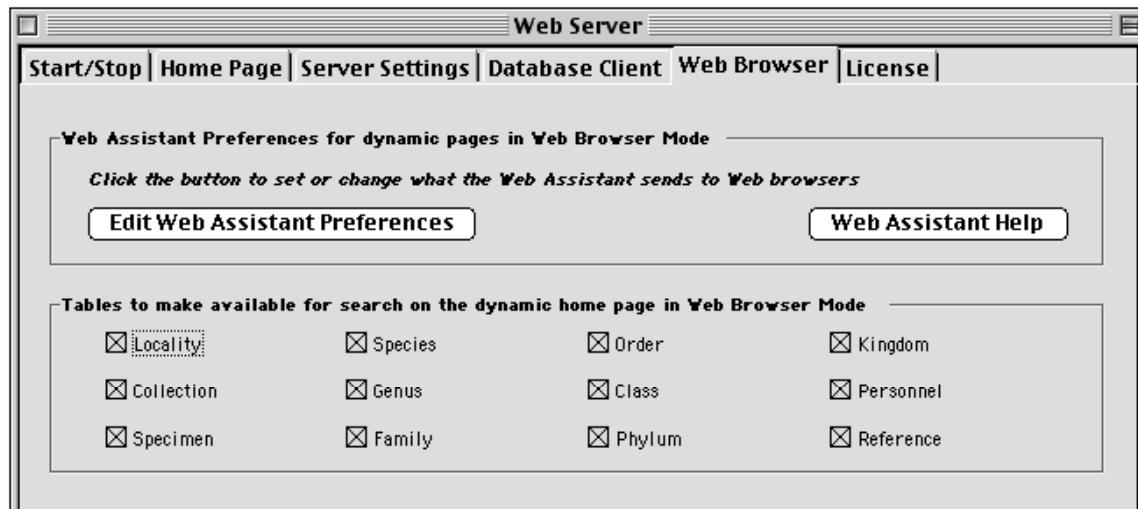


The settings on this tab control the Web page background used in Database Client Mode.

- **Use Biota's default colors.** With this option, the Web page background in Database Client Mode depends on which table the record or records belong to, just as in Biota's desktop mode. The same default colors are used. (Changing the table color scheme in the Colors tab of the Preferences screen in the Special menu does not affect the default colors for Web pages.)
- **Use one of the colors below for all pages.** If you choose this option, you can then select one of the color swatches from the Biota default color scheme as the single color used for all Web pages in Database Client Mode, regardless of the table they represent.
- **Use custom background for all pages.** If you select this option, you can use a background of your own design for all pages in Database Client Mode. The popup menu offers two ways to enter your custom background swatch:
 - ◊ **Paste from Clipboard:** Copy the custom swatch to the Clipboard of your operating system, then select this item from the popup.
 - ◊ **Import from File:** Selecting this option displays a file navigation window. Find the image file you want to use for a custom page background and select it.

The Web Browser Tab

The Web Browser tab includes two panels with tools to control the Web server output in Web Browser Mode. The Web Assistant is an off-the-shelf 4D component that controls and produces dynamically generated Web pages in Web Browser Mode. In the upper panel, the “Edit Web Assistant Preferences” button displays a series of option screens.



In the lower panel, you can choose which Biota tables to make available for Web site visitors who wish to search the Data File in Web Browser Mode. For details, see Chapter 31, [“Web Browser Mode and the Web Assistant.”](#)

The License Tab



The “Check or Add License” button on this tab allows you to check whether a 4D Web Extension License has been installed on your computer. See the next section, [“Installing a 4D Web Extension License,”](#) later in this chapter, for details.

Installing a 4D Web Extension License

Biota's onboard Web server runs for one hour (with unlimited connections) each time you launch Biota. To enable the onboard Web server for unlimited (non-stop) service, you must buy a 4D Web Extension License and install it on your computer (see “[Relative Costs of Internet Strategies](#),” in Chapter 29).

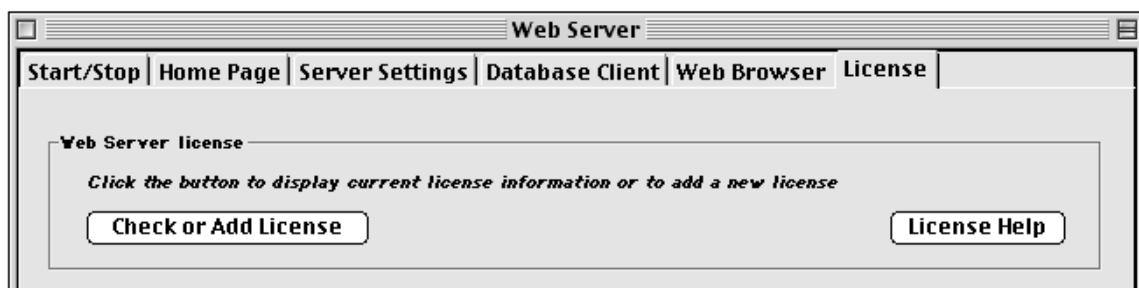
The license is not installed in Biota itself, but in a special, encrypted file inside the operating system folder of your computer. In Windows, the file is in the 4D folder within the Windows or WINNT folder. In Mac OS 9, the file is in the 4D folder within the MacintoshHD: System Folder: Application Support folder. In Mac OS X, the file is in the 4D folder within the MacintoshHD: Library: Application Support folder.

If you install a newer version of Biota, the license will continue to work, since it remains on your computer. If you move Biota to another computer, you can install the same license number again or move the 4D folder to the other computer.

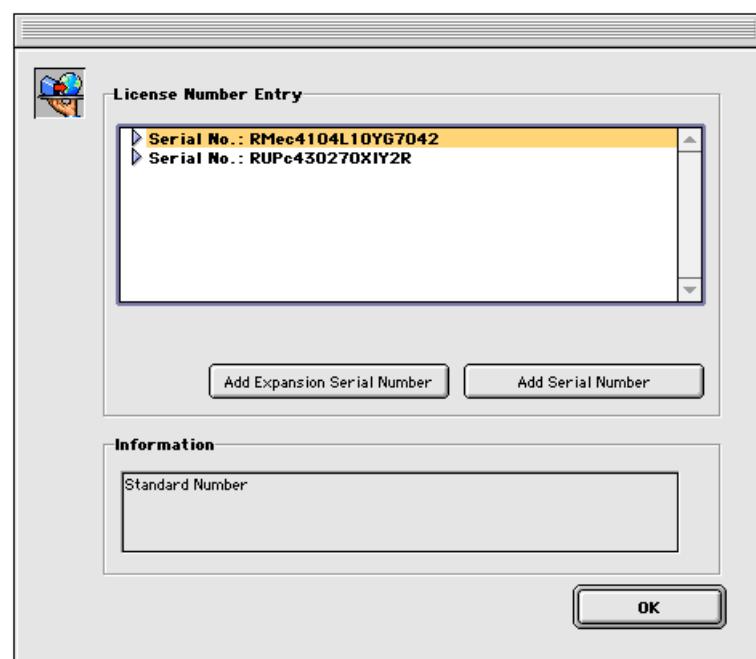
Once you have the license number for a 4D Web Extension, the method you must use to install it depends on whether you want to install the license in Biota4D (the client/server version) or in BiotaApp (the standalone version).

Installing a 4D Web Extension License for Biota4D

1. Choose Web Server from the Special menu, then click the License tab.



2. Click the “Check or Add License” button on the License tab. The License Number Entry window appears.
3. Click the triangle beside each entry in the list of serial numbers to find out what the license is for. If you have a Web Extension License installed, the detail line will read “Web.”



- To install a Web Extension License serial number for Biota4D, click the “Add Serial Number” button and enter the serial number, being careful to copy upper and lowercase letters precisely. (Note: The numbers below are fictitious.)

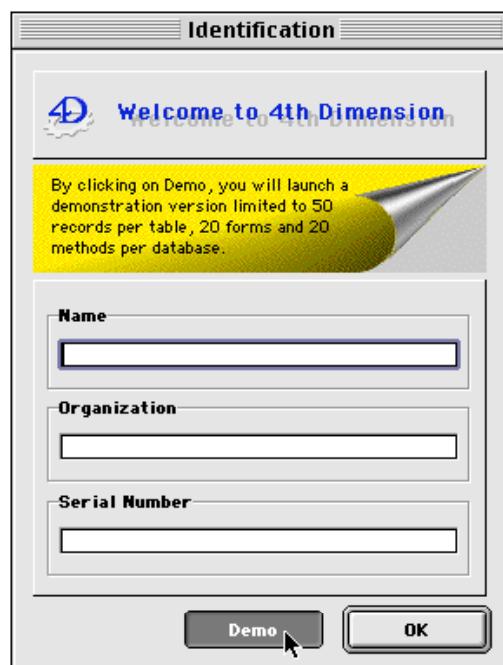


Installing a 4D Web Extension License for BiotaApp

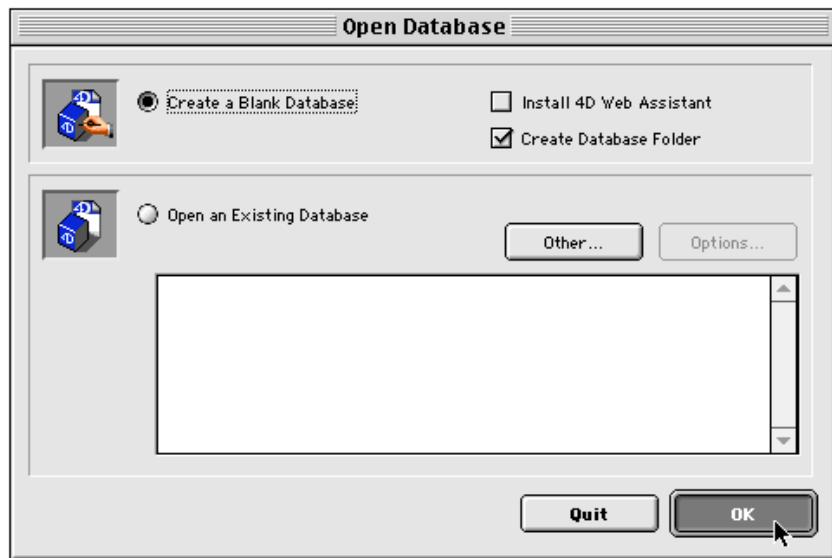
- To install a Web Extension License serial number for BiotaApp, you will need a copy of 4th Dimension. A free Demo version will do; there is no need to purchase a copy. A demo version is included on the Biota CD for this purpose.

NOTE: If you have 4D Server, you can use that instead, following the instructions in the previous section, even if you intend to use the Web server under BiotaApp.)

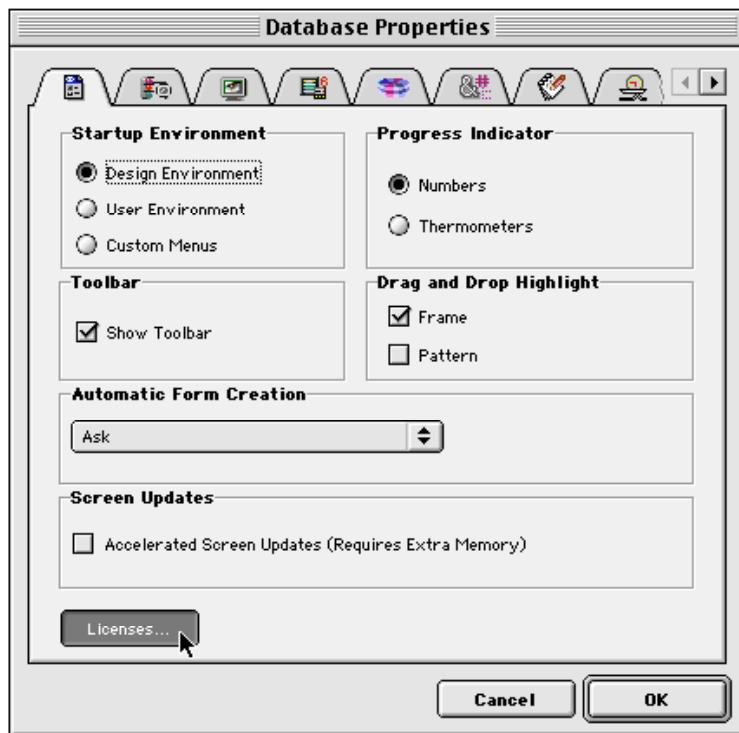
- Launch 4th Dimension in Demo mode. There is no need to fill in any of the fields.



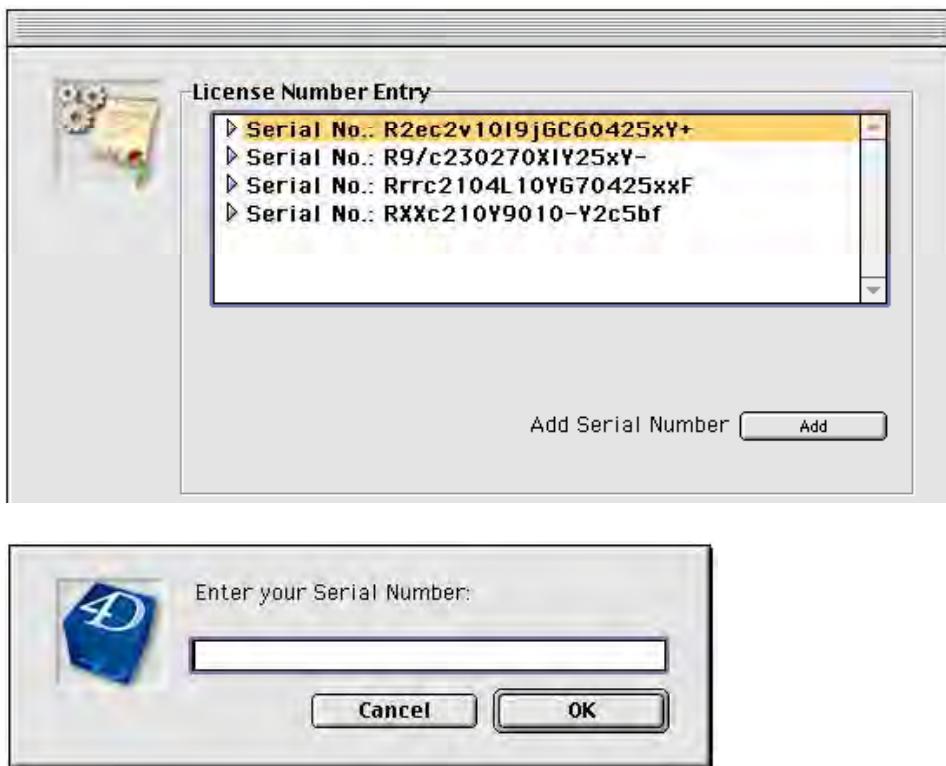
3. Use the default settings to Create a Blank Database. Click the “OK” button.



4. When the launch of 4th Dimension is complete, select Database Properties from the File menu. The Database Properties window appears.
5. Click the “Licenses” button at the bottom of the first tab of the Database Properties window. The Serial Number window appears, with an “Add Serial Numbers” button.



- Click the “Add Serial Numbers” button and enter the serial number in the request panel, being careful to copy upper and lowercase letters precisely. (Note: The numbers below are fictitious.)



- Close 4th Dimension.** You may delete or uninstall the program from your computer if you like.
- Launch BiotaApp**, then follow Steps 1 through 3 in “[Installing a 4D Web Extension License in Biota4D](#)” earlier in this chapter to verify that the license was installed.

Security and Passwords with the Web Server

Biota's onboard Web server gives others access to your Data File over the Web or a local network. Regardless of how well you set up security options in Biota or how trusted your visitors may be, Web-server-based access presents greater security concerns than desktop access to your Data File.

The next section explains how to limit Web access to your Data File using Biota's Password System. Here are some general suggestions.

- **Make regular backups** of your Data File (see “[Backup Strategies for Data Files](#)” in Appendix I).
- **Unless you must provide up-to-the-minute information**, consider posting a *copy* of your Data File for Web access running under BiotaApp, restricting access to your working copy of the Data File either to single-user access with a second copy of BiotaApp or to client/server access using Biota4D.

- If your institution maintains a security firewall and you need to give access to your Biota Data File over the Web, work with your IT Manager to develop a strategy for placing the Data File, running under a copy of Biota, outside the firewall.

Using Biota's Password System to Control Web Access

NOTES:

- a. At present, Biota's onboard Web server supports read-only access to Biota Data Files, regardless of settings in the Password system. (Read/write access may be added in a later version if there is sufficient demand for it.)
 - b. If you are unfamiliar with Biota's user password system, please review Chapter 26, “[Security: Passwords and Access Privileges](#),” before reading this section.
-

When you first launch a new copy of Biota, the user password system is inactive. Whoever signs on does so as Administrator. The Administrator has full, read-write access to all features and settings, with Super User privileges—including the privilege to enable or disable the user password system.

To enable the user password system, the Administrator enters and confirms a non-blank password using the Change Password item in the Special menu. (The user name “Administrator” can be changed to whatever you like using the Edit User Password System item in the Special menu. Here, “Administrator” refers to whichever user has been assigned Super User privileges. See “[Using the Password Editor](#)” in Chapter 26.)

- If you launch Biota's Web server **without activating** the user password system:
 - ◊ In Web Browser Mode (see Chapter 31, “[Web Browser Mode and the Web Assistant](#)”), Web visitors require no password to enter. They are automatically assigned “Guest” access privileges, as defined in the Web Assistant settings (see “[Setting Tables and Fields Preferences](#)” in Chapter 31). Guest access allows Read Only viewing of records, assuming you heed the Warning in Chapter 31, repeated below.

WARNING: Do **not** set tables to any mode but “r,” Read Only access, in the Web Assistant settings. Biota input screens include many error-checking procedures and warnings that are crucial to maintaining database integrity. The Web Assistant ignores all such procedures.

- ◊ In Database Client Mode (see Chapter 32, “[Database Client Mode](#)”) Web visitors require no password to enter. They are automatically assigned Read Only status, as defined in the section “[Users, User Names, and Access Privilege Levels](#)” in Chapter 26.
- If you launch Biota's Web server **after activating** the user password system:
 - ◊ In Web Browser Mode, Web visitors are presented with a standard Web browser request to enter a user name and password. Access is granted when the response matches any user name/password combination in the Biota Password system. (You can set up a special, “public” user name/password combination if you like, with “Browser” access privileges.) All visitors are automatically assigned “Guest” access privileges, as defined in the Web Assistant settings (see “[Setting Tables and Fields Preferences](#)” in Chapter 31). Guest access allows Read Only

viewing of records, assuming you heed the Warning in Chapter 31, repeated above.

- ◊ **In Database Client Mode,** Web visitors are presented with a standard Web browser request to enter a user name and password. Access is granted when the response matches any user name/password combination in the Biota Password system. (You can set up a special, “public” user name/password combination if you like, with “Browser” access privileges.)

Note: HTML does not offer any visual way to indicate that a button has been disabled. For this reason, Biota hides all disabled buttons in Database Client mode. All buttons that appear onscreen to the web visitor are active.

Chapter 31

Web Browser Mode and the Web Assistant

In Web Browser Mode, Biota uses 4D's Web Assistant (a built-in component of Biota) to generate standard HTML Web pages "on the fly" from your Biota Data File, based on queries from site visitors. Each user request to Biota's onboard Web server initiates an entirely new search and page generation, with no connection or relationship between successive requests from the same user, even if only moments apart. This "stateless" or "non-contextual" strategy is the classic way that Web servers work, allowing full use of the "Back" and "Forward" buttons in the Web browser window.

The alternative approach, used in Biota's Database Client Mode (see Chapter 32, "[Database Client Mode](#)"), maintains "state" or "context" on the server for each user between requests as long as the timeout period (see "[The Server Settings Tab](#)" in Chapter 30) has not elapsed. A familiar example of this "contextual" strategy on commercial Web sites is the "shopping basket" metaphor. Like most commercial sites that need to maintain context, Biota's Database Client Mode requires the visitor to use onscreen buttons, instead of the browser's navigation buttons.

Web Assistant Settings Files

In Biota's Web Browser Mode, you have full design control over which tables and fields are available to the site visitor for the construction of queries. You can also control many of the details of page appearance. The tools that control these options constitute 4D's Web Assistant, plus settings on the Web Browser Mode tab of the Web Server screen in Biota's Special menu (see "[The Web Browser Tab](#)" in Chapter 30).

How and Where Web Assistant Settings Are Saved

It is crucial to understand that the design choices you make using the Web Assistant are *not* stored in either Biota or in your Biota Data File. Instead, they are saved in special files within the "4D" folder in the operating system area of your hard drive.

Suppose you are using **BiotaAppWin2** (Windows) or **BiotaAppMac2** (Mac OS). Then the Web Assistant settings files (indicated as "[Web Assistant files]" below) are saved in a folder of the same name, placed as follows:

- **Windows.**

<root>\Windows\4D\4DWebAssistant\BiotaAppWin2\[Web Assistant files]

- **Windows NT.**

<root>\WINNT\4D\4DWebAssistant\BiotaAppWin2\[Web Assistant files]

- **Mac OS 9.**

MacintoshHD: System Folder: Application Support: 4D: 4DWebAssistant:
BiotaAppMac2: [Web assistant files]

- **Mac OS X.**

MacintoshHD: Library: Application Support: 4D: 4DWebAssistant: **BiotaAppMac2:** [Web assistant files]

In other words, the name of the folder that contains the Web Assistant settings files is the same as the *exact* name of the version of Biota that you are using, including any version designation that is part of the file name. (Windows file extensions do not form part of the folder name.)

NOTE: When you install Biota from the CD or from a download, a folder matching the name of the Biota version is automatically installed in the proper location. This prototype Web Assistant settings folder contains a special group of default settings, designed for general use with Biota. It is best to start with this group of settings in customizing the Web Assistant settings for your own needs. Make a copy of the prototype folder and its contents prior to beginning the customization so you can undo changes if you don't like the results.

Changing the Name of the Biota Application or Installing a New Version

If you change the name of the Biota application you are using or install a new version of Biota with a different version designation as part of its name, *you must change the name of the folder containing your Web Assistant settings to match these changes.*

Otherwise, the Web Assistant creates a new settings folder, containing Web Assistant default settings, to match the name of the new Biota application.

If you forget to change the folder name before launching the new version of Biota, you can simply delete the new folder that Web Assistant creates and rename the old one, which is not changed or deleted.

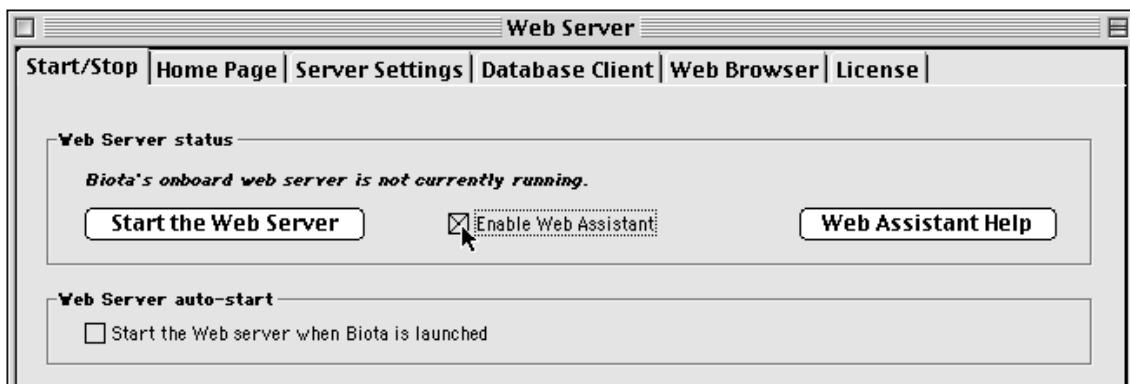
Enabling and Launching the Web Assistant and Web Browser Mode

Biota's onboard Web server can operate either with or without the Web Assistant enabled. If the Web Assistant is not enabled, the server supports only Database Client Mode (See Chapter 32, “[Database Client Mode](#)”), and Web Browser Mode cannot be launched from the Gateway Home Page described below (see “[Launching Web Browser Mode from a Gateway Home Page](#)” later in this chapter).

Enabling the Web Assistant and Web Browser Mode

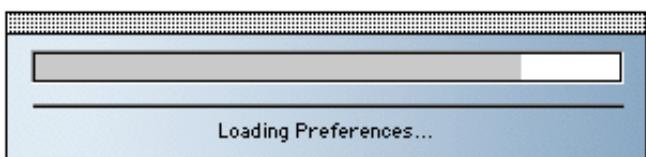
NOTE: Before launching the Web server, you should first verify that it has been properly set up. See “[Web Server Settings and Controls](#)” in Chapter 30.

To enable the Web Assistant and Web Browser Mode, check the “Enable Web Assistant” checkbox in the Start/Stop tab of the Web Server screen (from the Special menu), then click the “Start the Web Server” button.



If the Web server is already running when you check the “Enable Web Assistant” checkbox, Biota informs you that you must stop and restart the Web server before the change will take effect.

With the Web Assistant enabled, each time you launch Biota and start the Web server manually or launch Biota with the Web server set to start up automatically (by checking the box in the Web Server auto-start panel of the Start/Stop tab), the Web Assistant settings are loaded from special files in the operating system folder (see “[How and Where Web Assistant Settings Are Saved](#),” earlier in this chapter). A progress indicator appears.



If you later stop and restart the Web server without quitting Biota, settings remain in memory and are not reloaded.

Launching Web Browser Mode from a Gateway Home Page

When you install Biota from the CD or a downloaded installer, two prototype static Web (HTML) pages are installed in the same folder as the Biota application.

- **BiotaHomePage.html**
- **BiotaDatabaseClient.html**

A folder called WebImages is also installed, containing the background swatch (BiotaHomePageBackground.jpg) used for the two prototype Web pages.

Here is the full, default arrangement of folders and files:

```
[Biota Folder]
  [Biota Application Files]
    BiotaDatabaseClient.html
    BiotaHomePage.html
  WebImages [folder]
    BiotaHomePageBackground.jpg
```

The Web page file BiotaHomePage.html is intended as a Gateway Home Page to a Biota-based site that offers both Web Browser Mode and Database Client Mode to Web visitors.



- **The “Web Browser” link** initiates Web Browser Mode on the Biota server and displays the Web Browser home page, which is dynamically generated by Biota. The URL for this link is **/4DCGI/wbaHandleURL/HomePage**. For details, see “[Customizing the Gateway Home Page For Web Browser Mode](#),” below.
- **The “Database Client” link** displays the static HTML page BiotaDatabaseClient.html, which is used exclusively in Database Client Mode. The URL for this link is **/4DMethod/WebDatabaseClient**. See Chapter 32, “[Database Client Mode](#).”

NOTE: To launch Web Browser Mode from a static Web page, the URL for the link must read, precisely: **/4DCGI/wbaHandleURL/HomePage**

Customizing the Gateway Home Page for Web Browser Mode

On your Web site, Web Browser Mode must be launched from a static Web page, such as the prototype Gateway Home Page (BiotaHomePage.html) described above (see “[Launching Web Browser Mode from a Gateway Home Page](#),” earlier in this chapter).

- **Either: Design your own Gateway Home Page** for Web Browser Mode, incorporating the URL “hook” for Web Browser Mode (**/4DCGI/wbaHandleURL/HomePage**). You can use any Web-authoring application to create the page.
- **Or: Modify the prototype Gateway Home Page** (BiotaHomePage.html) to suit your needs. For a start, you will want to change the header to read something besides “Your Database Name Here,” which you can do in your Web-authoring application. (For instructions on how to change the title displayed on *dynamically* generated pages in Web Browser Mode, see “[Using the Web Assistant HTML Editor](#),” later in this chapter.)

The prototype Gateway Home Page uses graphic design elements (header, colors) from the dynamically generated Web browser pages that are produced by Biota based on the prototype Web Assistant settings. These design elements can be copied to other static pages if you wish, or you can design and implement your own header and footer elements.

If you want to use the prototype Gateway Home Page but prefer a different background, you have two options. You can prepare a new background swatch in jpeg format, name it BiotaHomePageBackground.jpg, and substitute it for the file of the same name that is installed with Biota; or you can use your Web-authoring application to apply a different background.

NOTES:

- a. To learn how to change the page title on dynamically generated pages in Web Browser Mode, see “[Using the Web Assistant HTML Editor](#),” later in this chapter.
 - b. To learn how to customize the page background used for dynamically generated pages in Web Browser Mode, see “[Using the Web Assistant HTML Editor](#),” later in this chapter.
 - c. To learn how to customize the page background for dynamically generated pages in Database Client Mode, see “[The Database Client Tab](#),” in Chapter 30.
-

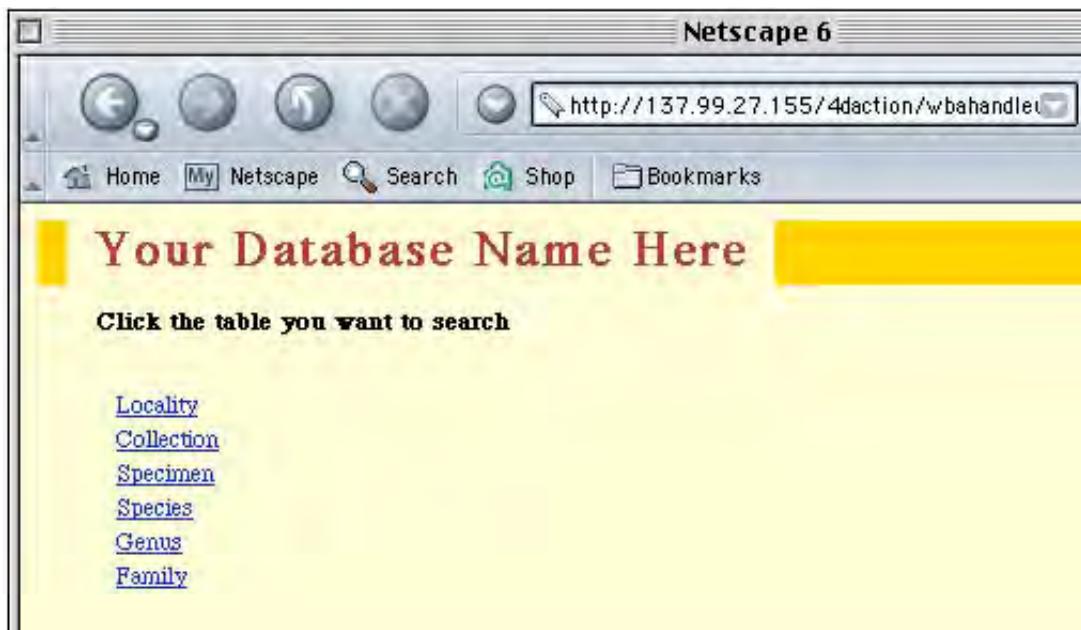
Customizing Dynamic Pages for Web Browser Mode

You can customize the Web pages that Biota creates in Web Browser Mode using the settings and tools on the Web Browser tab of the Web Server screen (Special menu).

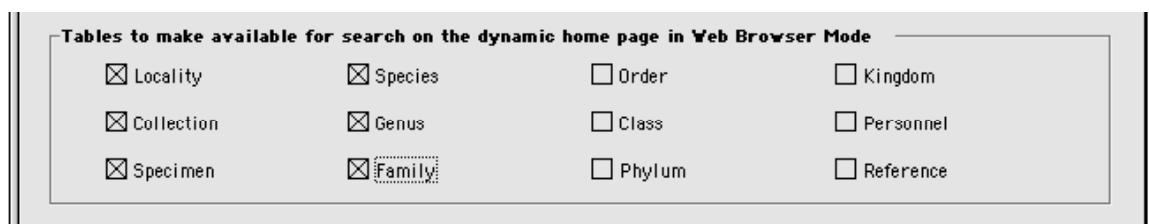


Setting the List of Tables Available for Search

When a Web visitor clicks the link in a Gateway Home Page that launches Web Browser Mode (see “[Launching Web Browser Mode from a Gateway Home Page](#),” earlier in this chapter), a dynamically-generated Web Browser home page appears, listing the Biota tables you have chosen to make available for user searches.



In the Web page shown above, six tables have been made available by checking the corresponding boxes in the lower panel of the Web Browser tab of the Web Server screen (Special menu), as illustrated below.



You can choose to make available any or all of the 12 Core Tables listed in the panel. As described in detail below (see “[Setting Tables and Fields Preferences](#)”), text data and images in Peripheral Tables linked to these Core Tables may also be made available in Web Browser Mode, but only through searches based on the Core Tables you enable in the panel illustrated above. (See Chapter 3, “[Key Concepts](#)” for the distinction between Core and Peripheral Tables.)

Web Assistant Settings

WARNING: Before working with Web Assistant preferences, be certain that the name of the copy of Biota you are using matches the name of the Web Assistant settings folder you intend to use. For help, see “[Web Assistant Settings Files](#),” earlier in this chapter.

NOTE: When you install Biota from the CD or from a download, a prototype Web Assistant settings folder matching the name of the Biota version is automatically installed in the proper location. The prototype folder contains a special group of default settings, designed for general use with Biota. It is best to start with this group of settings in customizing the Web Assistant settings for your own needs. Make a copy of the prototype folder and its contents prior to beginning the customization so you can undo changes if you don’t like the results.

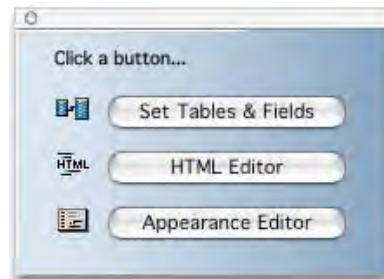
To access the **Web Assistant settings**, choose Web Server from the Special menu, go to the Web Browser tab, and click the “Edit Web Assistant Preferences” button.



The Web Assistant tool palette appears. (If the Web Assistant settings have not already been loaded, they will load first.)

The Web Assistant tool palette has three buttons:

- **The “Set Tables and Fields” button** displays a settings screen controlling which Biota tables and fields are made accessible to Web visitors in Web Browser Mode.
- **The “HTML Editor” button** displays an editor for customizing Web page header and footer information for HTML pages generated in Web Browser Mode.
- **The “Appearance Editor” button** displays a screen that allows you to customize the appearance of pages in Web Browser Mode.



Setting Tables and Fields Preferences

- Click the “Set Tables & Fields” button in the Web Assistant palette. The Set Tables and Fields setup window appears. (Be patient! It may take a few seconds to load).



- In the “Section to Update” panel, select “User Access.”

In the “User Access” panel:

- The “Users” list on the left shows all Biota users with password access. (See Chapter 26, “[Security: Passwords and Access Privileges](#).”) If you have enabled Biota’s password system, you can create different settings for each user, if you wish. If you have not enabled the password system, only the Guest user settings are relevant; site visitors are assigned Guest access by default.
- The Tables list in the middle displays every visible table in Biota’s structure. See Chapter 3, “[Key Concepts](#),” and Appendix A, “[Biota Tables, Fields, and Relational Links](#)” for more information on tables and their relations to one another.
- The “Tables Available to Use” list on the right displays the tables for which information will be available to the selected user. The illustration above shows only the tables available to Guest visitors, as set up in the prototype Web Assistant settings files that are installed with Biota. See “[Web Assistant Settings Files](#),” earlier in this chapter.

NOTE: You set the Core Tables available for search (for all users) in the Web Browser tab of the Web Server screen (Special menu), as explained in the section, “[Setting the List of Tables Available for Search](#),” earlier in this chapter. Each table made available for search *must also* be included in the “Tables Available to Use” list in the Web Assistant “Set Tables and Fields” screen illustrated above. If you want to make available data from Peripheral Tables that are linked to these searchable tables as well, you must include those Peripheral Tables in the Web Assistant Set Tables and Fields screen. For example, to make Species images available to Web visitors, include the Image Archive table as well as the Species table; to make Collection Notes available, include the Collection Notes table as well as the Collection table.

3. **Create the “Tables Available to Use” list:**

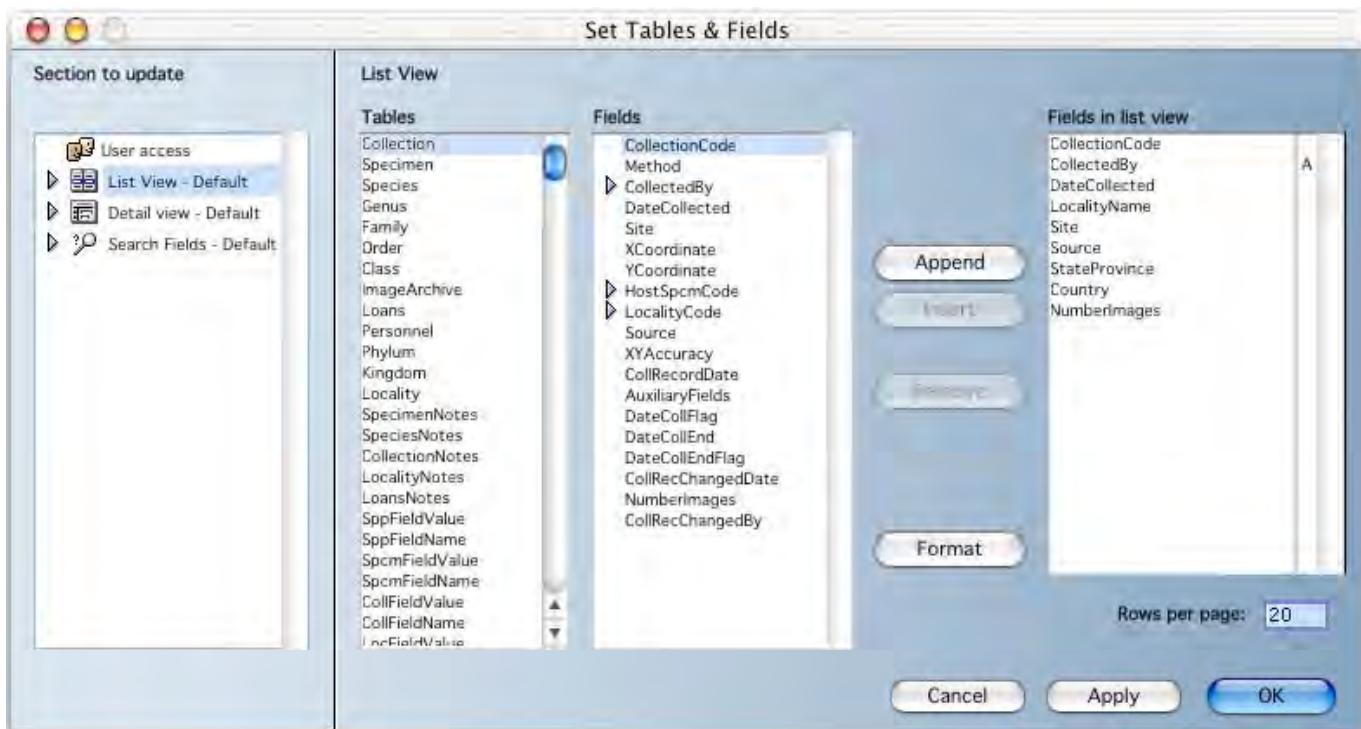
- **To make data for a table available** to Web visitors, select it from the “Tables” list and click the Append or “Insert” button. Using the “Remove,” “Append,” and “Insert” buttons, you can change the order to suit your needs.
 - **To hide all data for a table** from site visitors in Web Browser Mode, select the table in the list on the right and click the “Remove” button.
4. **To make a Core Table available for search** (see “[Setting the List of Tables Available for Search](#),” earlier in this chapter), a check mark must appear to the left of the table name in the “Tables Available to Use” list. The Web Assistant includes these checked tables in the navigation bar that it places on each Web page. To add a check mark, click to the left of the table name. To remove a check mark, click on it.
5. **The column of lowercase letters** (all “r” initially) to the right of the table names in “Tables Available to Use” list control access level to each table, for the selected user in the “User’s” list. The letter “r” allows Read Only access: the visitor cannot create, modify, or delete records.

WARNING: Do **not** set tables to any mode but “r,” Read Only access, in the Web Assistant settings. Biota input screens include many error-checking procedures and warnings that are crucial to maintaining database integrity. The Web Assistant ignores all such procedures.

6. In the “Section to Update” panel, select “List View—Default.” This screen (List View) controls the characteristics of record listing pages (record tables) in Web Browser Mode.



7. In the “Tables” list, click the name of the table for which you want to view or modify the settings. In the example below, the Collection table has been selected.



- The “Fields” list shows all fields in the Collection table (not in alphabetical order). Each field that is a Linking Field (foreign key) for a Parent table displays a triangle. If you click a triangle in this list, fields in the linked Parent table become available. In the example below, the LocalityCode field has been expanded to show the fields in the Locality table.

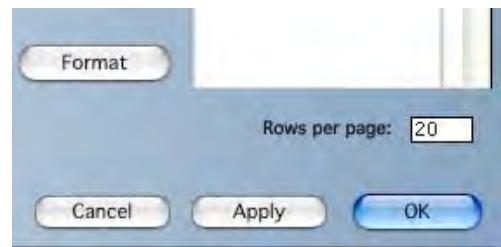


NOTE: There is no point in creating a field list for any tables other than the Core Tables made available for search (see [“Setting the List of Tables Available for Search,”](#) earlier in this chapter) and checked in the “Tables Available to Use” list in the “User Access” screen ([Step 4](#), above).

8. Create the “Fields in List View” list:

- To include a field, select it from the list in the center and click the “Append” or “Insert” button. Using the “Remove,” “Append,” and “Insert” buttons, you can change the order of fields to suit your needs.
- To remove a field from record listing screens in Web Browser Mode, select it from the list on the right and click the “Remove” button.

9. **To set the maximum number of records per Web page** in Web Browser Mode, enter the number in “Rows Per Page” box in the lower right-hand corner of the “List View” panel. You can enter a different number for each Core Table checked in the “Tables Available to Use” list in the “User Access” screen ([Step 4](#), above).



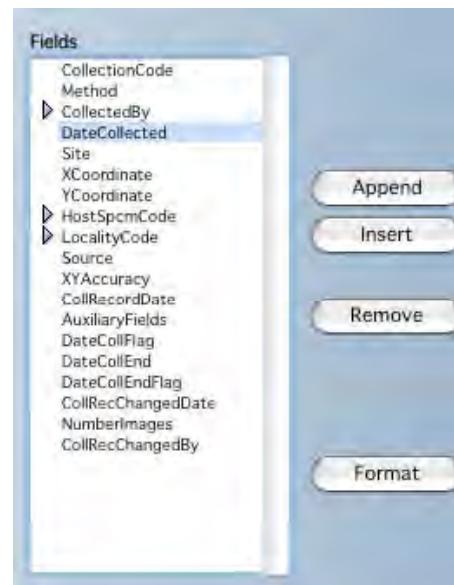
The smaller the number, the faster the browser will be able to display the page. Avoid using very large numbers, which may exceed the memory settings of some Web browsers.

NOTE: If you include the tag <!--PrevNext--> in the HTML Header and/or Footer, the Web Assistant automatically creates links to additional pages if the number of records to be displayed exceeds the limits you set. See “[Using the Web Assistant HTML Editor](#)” later in this chapter.

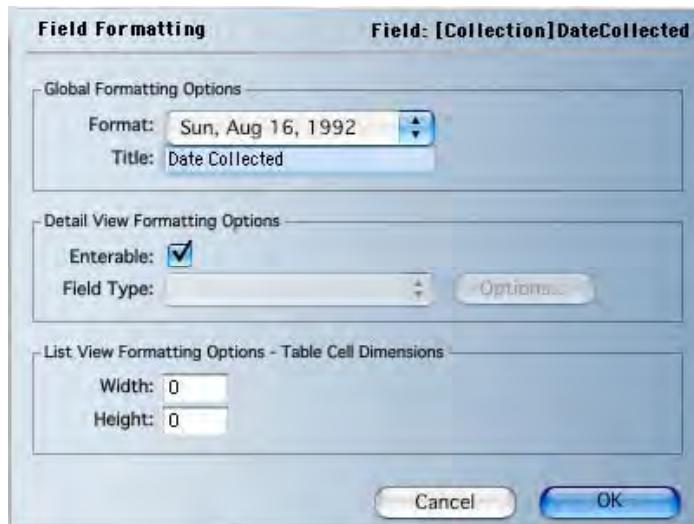
10. **To specify that records be sorted on a particular field**, click to the right of a field name (between the black line and the scroll bar) in the “Fields in List View” panel. An “A” will appear indicating the records displayed will be sorted on this field in ascending order on pages in Web Browser Mode. Click the “A” to switch it to a “D.” The fields will now be sorted in descending order. Another click will clear the “D,” indicating that the records will not be sorted.

NOTE: It is best to choose only indexed fields for sorting. Consult Appendix A, “[Biota Tables, Fields, and Relational Links](#)” to see which fields are indexed. Otherwise, Web page display will be slow.

11. **To change the formatting of a field in List view (record listing Web pages)**, select the field in the “Fields” list and click the “Format” button. The DateCollected field has been selected here. (Be sure to click the field name in the “Fields” panel, not in the “Fields in Detail View” panel.)



The “Field Formatting” screen appears.



- **“Global Formatting Options” panel** of the “Field Formatting” screen. For certain field types (such as Date, in this example), the “Format” popup list offers alternative formats in the “Global Formatting Options” panel.

The “Title” entry area in this panel allows you to modify the field name. In this example, a space character has been added between “Date” and “Collected” to make the DateCollected field name more legible. (This modification has been applied to all such fields in Biota’s prototype Web Assistant settings.)

Note: Unfortunately, the 4D Web Assistant does not offer international date formats.

- **“Detail View Formatting Options” panel** of the “Field Formatting” screen. Ignore these settings, which apply only to detail view screens in read-write mode, which you should not use with Biota (see the [Warning in Step 5](#), above).
 - **“List View Formatting Options” panel** of the “Field Formatting” screen. You can adjust the Width of table cells in Web page listing screens using the bottom panel. If you leave the default setting of zero, the Web Assistant adjusts the width based on content, which works quite well. (The Height setting has no effect on Biota fields.)
12. In the “Section to Update” panel on the left, select “Detail View—Default.” This screen (Detail View) controls the characteristics of record detail pages in Web Browser Mode. (See next page.)



The “Detail View” screen operates in exactly the same way as the “List View” screen but controls which fields appear on detail (single record display) Web pages and the order in which these fields appear.

13. In the “Section to Update” panel on the left, select “Search Fields—Default.” This screen (Search Fields) allows you to determine, table by table, which fields will be offered to site visitors for queries.



14. **Select the Table, then the Fields you want to include in the query popup list** for that table. Construct and order the list of Search Fields using the “Remove,” “Append,” and “Insert” buttons.

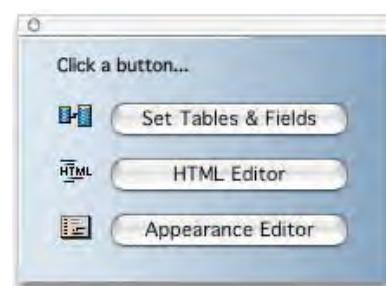
Note: There is no point in setting query fields for any tables other than the Core Tables made available for search (see “[Setting the List of Tables Available for Search](#),” earlier in this chapter) and checked in the “Tables Available to Use” list in the “User Access” screen ([Step 4](#), above).

15. **For each Table, choose a query format by** clicking one of the radio buttons in the lower right corner of the Search Fields screen: either a Conjunctive Search format or a Search by Example format. Conjunctive search screens are recommended, but you can try both and decide for yourself.
16. **Click the “Apply” button** to apply new settings for the Set Tables and Fields window immediately, if you wish.
17. **Click the “OK” button** to save changes for the Set Tables and Fields window.

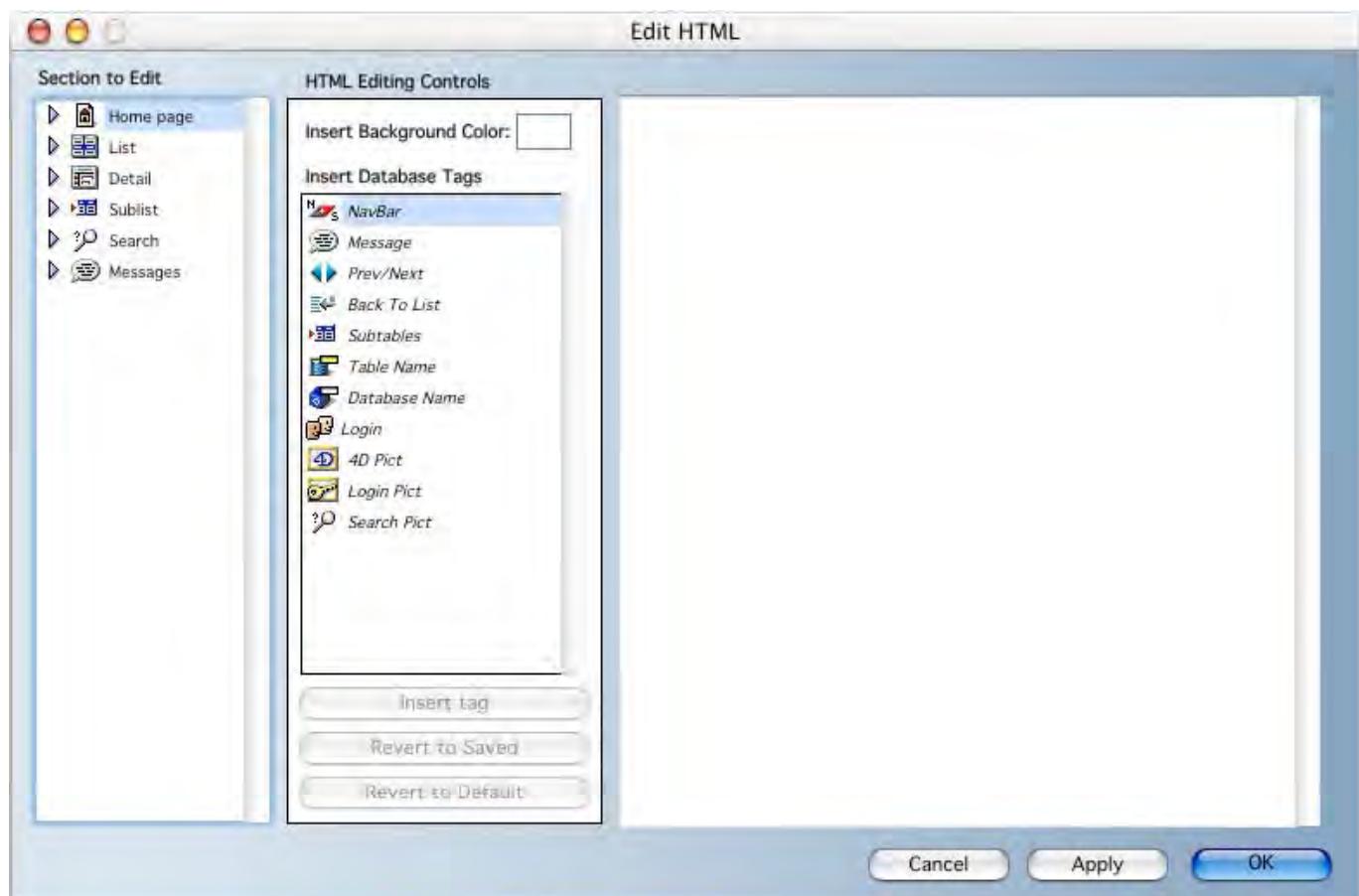
Using the Web Assistant HTML Editor

NOTE: If you prefer, you can edit the HTML Header and Footer code directly in the appropriate text file within the Web Assistant folder (see “[How and Where Web Assistant Settings Are Saved](#),” earlier in this chapter). Alternatively, you can paste HTML material into the “Edit HTML Text” panel. However, if you do edit files directly in the Web Assistant folder, you should do the editing (or at least check the code) in a simple text editor. Web authoring tools are likely to automatically add lines that will make nonsense of the dynamically generated body code that Biota places between header and footer code that you can edit.

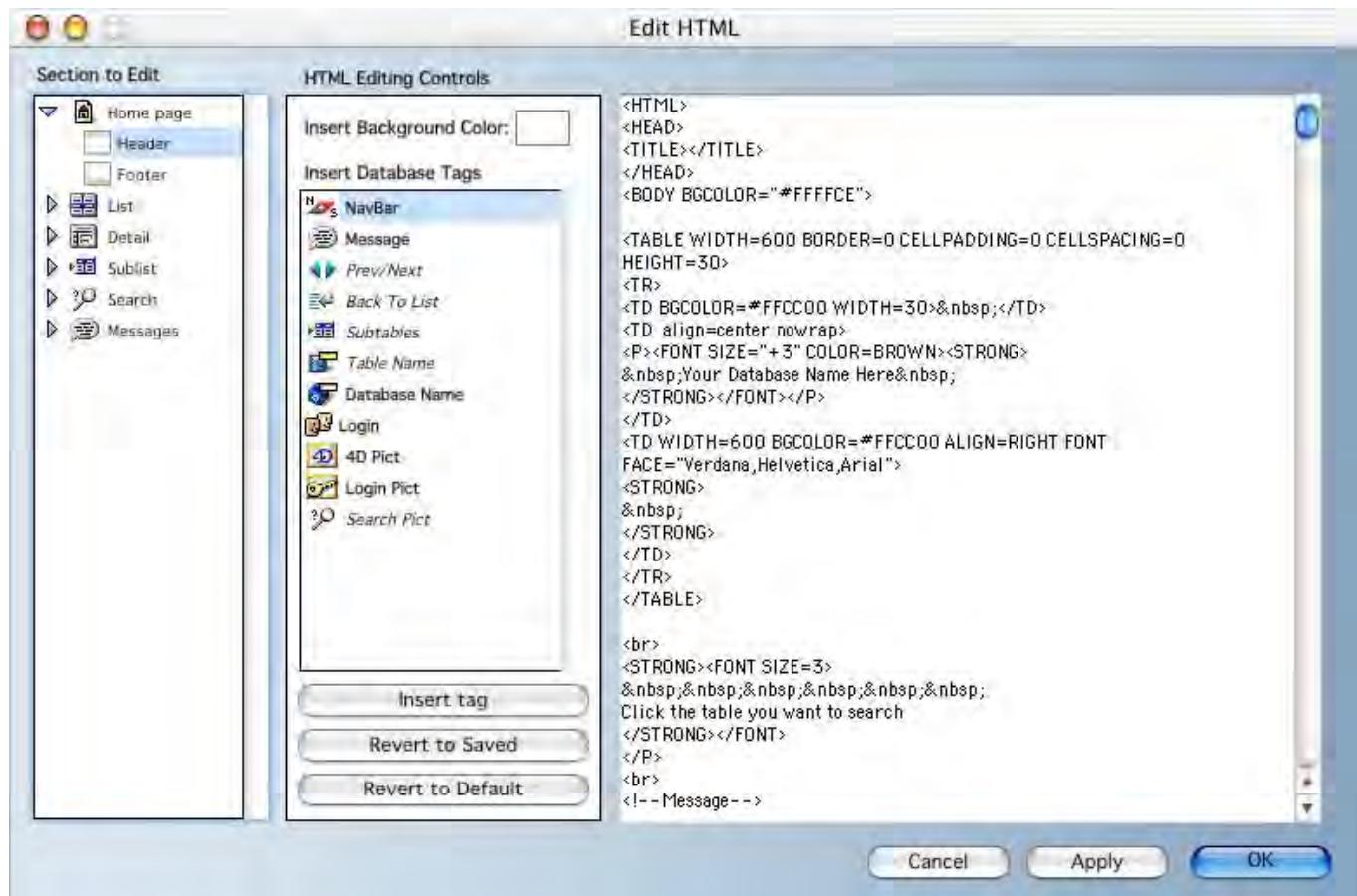
1. Click the “HTML Editor” button in the Web Assistant palette.



The “Edit HTML” screen appears.



2. Click the triangle next to a page type (e.g., “Home Page,” “List,” or “Detail”) in the “Section to Edit” list, then select either “Header” or “Footer.” In the image below, the triangle by the “Home Page” entry in the “Section to Edit” list on the left has been clicked to expand the list, and the Header entry has been selected, displaying the HTML for the dynamically generated Tables Home Page that Biota displays first in Web Browser Mode.



3. Edit the HTML to make changes in the Header or Footer for each of the page types in the “Section to Edit” list on the left. (See [Step 4](#) for instructions on changing page titles and [Step 5](#) for instructions on changing page background color.)
- You can replace header and footer HTML coding with any legal HTML, but be aware that the Header and Footer for each page type must comply with proper HTML syntax when taken together to form a complete page.

NOTE: These headers and footers are simply inserted above and below the HTML automatically generated by Biota. They do not correspond to the HTML <HEAD> and <FOOTER> tags. However, they may contain these tags.

- The “HTML Editing Control” panel lists special 4D tags that the Web Assistant uses to place objects, variables, and repeated HTML code in the page. You can recognize these special tags in the existing Header and Footer code by looking

for tags of the form: <!--TagName-->. The onboard Web server looks for these tags and inserts the appropriate code.

The best way to see what these tags do is to try them out. Select a tag from the list, place the cursor where you want to insert the tag in the HTML panel, and click the “Insert Tag” button. To restore the HTML to its previous state, click the “Revert to Saved” button.

Notice that the navigation bar displayed on Web Browser Mode pages is not a part of the HTML headers you see here. Instead, the Web Assistant looks for a <!--NavBar--!> comment. When it sees this comment, it is replaced with links to the tables checked in the “Set Tables & Fields” dialog screen in [Step 4](#) in the section, “Setting Tables and Fields Preferences,” above.

If you include the tag <!--PrevNext--> in the HTML Header and/or Footer, the Web Assistant automatically creates links to additional pages if the number of records to be displayed exceeds the limits you set (see [Step 9](#) in “Setting Tables and Fields Preferences” earlier in this chapter).

NOTE: The Database Name tag inserts the name of your Biota *application*, not the name of the Data File.

4. **To change the title on dynamically generated pages in Web Browser Mode,** substitute your title for the words “Your Database Name Here” in the Header for each of the page types listed in the “Section to Edit” panel (omitting Sublist, which has no page title).
5. **To change the page background color in Web Browser Mode:**
 - (a) **In the “Section to Edit” panel, select a page type.**
 - (b) **In the HTML panel, select the page background color definition** (e.g., BGCOLOR="#FFFFCEV"). Do not select anything else, including spaces before and after these characters.
 - (c) **Click on the “Insert Background Color” box and select a color** from the dropdown palette that appears.
 - (d) **Check the syntax in the HTML panel.** The complete tag should read, for example: <BODY BGCOLOR="#CEFFFF" (including the quotes).
6. **Click the “Apply” button** to apply changes made in the HTML Editor.
7. **Click the “OK” button** to save changes made in the HTML Editor.

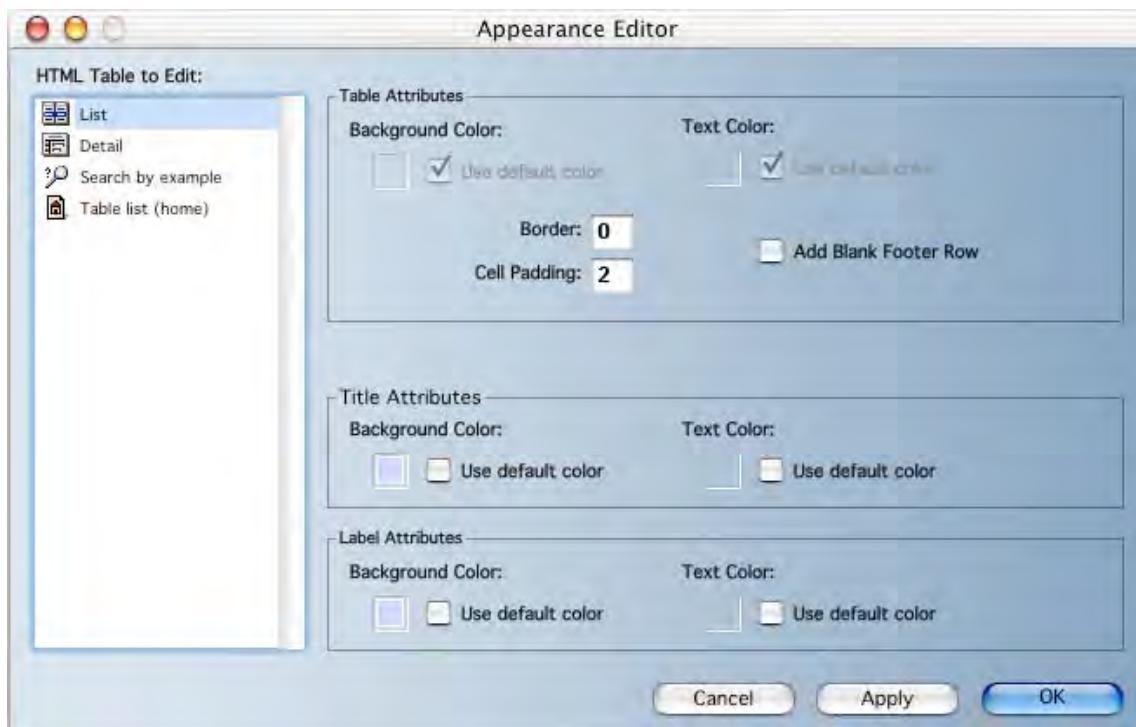
Using the Web Assistant Appearance Editor

The Appearance Editor controls various attributes of the body of Web pages dynamically generated by the Web Assistant in Web Browser Mode. You must use these controls if you wish to change these attributes, because you have no direct control over the HTML generated in the main body of these Web pages.

1. Click the “Appearance Editor” button in the Web Assistant palette.



The “Appearance Editor” screen appears.



2. Select a page type from the “HTML Table to Edit” list on the left.
3. To change the color scheme for that page type, click on “Background Color” or “Text Color” in the “Table Attributes,” “Title Attributes,” or “Label Attributes” panel.
 - **Table Attributes** apply to the cells of the table.
 - **Title Attributes** apply to the name of the Biota table (e.g., Specimen, Locality...) displayed at the top of a page.
 - **Label Attributes** apply to field labels (e.g., Specimen Code, Locality Name...).

NOTE: The Background Color setting for the Table List page does not seem to do anything.

4. **Choose a new color** from the dropdown palette that appears.
5. **To change the appearance of the record tables** in Web Browser Mode, change the Border or Cell Padding settings.
6. **Click the “Apply” button** to apply changes made in the Appearance Editor.
7. **Click the “OK” button** to save changes made in the Appearance Editor.

Chapter 32

Database Client Mode

In both Database Client Mode and Web Browser Mode (Chapter 31, “[Web Browser Mode and the Web Assistant](#)”), Biota’s onboard Web server generates Web pages dynamically, and the site visitor requires only an ordinary Web browser to access Biota. Unlike Web Browser Mode, however, in which each action by a site visitor initiates a new and independent request from Biota’s Web server, the site visitor in Database Client Mode maintains a single, “private” connection with Biota’s Web server throughout a work session.

- **Advantages of Database Client Mode.** This mode allows the user to take advantage of many of the same powerful query and browsing tools that Biota offers in desktop mode, including Taxa for Places and Places for Taxa, the Query Editor, and use of Record Sets for sequential queries.
Database Client Mode, like desktop mode, supports record browsing over any number of levels. For example, if a Family record is displayed by a query, the site visitor can show all Genus records for the family, display a Genus record, then display all Species records for the genus and all Specimen records for a species, all without initiating a new search. In contrast, Web Browser Mode allows only one level of child record access (e.g., all Genus records for a family may be displayed from the Family record, but to find linked Species or Specimen records, a new search at the lower level is required).
- **Disadvantages of Database Client Mode.** There are two main disadvantages of Database Client Mode, in comparison with Web Browser Mode. First, navigation is strictly by on-screen buttons; the Internet browser Back and Forward buttons cannot be used. This may be frustrating to some visitors. Second, with greater power comes a somewhat steeper learning curve. Casual Web site visitors may not be willing to learn how to use the search tools in Database Client Mode, although they have been designed to be as intuitive as possible.

Enabling and Launching Database Client Mode

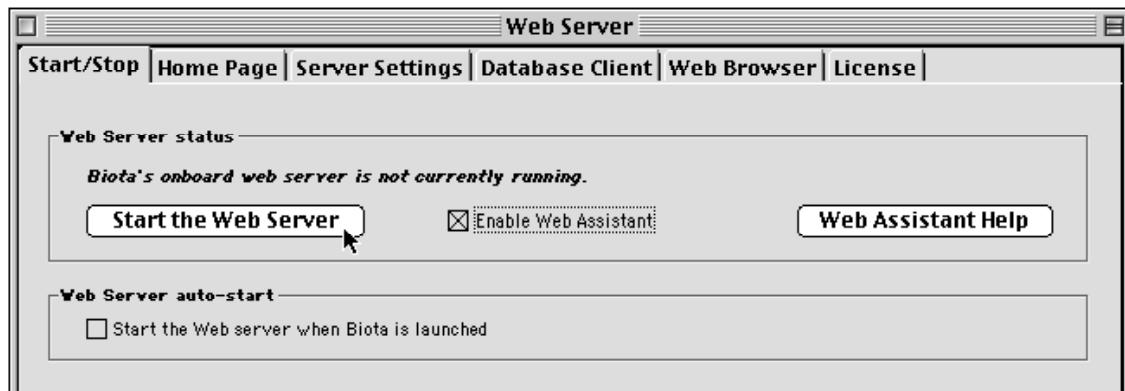
Biota’s onboard Web server can operate exclusively in Database Client Mode, exclusively in Web Browser Mode, or in both at once. The mode that is invoked depends upon the request sent to the Web server from the visitor’s Web browser.

For Web Browser Mode, the Web Assistant must be enabled. If not, Biota’s Web server supports only Database Client Mode (See Chapter 31, “[Web Browser Mode and the Web Assistant](#)”).

Enabling Database Client Mode and Changing Settings

NOTE: Before launching the Web server, you should first verify that it has been properly set up. See “[Web Server Settings and Controls](#)” in Chapter 30.

- To enable **Database Client Mode** in the Biota Web server, simply choose Web Server from the Special menu, then click Start the Web Server.



NOTE: If you want to enable Web Browser Mode at the same time, check the Enable Web Assistant box before launching the Web server. Otherwise, leave it unchecked.

- To change settings for **Database Client Mode**, follow the instructions in the section “[Web Server Settings and Controls](#)” in Chapter 30. All settings described in that section affect Database Client Mode, with the exception of the Web Browser tab.

Launching Database Client Mode from a Static Web Page

When you install Biota from the CD or a downloaded installer, two prototype static Web (HTML) pages are installed in the same folder as the Biota application.

- **BiotaHomePage.html**
- **BiotaDatabaseClient.html**

A folder called **WebImages** is also installed, containing the background swatch (**BiotaHomePageBackground.jpg**) used for the two prototype Web pages.

Here is the full, default arrangement of folders and files:

```
[Biota Folder]
  [Biota Application Files]
    BiotaDatabaseClient.html
    BiotaHomePage.html
  WebImages [folder]
```

BiotaHomePageBackground.jpg

The HTML file **BiotaHomePage.html** is intended as a Gateway Home Page to a Biota-based site that offers both Web Browser Mode and Database Client Mode to Web visitors. For suggestions on customizing the Gateway Home Page, see “[Customizing the Gateway Home Page For Web Browser Mode](#)” in Chapter 31.



- The “**Web Browser**” link initiates Web Browser Mode on the Biota server and displays the Web Browser home page, which is dynamically generated by Biota. The URL for this link is **/4DCGI/wbaHandleURL/HomePage**. For details, see “[Customizing Dynamic Pages for Web Browser Mode](#),” in Chapter 31.
- The “**Database Client**” link displays the static HTML page **BiotaDatabaseClient.html**, which is used exclusively in Database Client Mode. The URL for this link is **/4DMethod/WebDatabaseClient**. The page **BiotaDatabaseClient.html** is shown on the next page of this manual.

The static HTML page **BiotaDatabaseClient.html** shown below has three menus: Find, Display Set, and Special. Together, these menus contain all the commands currently allowed in Database Client Mode. The menus and commands are detailed in the next section in this chapter, “[Customizing the Static Web Page that Launches Database Client Mode](#).”

NOTE: Watch the Biota Web site (<http://viceroy.eeb.uconn.edu/biota>) for news on additional Database Client Mode commands in Biota updates.

BiotaDatabaseClient - Netscape 6

Home My Netscape Search Shop Bookmarks

Your Database Name Here

FIND	DISPLAY SET	SPECIAL
Using the Query Editor	Specimen Set	About Biota
Specimens for a Species	Collection Set	Empty Record Sets
Lower Taxa for a Higher Taxon	Locality Set	Return to Homepage
Species or Specimens for a Locality or Collecting Event	<hr/>	
	Species Set	
	Genus Set	
All Specimens	Family Set	
All Collections	Order Set	
All Localities	Class Set	
All Species	Phylum Set	
All Genera	Kingdom Set	
All Families	<hr/>	
All Orders	Personnel Set	
All Classes	Reference Set	
All Phyla		
All Kingdoms		
<hr/>		
All Personnel		
All References		

Customizing the Static Web Page That Launches Database Client Mode

On your Web site, Database Client Mode must be launched from a static Web page, such as the prototype page (BiotaDatabaseClient.html) described above (see “[Launching Database Client Mode from a Static Web Page](#),” earlier in this chapter).

- ***Either:*** Design your own static Web page for Database Client Mode, incorporating the command-URL links detailed in the section “[Customizing Command Links](#),” below, using any Web-authoring application.
- ***Or:*** Modify the prototype page (BiotaDatabaseClient.html) to suit your needs. For a start, you will want to change the header to read something other than “Your Database Name Here,” which you can do in your Web-authoring application.

Customizing Graphic Elements and Page Background

The prototype page (BiotaDatabaseClient.html) uses graphic design elements (header, colors) from the dynamically generated Web browser pages that are produced by Biota based on the prototype Web Assistant settings (see Chapter 31, “[Web Browser Mode and the Web Assistant](#)”). These design elements can be copied to other static pages if you wish, or you can design and implement your own header and footer elements.

If you want to use the prototype page but prefer a different background, you have two options. You can prepare a new background swatch in jpeg format, name it BiotaHomePageBackground.jpg, and substitute it for the file of the same name that is installed with Biota; or you can use your Web-authoring application to apply a different background.

NOTES:

- a. To learn how to customize the page background for dynamically generated pages in Database Client Mode, see “[The Database Client Tab](#)” in Chapter 30.
 - b. To learn how to customize the page background used for dynamically generated pages in Web Browser Mode, see “[Using the Web Assistant HTML Editor](#)” in Chapter 31.
 - c. To learn how to change the page title on dynamically generated pages in Web Browser Mode, see “[Using the Web Assistant HTML Editor](#)” in Chapter 31.
-

Customizing Command Links

In Database Client Mode, you issue commands to Biota's onboard Web server through specially formatted command-URLs, which the Web server recognizes as 4D commands, rather than as Web addresses. You can place these command links on any static Web page, in any combination that suits your needs.

Using Command Links

The HTML code for a standard Web link, such as a link to the Web search engine Google, might read:

```
<p><a href="www.google.com">Search the Web at Google</a></p>
```

The URL in this code segment is

www.google.com

In its simplest form, the HTML code for the command-URL link that orders Biota's Web server to display a list of all Family records reads:

<p> All Families</p>

The URL in this code segment is:

/4DMethod/AllFamilies

All Database Client Web page command-URL links have the same format:

/4DMethod/*CommandName*

In this format, **CommandName** represents one of the Database Client Commands in the table below. The table columns correspond exactly to the menus Find, Display Set, and Special on the prototype Web page BiotaDatabaseClient.html:

Table 32.1. Commands available for use in Database Client Mode

Find commands	Display commands	Special commands
SearchEd	DisplaySpecimen	AboutBiota
SpcmsForASpecies	DisplayCollection	EmptySets
LowTaxForHigh	DisplayLocality	GoToHomePage
SpcmSppForLC	DisplaySpecies	
AllSpecimens	DisplayGenus	
AllCollections	DisplayFamily	
AllLocalities	DisplayOrder	
AllSpecies	DisplayClass	
AllGenera	DisplayPhylum	
AllFamilies	DisplayKingdom	
AllOrders	DisplayPersonnel	
AllClasses	DisplayReference	
AllPhyla		
AllKingdoms		
AllPersonnel		
AllReferences		

NOTE: You must follow the syntax **/4DMethod/*CommandName*** precisely, with no space characters, and substitute one of the Commands in the table above for **CommandName**. Examine the HTML in the prototype Web page BiotaDatabaseClient.html if you are in doubt.

Differences from the Corresponding Desktop Commands

The commands available for use in Database Client Mode are, in general, identical in function to the corresponding menu items in desktop mode (BiotaApp or Biota4D under 4D Client). There are some important exceptions, however, made necessary or appropriate by the nature of Web clients and the limitations of HTML.

- **For all Database Client Mode find (query or record-finding) commands** (the Find menu or first column in [Table 32.1](#)), a Record Set for the target table is automatically created for the set of records found, rather than offering the site visitor a choice as is done in desktop mode (see “[Record Sets](#)” in Chapter 3).
- **Database Client Mode Display commands** (the Display menu or second column in [Table 32.1](#)) are identical to their desktop counterparts. Each displays the current Record Set for the indicated table, as long as the connection has not timed out (see “[The Server Settings Tab](#)” in Chapter 30).

Note: Biota maintains a “private” Record Set for each Biota Core Table for each Web site visitor. If you use Biota in desktop mode simultaneously, your own Record Sets are unaffected by the activities of Web site visitors.

- **The Query Editor in Database Client Mode** functions identically (despite necessary differences in the interface) to its desktop counterpart (see “[The Query Editor, a General Purpose Tool for Finding Records Based on Content](#)” in Chapter 12).
- **The Database Client Mode command “Specimens for a Species” (`SpcmsForASpecies`)**, which finds all Specimen records linked to a particular Species record, has no exact counterpart in desktop mode. It takes the place of the query “Find All Specimens for the Species...” in the desktop command “Lower Taxa for Higher Taxa” (in the Find menu) (see “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12).
- **Accordingly, the Database Client Mode command “Lower Taxa for a Higher Taxon” (`LowTaxForHigh`)** supports all the same queries as its desktop counterpart except “Find All Specimens for the Species....”
- **The Database Client Mode command “Specimens or Species for a Locality or Collecting Event” (`SpcmSppForLC`)** corresponds exactly to its counterpart in desktop mode, “Specimens or Species for Places” (in the Find menu) (see “[Finding Specimen or Species Records for Places \(Collections or Localities\)](#)” in Chapter 12). This command (as in desktop mode) requires a Record Set to already be established for the criterion table.

Chapter 33

Exporting Static Web Pages

Biota supports four different strategies for providing access to a Data File over the Internet or a local network (Chapter 29, “[Internet Strategies](#)”). Although Biota has its own Web server (Chapter 30, “[Biota’s Onboard Web Server](#)”), you may prefer to export a set of Web pages (HTML files and associated image files) that can be uploaded to a dedicated Web server.

There are a number of reasons you may prefer this strategy. Your institution may have a firewall policy that prevents you from running Biota’s Web server or makes it impossible to serve visitors outside the institution. Or, you may have only modem access to the Internet. If you have free or inexpensive use of a dedicated Web server, producing static Web pages may be less expensive than the cost of the 4D Web Extension License required to fully enable Biota’s Web server (see “[Relative Costs of Internet Strategies](#)” in Chapter 29).

Biota’s Create Web Pages tool guides you through the setup process for the completely automated export of hyperlinked Web pages, ready to post on a Web server. You can export hierarchically-linked pages for any range of taxonomic levels (including intermediate levels such as Subfamily), for Record Sets that you define with either a top-down or bottom-up search in the taxonomic hierarchy.

If you include Specimen records, you can select any set of fields in the Specimen, Collection, or Locality tables for inclusion as Specimen data. You can include an image for each Species record. Other options include control over page length, custom page footnotes, hyperlinking of host and “guest” Specimen records, and the translation of non-ASCII characters to HTML character codes.

Choosing a Strategy for Exporting Web Pages

Before you begin, you must decide whether to base the scope of the taxonomic records to be exported to Web pages on a *top-down* or a *bottom-up* search of tables in the taxonomic hierarchy. If you choose a bottom-up search, you may also choose to restrict the export by Collection or Locality. In any case, if you include the Specimen level, you can export data for each selected Specimen record based on related information in the Collection and Locality tables, as well data from the Specimen table itself. (See Appendix A, “[Biota Tables, Fields, and Relational Links](#)” to review Biota’s table structure.)

- **The top-down strategy** is based on the Lower Taxa for Higher Taxa tool of the Find menu (see “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12), which the Create Web Pages procedure presents if you choose this strategy. Some typical queries you could construct using this tool are “Find all Species for the Order Orthoptera,” “Find all Specimens for the Family Fringillidae,” or “Find all Specimens for the Genus Record Set” (where the Genus Record Set contains all genera of Galápagos finches, for example).

With this strategy, Biota will ask you to choose a *criterion* table at a higher taxonomic rank than the *target* table. The search can be based on a single higher taxon record (e.g., an Order record) or a higher taxon Record Set (e.g., the current

Order Record Set) in the criterion table. Biota finds all linked records down to the level of the target table (e.g., Species or Specimen).

The exported Web pages, organized by the taxonomic hierarchy, will include the criterion and target levels you choose, all obligatory intervening ranks, and any optional ranks (e.g., Subfamily) that you indicate later in the setup.

- **The bottom-up strategy** is based on the Higher Taxa for Lower Taxa tool of the Find menu (see “[Finding Records for Higher Taxa Based on Lower Taxa](#)” in Chapter 12), which the Create Web Pages procedure presents if you choose this strategy. Some typical queries you could construct using this tool are “Find all Genera for the Specimen Record Set” or “Find all Orders for the Species Record Set.”

With this strategy, Biota will ask you to choose a criterion table at a lower taxonomic rank than the target table. The search is based on the current Record Set at the criterion level. Biota finds all records linked to the criterion Record Set, at ranks up to and including the target level.

The exported Web pages, organized by the taxonomic hierarchy, will include the criterion and target levels you choose, all obligatory intervening ranks, and any optional ranks (e.g., Subfamily) that you indicate later in the setup process.

- **To create Web pages based on a particular set of Locality or Collection records**, you must use a two-stage strategy. First, create a Locality or Collection Record Set for the records of interest. Then use the Specimens or Species for Places tool (see “[Finding Specimen or Species Records for Places...](#)” in Chapter 12) to create a Specimen or Species Record Set based on links to the Locality or Collection Record Set. Finally, choose the bottom-up option (described above), based on the Specimen or Species Record Set.

Using this strategy, you can create Web pages (for example) for all Specimens in the Collections from a particular site or for all Species from a particular country or province. In either example, you could also include linked records up to the level of, say, Family or Order.

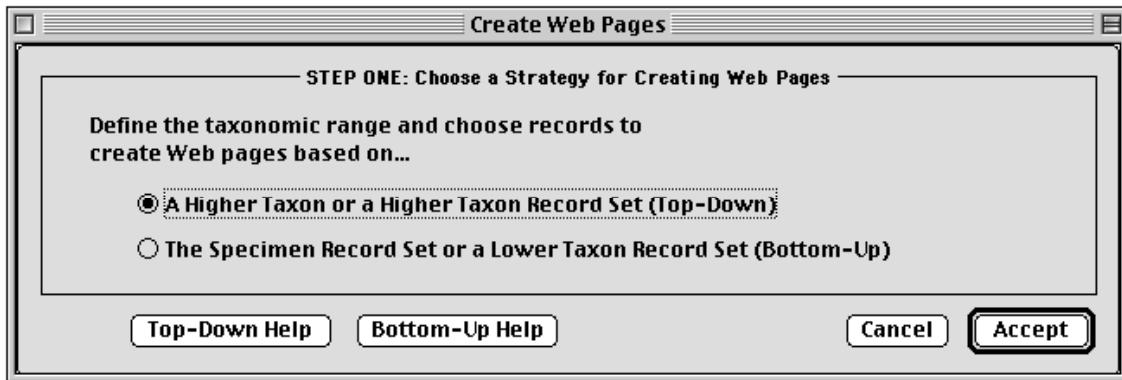
Exporting Web Pages: Step by Step

Warning: Before beginning, be certain that you have enough space available on your hard disk for the exported files.

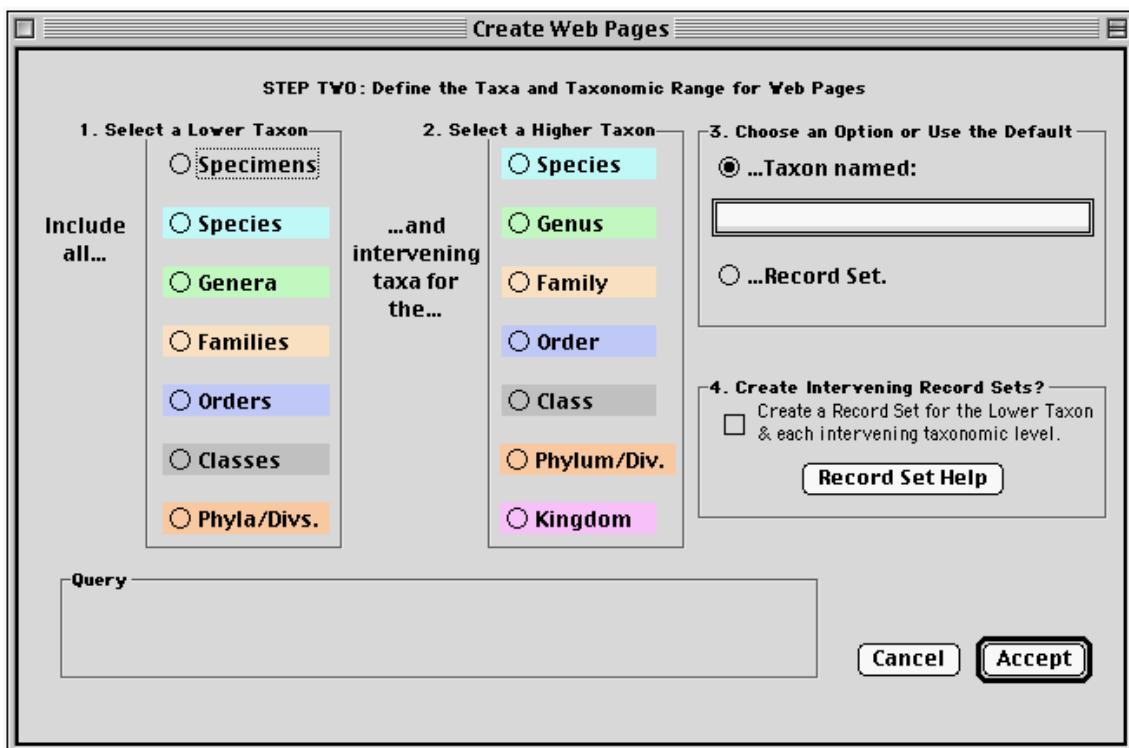
Here are the steps to follow to create Web pages, once you have settled on a strategy (see “[Choosing a Strategy for Exporting Web Pages](#),” above):

1. **Define the appropriate criterion Record Set**, using tools from the Find menus (see Chapter 12, “[Finding and Updating Records](#)”). See the guidelines in the previous section. (If you intend to use the *top-down* strategy based on a single higher taxon record, there is no need to create a Record Set. You may proceed directly to the next step.)

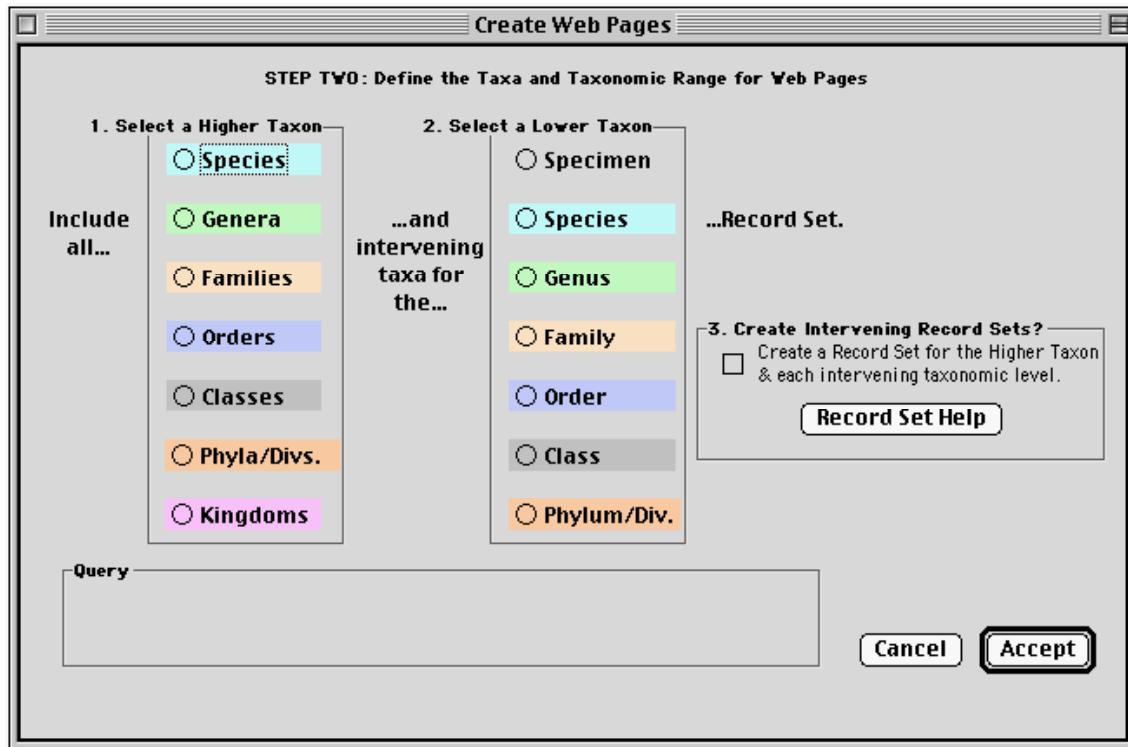
2. From the Im/Export menu, choose Create Web Pages. The Strategy option screen appears.



3. Choose either the “Top-Down” strategy (the default) or the “Bottom-Up” strategy and click the “OK” button.
- If you choose the “Top-Down” strategy, a special version of the Lower Taxa for Higher Taxa tool appears. If you are not familiar with this tool, see “[Finding Records for Lower Taxa Based on Higher Taxa](#)” in Chapter 12.



- If you choose the “Bottom-Up” strategy, a special version of the Higher Taxa tool appears. If you are not familiar with this tool, see “[Finding Records for Higher Taxa Based on Lower Taxa](#)” in Chapter 12.

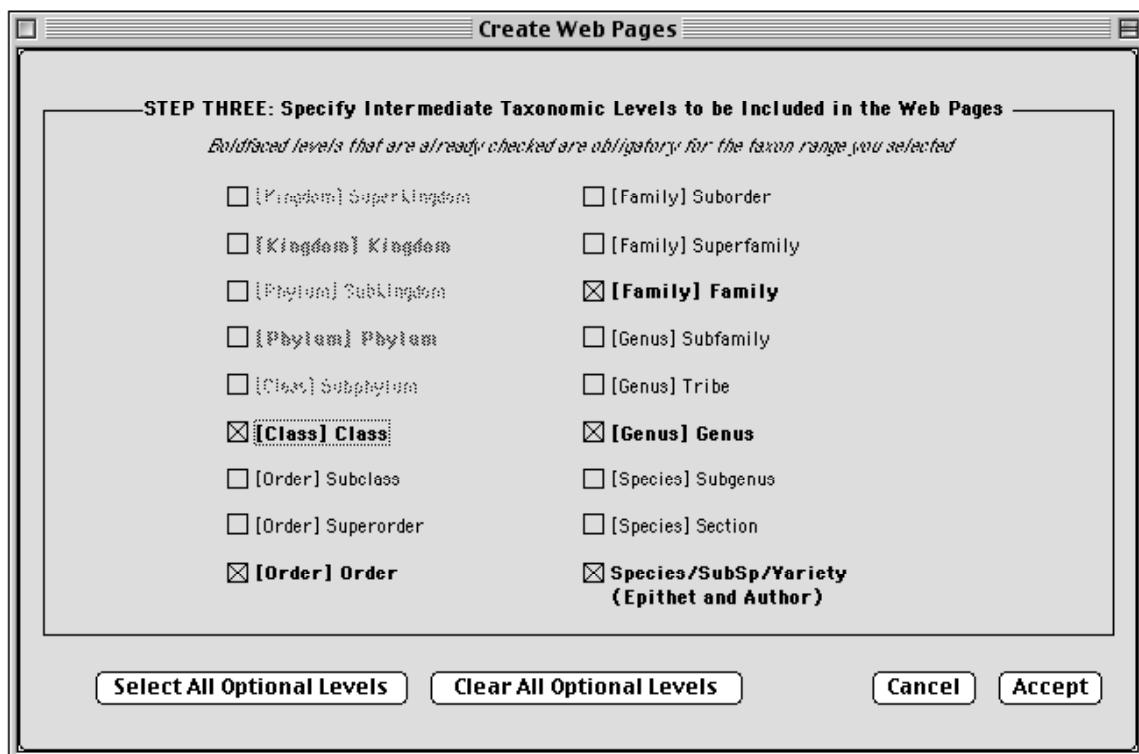


4. Set up the appropriate query in one of the screens above.

NOTE: It is not necessary to check the “Create Intervening Record Sets?” box to create the Web pages, but it might help you check the pages against records in the Data File. Use the Display menu to see the Record Sets created.

5. Click the “Accept” button in the search screen. Biota performs the search, which may take a few moments.

The Intermediate Taxonomic Level option **screen appears**.



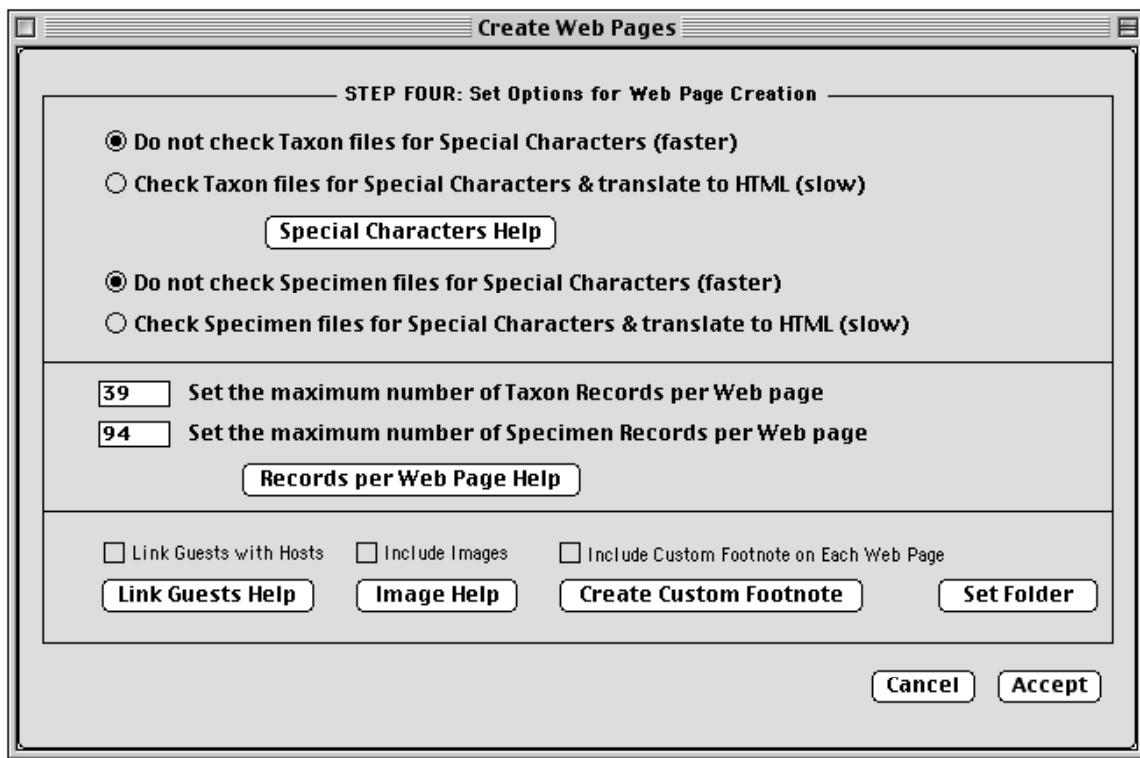
6. Click the check box for each intermediate taxonomic rank that you want Biota to recognize in creating the Web page hierarchy.

Any ranks above or below the criterion and target ranks (tables) are dimmed (disabled). (In the example above, the criterion table was Class and the target table was Specimen.)

All *obligatory* ranks within the taxonomic scope you chose in the previous step are automatically enabled and cannot be manually disabled (it would make no sense to disable them).

You can use the “Select All Optional Levels” and “Clear All Optional Levels” buttons to speed up the selection process, if you wish.

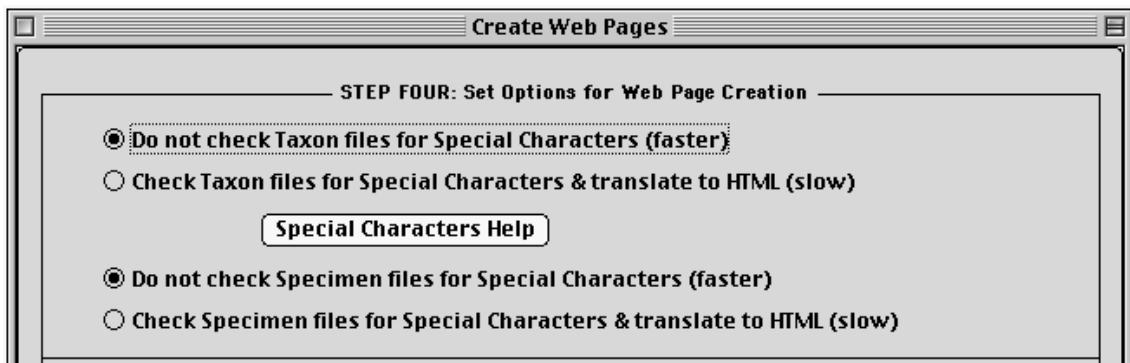
7. Click the “Accept” button in the Intermediate Taxonomic Level option screen (above). The Web Page options screen appears (below).



If you included the Specimen table in the taxonomic scope you specified in [Step 4](#), above, the options screen will appear as illustrated above. If the Specimen table was not included, all options that apply to Specimen records will be dimmed (disabled).

The next five steps treat each of the options in the Web Page options screen, one at a time.

8. Set options for HTML translation of special characters.



Hypertext Markup Language (HTML), which Web browsers interpret, does not recognize characters with diacritical marks and a few other special characters.

If the records you are exporting contain HTML special-meaning characters (& < >), characters with diacritical marks (á é í ó ú à è ì ò ù â ê î ô û ã õ ö ñ and uppercase equivalents), inverted punctuation marks (¿ or ¡), or German ß, these characters will not display correctly with a Web browser unless you select one or both of the “Check...files for Special Characters and translate to HTML” options.

The two sets of option buttons in the top panel of the Web Page options screen (above) allow you to instruct Biota to ignore or to check and translate special characters for taxon files (Species, Genus, Family,..., Kingdom, using the upper pair of buttons) or data associated with Specimen records, including associated Collection and Locality data (using the lower pair of buttons).

NOTE: If you do *not* have any special characters in your records, or you are doing a test run, the export will run considerably faster if you do *not* ask Biota to check for special characters. Biota translates the degree and second symbols (characters ° and ") in latitudes and longitudes correctly with either setting, so it is not necessary to ask for character translation if these are the *only* special characters in your data.

9. Set guidelines for the maximum number of Taxon Records or Specimen Records per Web page.



These two numeric entry areas allow you to specify *guidelines* for the maximum number of taxon records (Species records, Genus records, Family records, etc.) records or Specimen records (including associated Collection and Locality data) per Web page. You can change the numbers to any value you wish.

Here are the rules Biota follows:

- **When the Web Page options screen first appears**, these values (above) are set to the highest *total* number of taxa for any selected rank (39 records, in the example above), and to the *total* number of Specimen records to be included on the Web pages (94 records in the example above), respectively.
 - **If you leave these values as they stand**, all taxa within a taxonomic rank will be displayed on a single Web page, and all Specimen records will be displayed on a single Web page. The longest of the taxon pages will have the number of records indicated in the upper box (usually, the page for the lowest rank in the taxonomic scope you defined). The single Specimen page will include the number of records indicated in the lower box.
 - **All records for a given taxon always appear on the same Web page**, regardless of the maximum records setting, and regardless of how many records there may be for the taxon. For example, if you have set a maximum of 50 records per taxon page, and you ask Biota to create a Web page that includes a genus with 75 Species, all 75 will nonetheless appear on a single Web page—but Biota will begin a new page for the next genus.
 - **Likewise, all Specimen records linked to a given Species record will appear on the same Web page**, regardless of the numerical limit you set for Specimen records.
 - **If the numerical limit you set has not been reached** at the end of a set of taxon records or the end of a conspecific group of Specimen records, Biota includes the next taxon of the same rank, or the next group of conspecific Specimen records, on the same Web page as the previous taxon or group.
 - **If you want to specify only one taxon per Web page**, regardless of how many or how few records it contains, set the Taxon Record numerical limit to 1. The second rule (above) guarantees the desired result.
 - **If you want to specify only one group of conspecific Specimen records per Specimen Web page**, regardless of how many or how few Specimen records are linked to each Species, set the Specimen record numerical limit to 1. The second rule (above) guarantees the desired result.
- 10. Specify whether to link guest Specimen records with host Specimen records.**

Hypertext links are a natural way to navigate from “guest” Specimen records to the associated host Specimen record at a Web site (see Chapter 24, “[Host-Guest Relations](#),” for a full discussion of host–guest relations).

If you create a Specimen Record Set that includes not only guest Specimen records but also the host Specimen records with which they are linked (see “[Finding Host and Guest Records](#)” in Chapter 24), Biota will automatically create the hypertext links between guests and their hosts on the appropriate Specimen Web pages, as illustrated below.



Species *Rhinoseius haplophaedia* Ohmer et al. 1991

Specimen Code: JLL13339:05; Collection Code: JLL13339H; Collected By: J.L. Luteyn; Date(s) Collected: 15 Nov 1989; [Host Spcm Code: JLL5674\(Ex Rhinoseius haplophaedia, Ericaceae\)](#); State/ Prov: Pichincha; Country: Ecuador; Loc Latitude: 0°4'S; Loc Longitude: 78°38'W

Specimen Code: JLL13339:06; Collection Code: JLL13339H; Collected By: J.L. Luteyn; Date(s) Collected: 15 Nov 1989; [Host Spcm Code: JLL5674\(Ex Rhinoseius haplophaedia, Ericaceae\)](#); State/ Prov: Pichincha; Country: Ecuador; Loc Latitude: 0°4'S; Loc Longitude: 78°38'W

Specimen Code: JLL13339:07; Collection Code: JLL13339H; Collected By: J.L. Luteyn; Date(s) Collected: 15 Nov 1989; [Host Spcm Code: JLL5674\(Ex Rhinoseius haplophaedia, Ericaceae\)](#); State/ Prov: Pichincha; Country: Ecuador; Loc Latitude: 0°4'S; Loc Longitude: 78°38'W

Species *Rhinoseius luteyni* sp. n.

Specimen Code: JLL14400:01; Collection Code: JLL14400H; Collected By: J.L. Luteyn; Date(s) Collected: 4 Apr 1992; [Host Spcm Code: JLL14400\(Ex Rhinoseius luteyni, Ericaceae\)](#); State/ Prov: Cotopaxi; Country: Ecuador; Loc Latitude: 0°58'S; Loc Longitude: 78°56'W

Specimen Code: JLL14400:02; Collection Code: JLL14400H; Collected By: J.L. Luteyn; Date(s) Collected: 4 Apr 1992; [Host Spcm Code: JLL14400\(Ex Rhinoseius luteyni, Ericaceae\)](#); State/ Prov: Cotopaxi; Country: Ecuador; Loc Latitude: 0°58'S; Loc Longitude: 78°56'W

NOTES:

- a. Be certain to include [Collection] Host Specimen Code among the fields you select for export with each Specimen record, in [Step 17](#), below.
- b. Biota does not check to see if you have included the proper records for the links to work. If you fail to include the host Specimens, the links from the guest Specimens are created properly, but there are no target host records.
- c. This option is disabled if you did not include the Specimen table in the taxonomic scope of the search.

11. Specify whether to include an image with each Species record that has associated images.

If this option is checked, Biota will export one Image for each Species record in the selection, if that Species has any associated Image Archive records. (See Chapter 19, “[Images](#),” for full information on the Image Archive and its relation to Species records).



An option screen appears.

12. Choose the Web page display option you prefer for Species images.

- **To display the images automatically on the Web page** when it is displayed, choose the first option, “On Species page, display images and text together.”

- **To display hyperlinks to the images on the Web page,** choose the second option, “On Species pages, display links to images, instead of the images themselves.” In this case, when

the Web site visitor clicks an image link, the image is displayed in a new window, labeled with the Image Name from the Image Archive record.

In either case, each image is exported to its own file, which is automatically linked with the appropriate Species record on a Species Web page. This option is disabled

 Many images per Web page may cause Web pages to load slowly. What do you want to do?

- On Species pages, display images and text together.
- On Species pages, display links to images, instead of the images themselves.

Cancel

OK

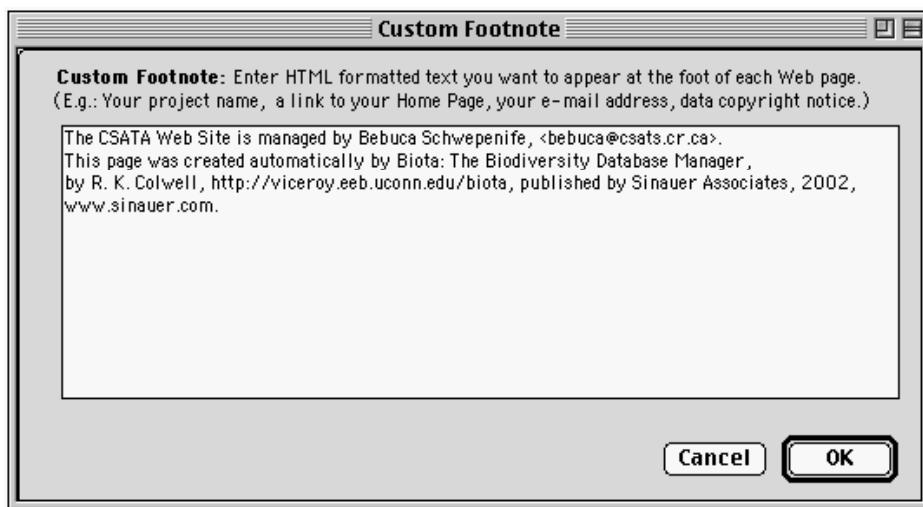
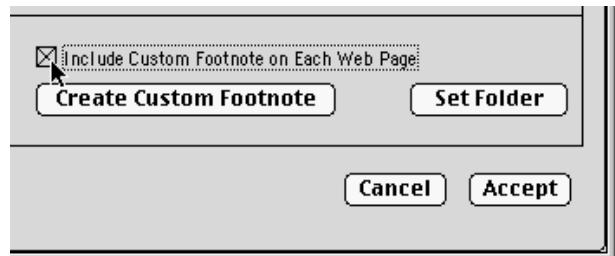
if you did not include the Species table in the taxonomic scope of the information to be exported.

- **The Image exported**—if more than one Image is linked to a particular Species record—is the *first* Image for the Species, according to the Image order you have determined in the Image tab of the Species input screen. (To make a different Image than the first one, see “[Changing the Order of Linked Image Records in the Input Screen](#)” in Chapter 19.)
- **The JPEG format is used for all Images exported by the Export Web Pages tool**, regardless of the format of the original image record or external file.
- **File names for Image files, when exported**, consist of the Species Code with the extension *.jpg*.

13. Specify a custom footnote to be included on each Web page, if you wish.

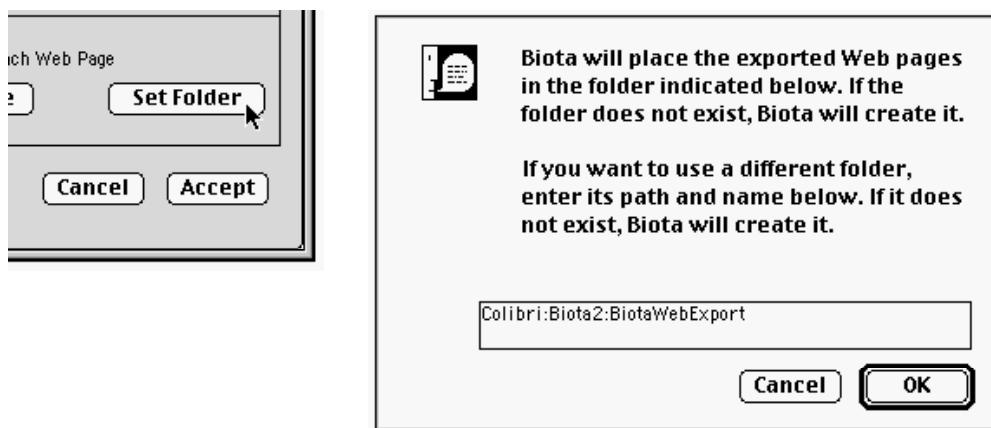
- a. **Click the checkbox “Include Custom Footnote on Each Web Page”** in the Web Page options screen.
- b. **Click the “Create Custom Footnote” button.**

The Custom Footnote editing window appears. (It will be blank unless you have previously entered text in the footnote window during this Biota session.)



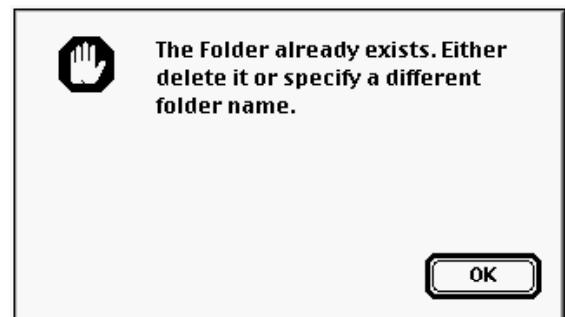
- c. **Enter whatever you wish to include in the footnote** (e.g., your project name, Web-site name, email address, data copyright notice, disclaimers, etc.). You can enter text only, or HTML coded objects such as hypertext links (e.g., a link to your home page) or image references for project or institutional logos.
- d. **Click the “OK” button in the Custom Footnote window to accept the entry.** The footnote button now reads Edit Custom Footnote (instead of Create Custom Footnote), to indicate that a footnote entry now exists.

- 14. To set the destination folder for the exported Web files**, click the “Set Folder” button. A request screen appears, showing the default folder name (“BiotaWebExport”), with full path information. The default path places the folder within the same folder as your Biota Data File.

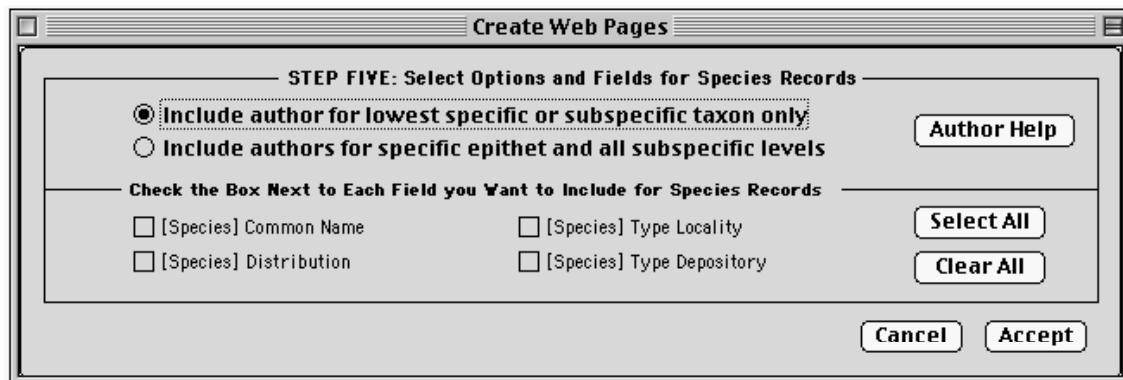


NOTE: In the illustration above, the default “BiotaWebExport” folder will be created (or used, if it already exists) on a hard disk called “Colibri,” within a folder called “Biota2.” The path name “Colibri:Biota2:” is the Mac OS path (without the quotes). The same path would be rendered “Colibri\Biota2\” in Windows (without the quotes).

- **If you want Biota to use the default destination folder**, click the “OK” button.
 - **If you want to use or create a different destination folder**, enter the path and folder name, then click the “OK” button.
 - ◊ **If accepted**, your entry will remain in effect until you quit Biota or change it again.
 - ◊ **If Biota cannot find or create the folder you have indicated**, you will see an error message. The most likely problem is a bad path. Click the “Set Folder” button again and try to reenter the path and folder name, or use the suggested default instead.
 - **In either case, if you designate a folder that already exists**, Biota will not accept it, to prevent overwriting Web files you might want to keep. In this event, you must either delete the existing folder or specify a different folder name.
- 15. Click the “Accept” button in the Web Page options window** to accept the settings from Steps 8–14, above. If you have included the Species level in the taxonomic scope ([Step 3](#), above), the Options and Fields for Species Records appears.

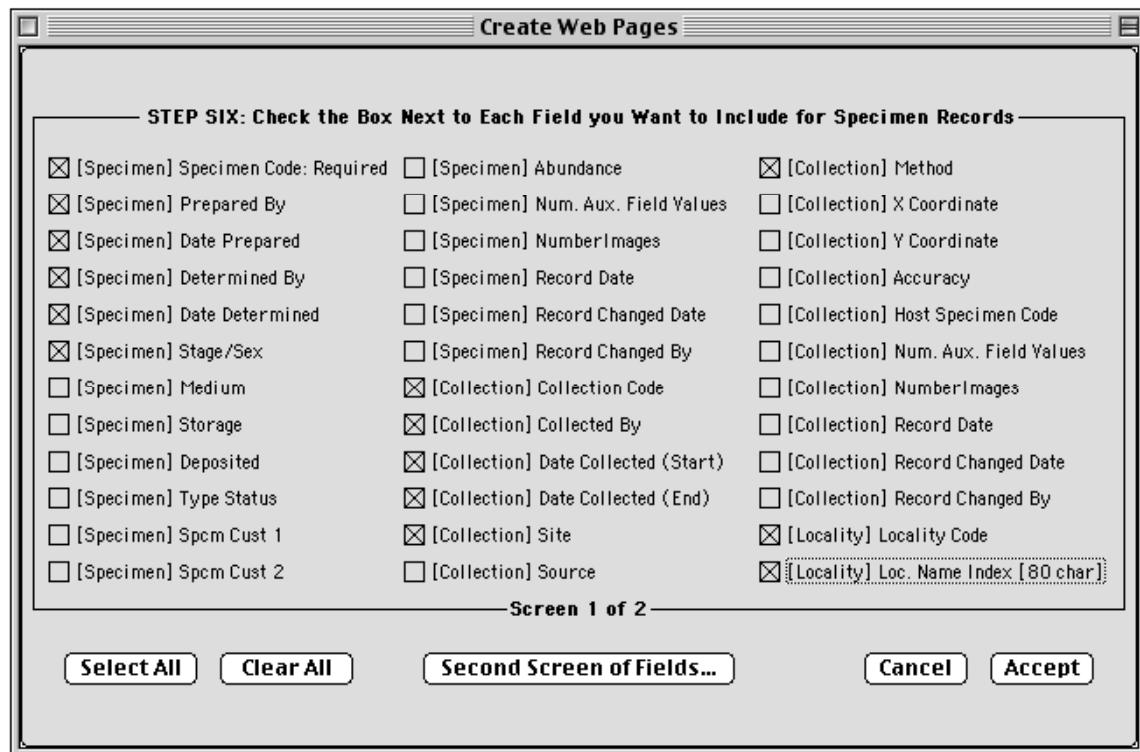


- **Include Author options.** The pair of options in the upper panel of the screen controls the format and content of species and infraspecific taxon names in the Species Web pages to be exported.



- ◊ **Include author for lowest specific or infraspecific taxon only.** If you choose this option (the default) full trinomials or tetrynomials appear, where appropriate, followed by the author field for the *lowest* level included (e.g., *Metrioptera roeseli* subsp. *roeseli* var. *diluta* Charpentier). Authors for higher levels are not included.
 - ◊ **Include author for specific epithet and all infraspecific levels.** If you choose this option, the Author fields for *all* levels (species and below) are included (e.g., *Beta vulgaris* Linnaeus subsp. *nivea* Jones var. *odorata* Lopez)
 - **Checkboxes for fields of the Species table.** Any of the four fields Common Name, Distribution, Type Locality, and Type Depository may optionally be included for each Species record on Species Web pages, as indicated in the panel of the Species options screen illustrated above. You can use the "Select All" and "Clear All" buttons to speed the selection process if you wish.
- 16. Click the “Accept” button in the Options and Fields for Species Records screen to accept the settings.**
- **If you did not include the Specimen table** in the taxonomic scope for the Web pages, the creation of the Web pages begins now. Skip to [Step 19](#), below.

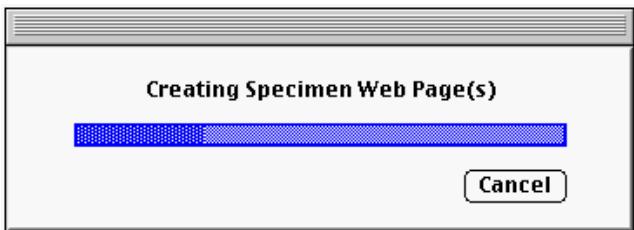
- If you included the Specimen table in the taxonomic scope for the Web pages, the Specimen/Collection/Locality Field Options screen appears. Notice that there are two screens of fields available, including every field in the Specimen, Collection, and Locality tables—more than 100 fields in all.



- To access the second screen, click the “Second Screen of Fields” button.
17. In the Field Options screen (above), check each field for which you want Biota to export information for each Specimen record in the selection. The Specimen Code field is obligatory. You can use the “Select All” and “Clear All” buttons to speed the selection process if you wish.

NOTE: If you checked the Link Guests with Hosts box in the Web Page options screen in [Step 10](#), above, be certain to include [Collection] Host Specimen Code among the fields you select for export with each Specimen record.

18. Click the “Accept” button in the Field options screen (above) to launch the Web page export. Biota posts a series of progress indicators (example below) as the



pages are made for each table. You can carry out other activities with Biota (or other applications) while the pages are being created in the background, as long as you do not open any records in input screens that might be involved in the export.

19. To abort the creation of Web pages, click the “Cancel” button in any progress window (example above).
20. Check the Web pages using a Web browser when the process is complete. Using the Open File command from the File menu of Netscape or Internet Explorer, or the equivalent command in another Web browser, open the page for the highest taxonomic rank. Use the hypertext links to move up and down the taxonomic hierarchy.
21. Move the Web pages to a Web server and add additional material to the pages (species descriptions, backgrounds, headers, etc.), if you wish. You will need to create a link or links in your home page to direct visitors to the Biota pages.

PART
9

Appendixes

Appendix A

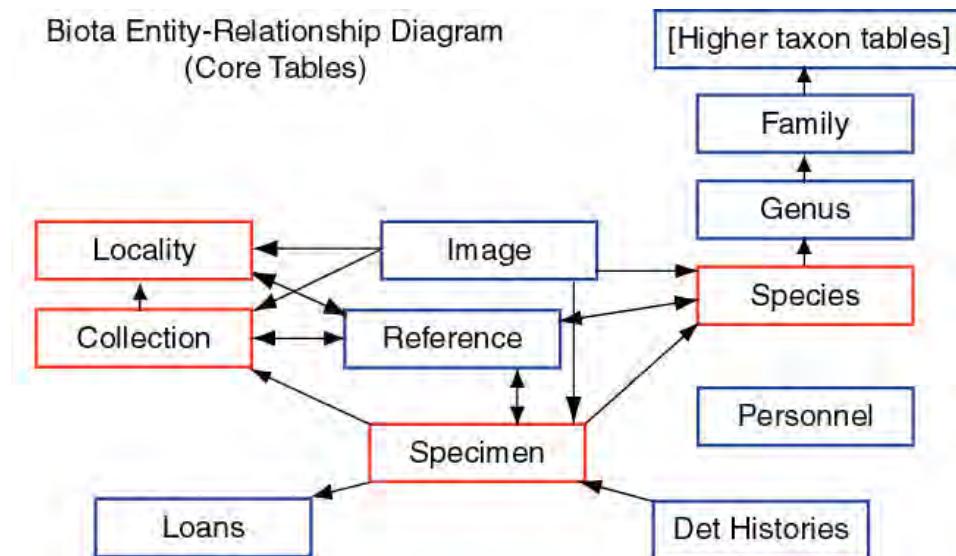
Biota Tables, Fields, and Relational Links

This appendix provides details of Biota's tables and fields, and their relational links. For an overview of Biota's structure and explanation of the links between tables, please see [Chapter 3](#), especially the section on "[Tables](#)" (repeated below) and "[Fields and Records](#)".

Overview of Tables

Core tables

The diagram below (in database jargon, an "entity-relationship" diagram), shows most of the links between Core Tables in Biota.



- **The taxonomic hierarchy** includes the *Specimen* table and a table for each of the seven obligatory levels of the Linnean classification system: *Species*, *Genus*, *Family*, *Order*, *Class*, *Phylum*, and *Kingdom* (see Chapter 11, "[Input—Table by Table](#)").
- **The place hierarchy** has two levels. The *Collection* table records data for collecting events (including collector and collection date), whereas each record in the *Locality* table keeps track of the geographical site of one or more collecting events (see "[Collection Input](#)" and "[Locality Input](#)" in Chapter 11).
- **Literature references** are recorded in the *References* table. Reference records can be linked to records in the *Species*, *Specimen*, *Collection*, and *Locality* tables (see Chapter 20, "[References](#)").

- **Names and contact data** for collectors, preparators, borrowers, Project participants, and authors of Notes are recorded in the *Personnel* table (see “[Personnel Input](#)” in Chapter 11).
- **To allow several projects to share the same Data File**, the *Project* table keeps track of project names and descriptions, and provides project-specific views of Auxiliary Fields (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”). (Not shown in the diagram.)
- **To keep track of specimen loans**, the *Loans* table records which specimens have been loaned, borrowed, and returned (see Chapter 21, “[Specimen Loan System](#)”).

Peripheral Tables

In addition to the 14 Core Tables, Biota’s relational structure encompasses an additional 20 *Peripheral Tables* (see Appendix A, “[Biota Tables, Fields, and Relational Links](#).”). Peripheral Tables keep track of supporting or ancillary data related to Core Table records.

For data entry, you will generally not need to think about what data the Peripheral Tables record or how they are linked to each other or to the Core Tables. But you will need to understand them fully if you wish to import data into Peripheral Tables or export data directly from them.

- **Images** are saved in the *Image Archive* table, which is linked with the Species, Specimen, Collection, and Locality tables (see Chapter 19, “[Images](#)”)
- **Notes** are saved in the *Specimen Notes*, *Species Notes*, *Collection Notes*, *Locality Notes* and *Loan Notes* tables (see “[Notes Input](#)” in Chapter 11).
- **User-Defined Auxiliary Field names and Auxiliary Field values** for the Species, Specimen, Collection, and Locality tables are recorded in four *Field Name* and four *Field Value* tables (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).
- **Entry choice lists (pick lists)** are enabled by settings in the *Lists* table. The list values themselves are saved in the *List Items* table (see Chapter 17, “[Default Entries and Entry Choice Lists \(Pick Lists\)](#)”).
- **Field name aliases** for re-namable fields are also saved in the *Lists* table (see Chapter 18, “[Renaming Fields](#)”).
- **Specimen determination histories** are kept in the *Det History* table (see Chapter 22, “[Determination Histories](#)”)
- **Personnel groups are defined** by records in the *Group* table (see “[Entering Personnel Data: The 'Group' Tab](#)” in Chapter 11).
- **References are linked to Species, Specimen, Collection, or Locality records** through entries in the *Reference Links* table (see Chapter 20, “[References](#)”).
- **Projects are linked to Auxiliary Field names** by means of records in the *Aux Index* table (see Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#)”).

Biota Fields and Relations: Table by Table

The Figures in this section are images captured directly from the “Design Environment” in Biota (not accessible to Biota users). The order of the fields is historical, not alphabetical, so you may have to scan down to find a field you are looking for.

NOTE: For detailed information on Field Types in relation to importing data into Biota, see “[Field Types and Field Lengths](#)” in Chapter 28.

Here are the conventions used in the following figures:

- **The Table Name** is at the top of each list of fields.
- **Boldfaced Field Names** are **indexed fields** (which allows faster sorts and queries on these fields, though all other except Text fields can also be sorted and queried).
- **Arrows show relations** between tables, through Key fields and Linking fields. The 4D convention is that the arrowhead appears at the “one” end of a “many-to-one” relation.
- **Field Type** is indicated in the second column of each Table as follows:
 - ◊ **A nn**, where **nn** is an integer: Alphanumeric field of length **nn** (e.g., A30 means an Alphanumeric field that holds up to 30 characters.)
 - ◊ **D**: Date field
 - ◊ **I**: Integer field
 - ◊ **L**: Long Integer field
 - ◊ **B**: Real number field
 - ◊ **T**: Text field (32,000 character limit)
 - ◊ **D**: Boolean field
 - ◊ **P**: Picture (Image) field
 - ◊ *: Vestigial (deleted) field

Links to the Figures on the Following Pages

[Figure 1](#): Specimen, Determination History, Loans, and Linked Peripheral Tables

[Figure 2](#): Specimen, Species, and Linked Peripheral Tables

[Figure 3](#): Species and Higher Taxon Tables

[Figure 4](#): Collection, Locality and Linked Peripheral Tables

[Figure 5](#): Personnel, Group, Project, and Aux Index Tables

[Figure 6](#): Project and Auxiliary Fields System Tables

[Figure 7](#): Reference System Tables, Image Archive Table, and List Items Table

[Figure 8](#): The Lists Table (with explanation of the function of the table)

Figure 1: Specimen, Determination History, Loans, and Linked Peripheral Tables

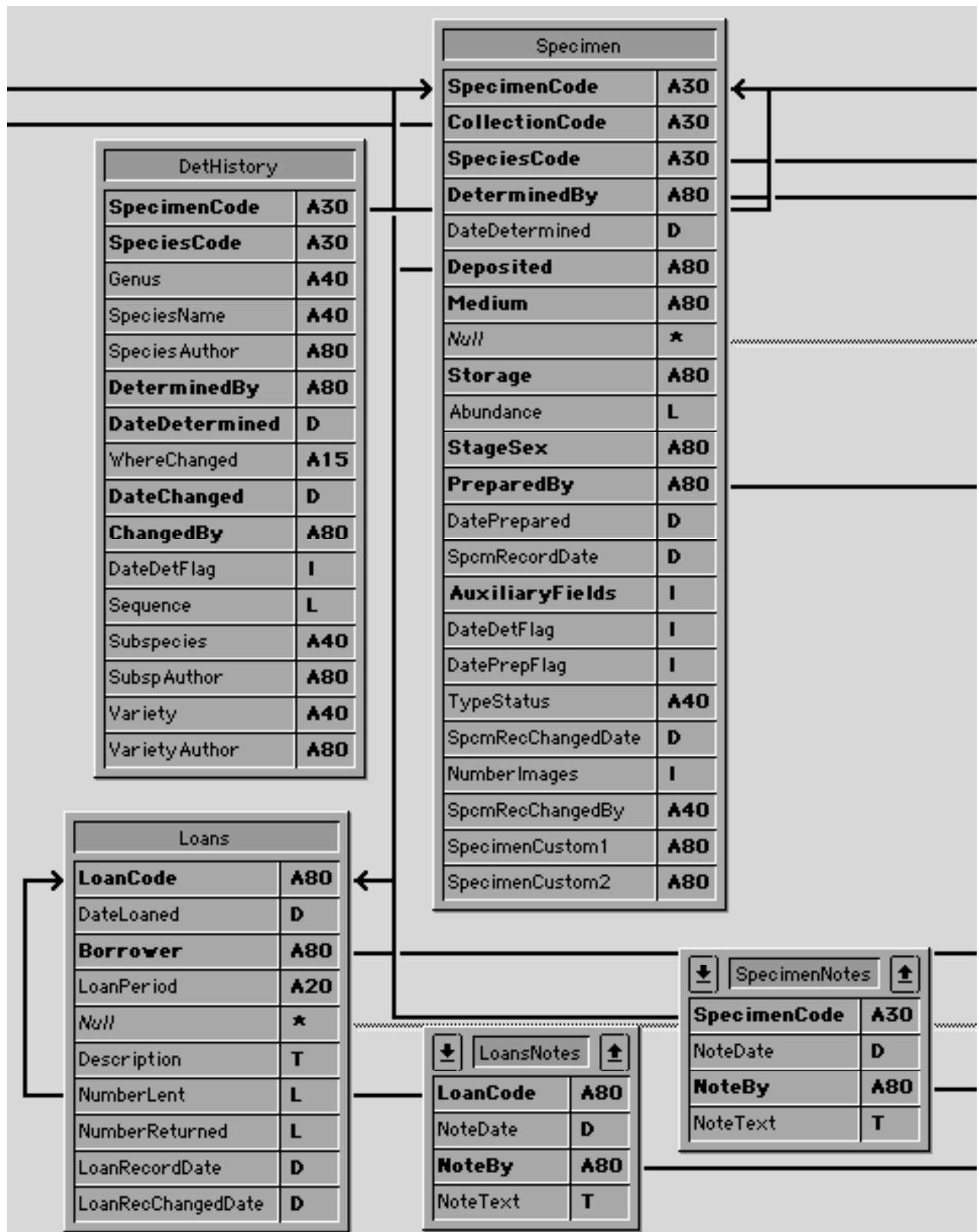


Figure 2: Specimen, Species, and Linked Peripheral Tables

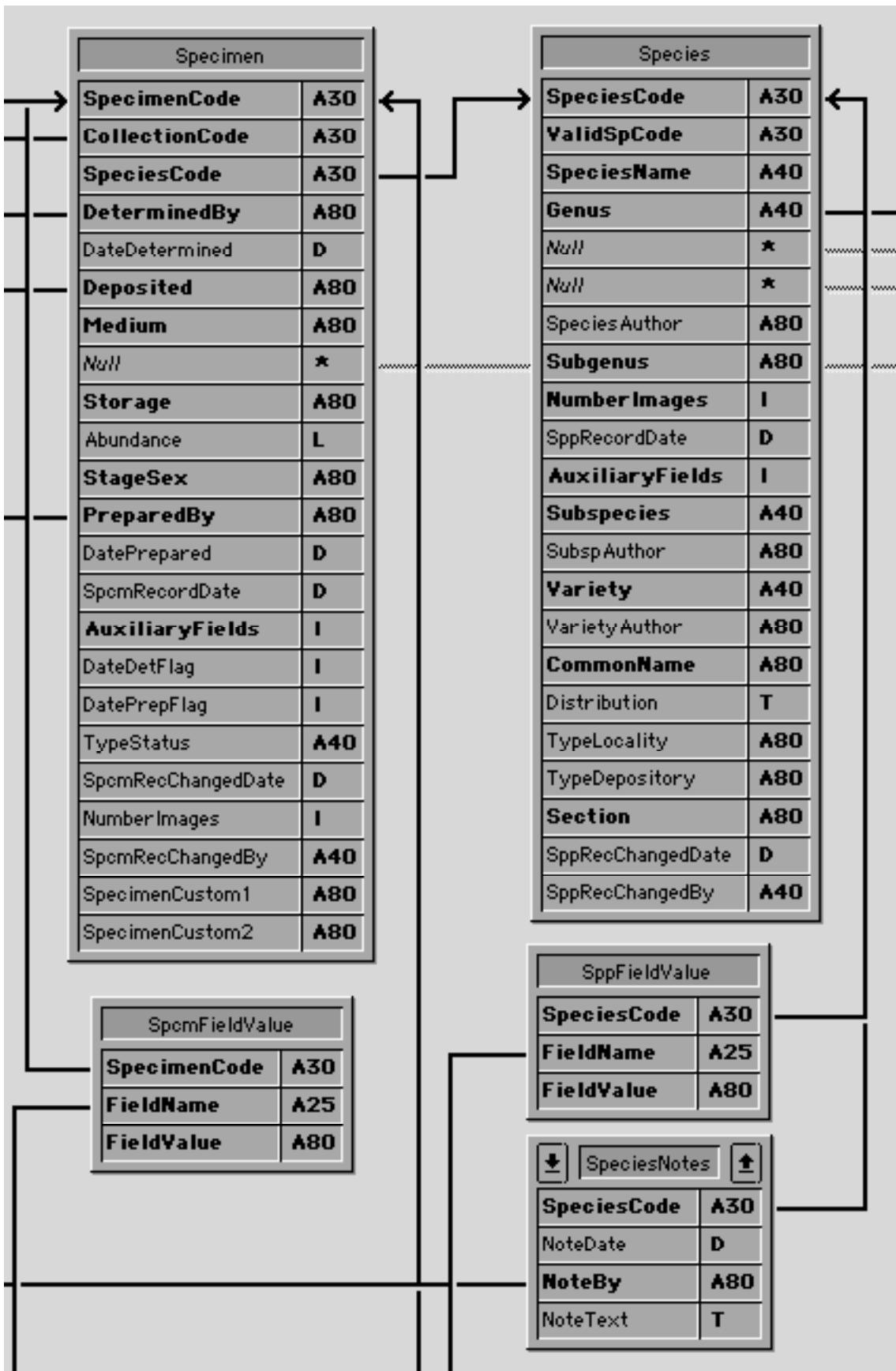


Figure 3: Species and Higher Taxon Tables

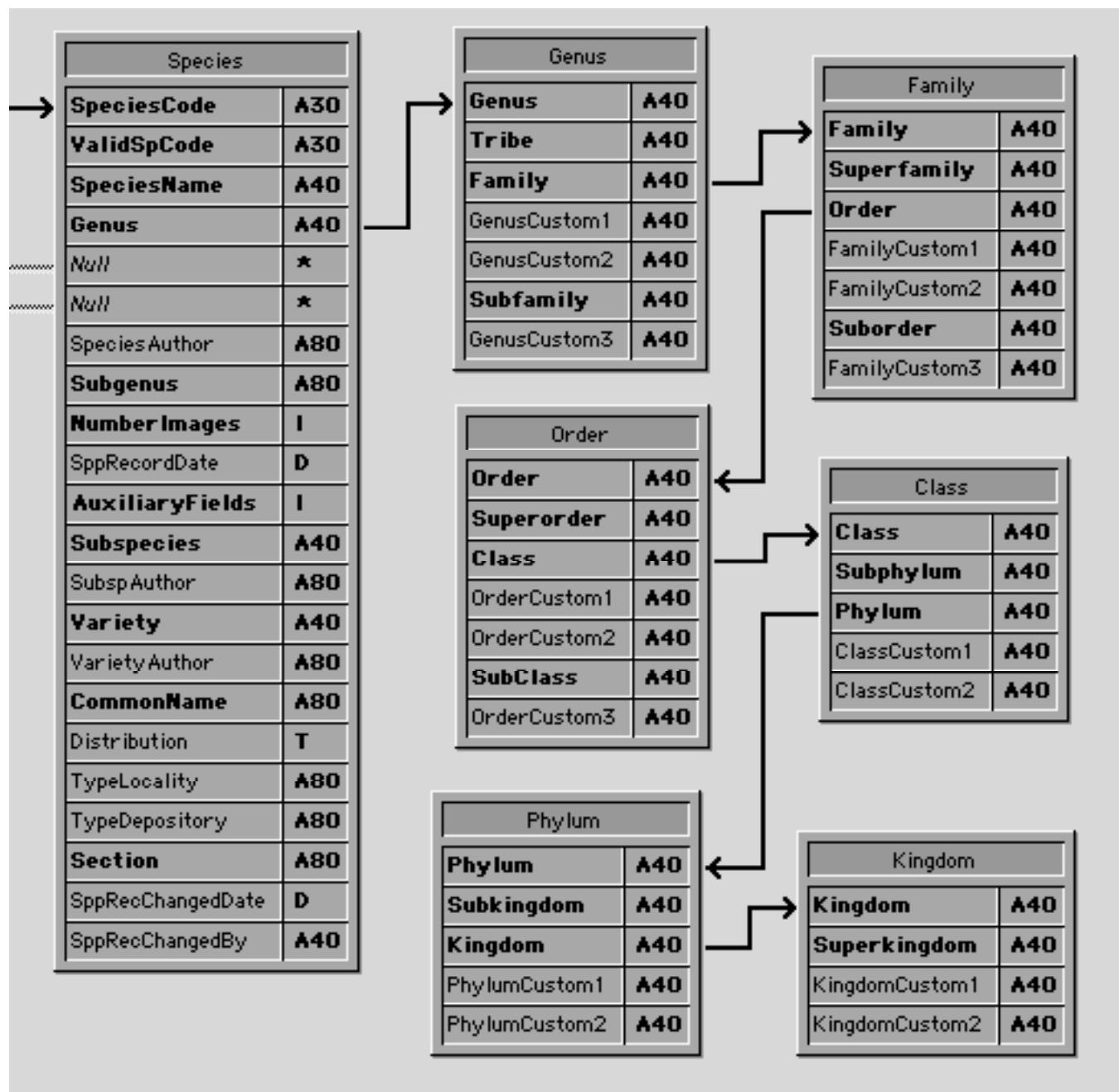


Figure 4: Collection, Locality and Linked Peripheral Tables

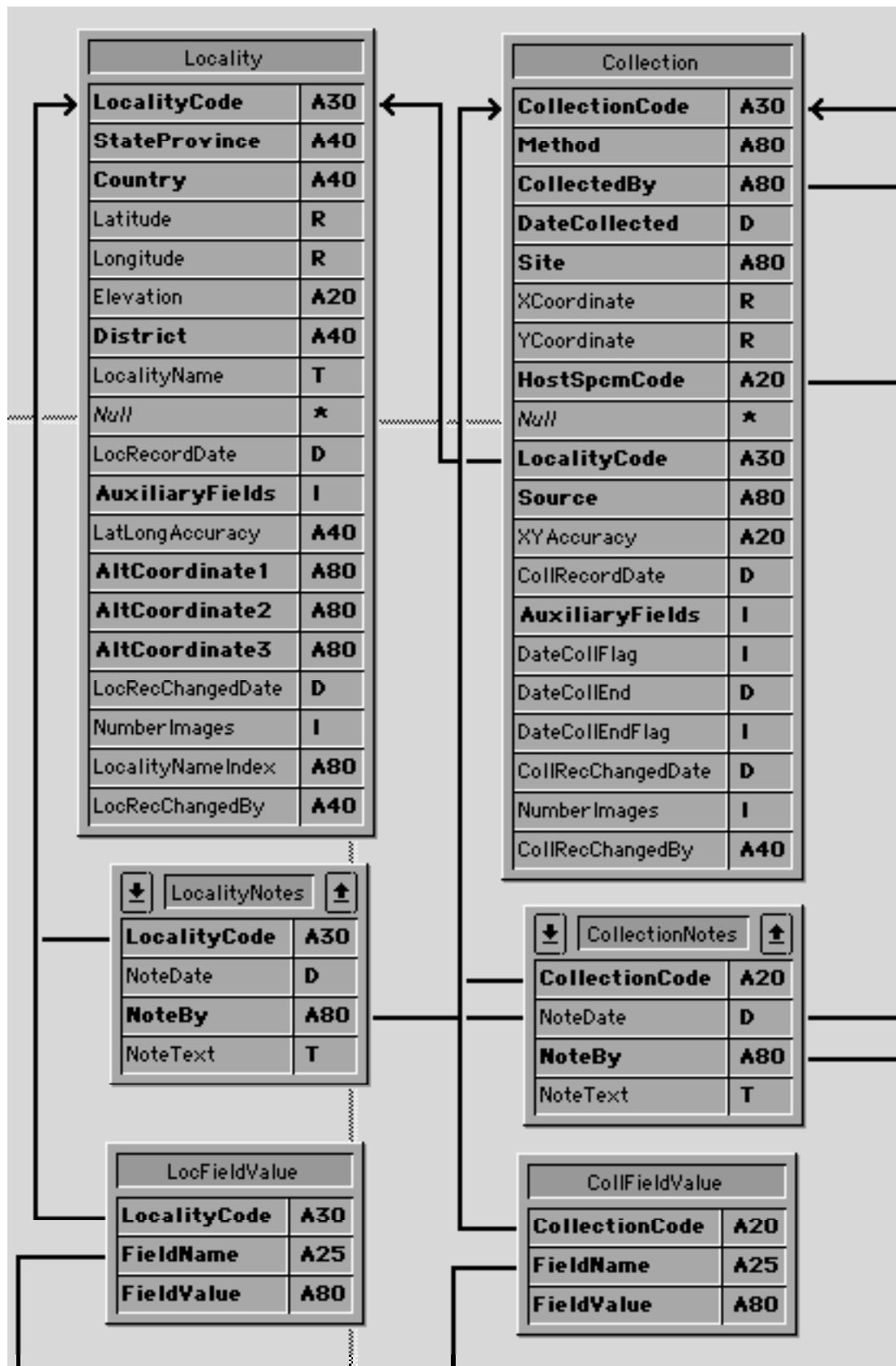


Figure 5: Personnel, Group, Project, and Aux Index Tables

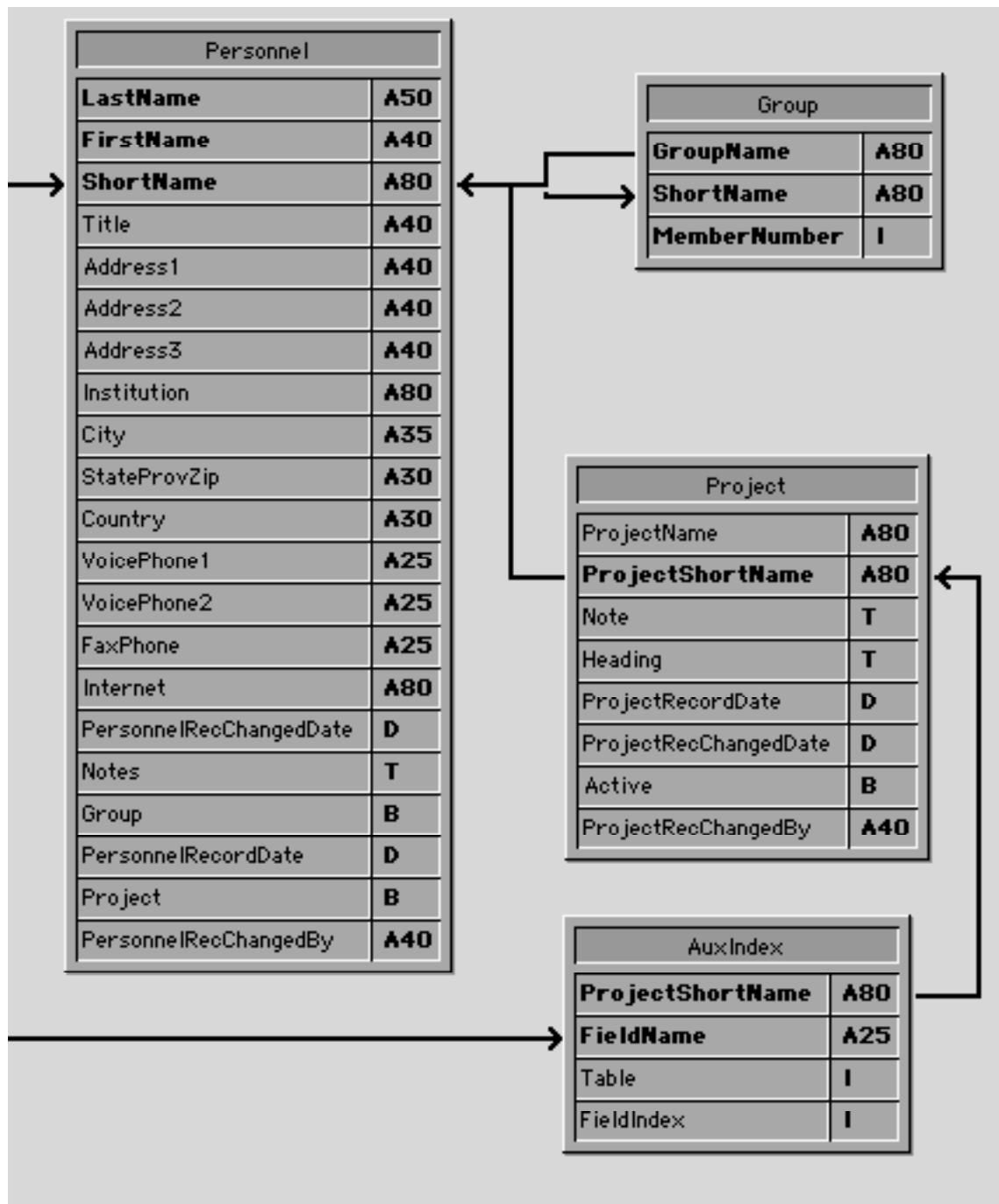


Figure 6: Project and Auxiliary Fields System Tables

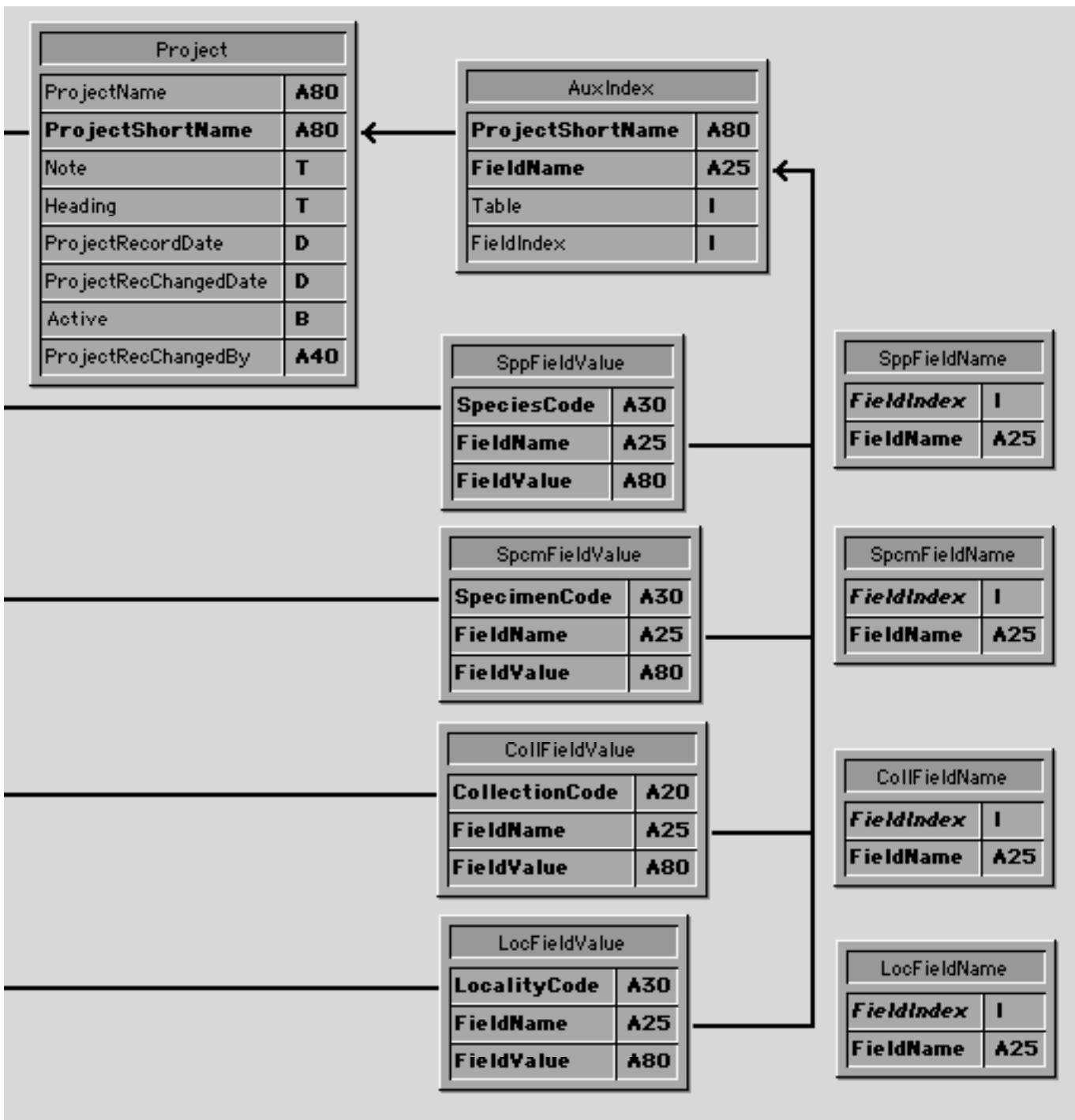


Figure 7: Reference System Tables, Image Archive Table, and List Items Table

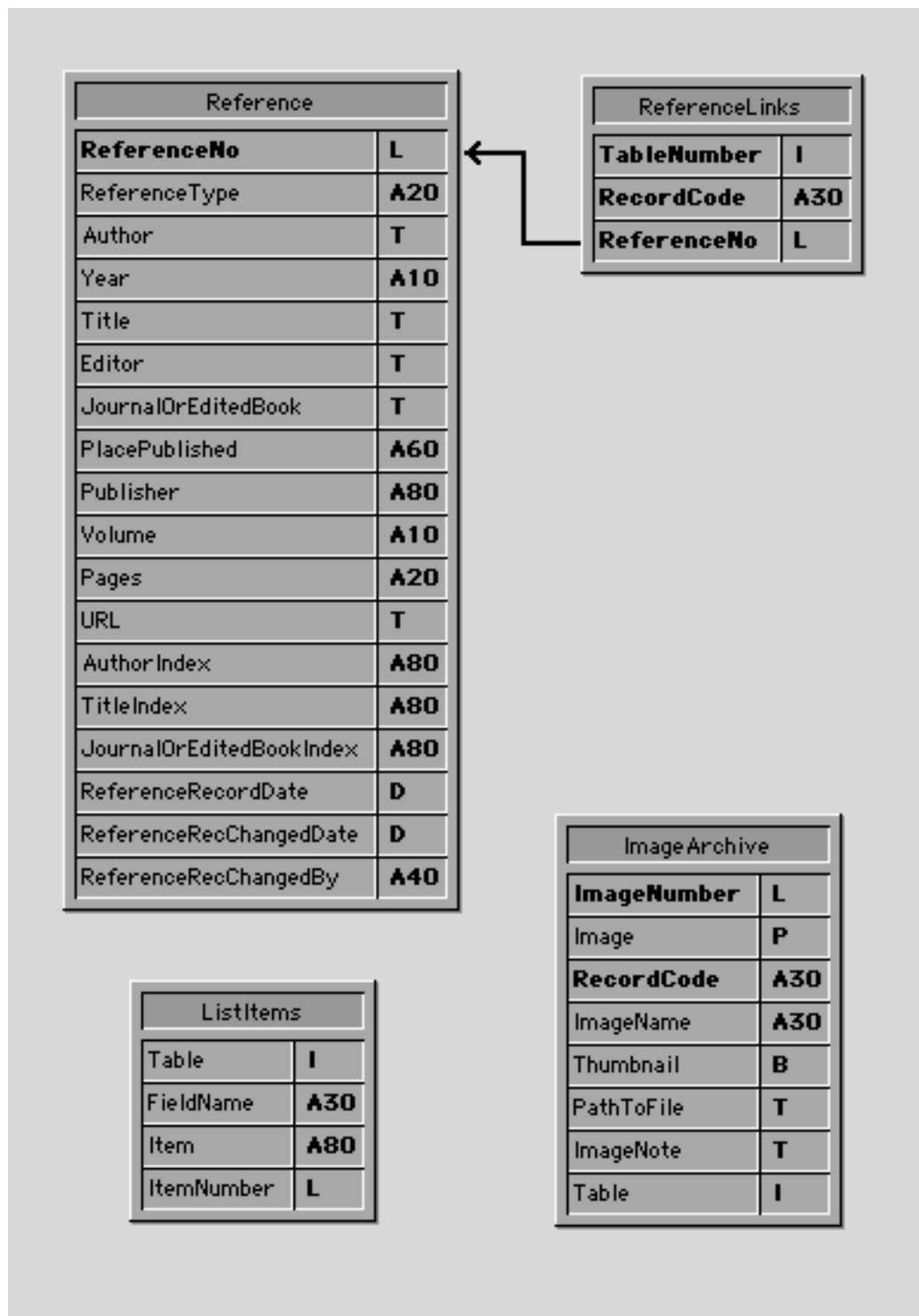


Figure 8: The Lists Table

The Lists table in Biota has two special purposes. It keeps track of Core Field Aliases that you define (see Chapter 18, “[Re-naming Fields](#)”) and it manages the Entry Choice Lists that you create (see “[Using Entry Choice Lists](#)” in Chapter 17).

For most users, the only reason you would ever deal directly with the Lists table is to transfer Lists records from one Biota Data File to another (to a new, blank one, for example). The procedure for exporting Lists records from one Biota Data File and importing them into another is detailed in Chapter 17, in the section “[Transferring Choice Lists to a Different Biota Data File](#).”

This section details the fields, default values, and required records for the Lists table. You should study this section if you intend to create the required records for import into the Lists table using another application (e.g., a spreadsheet application) or if you want to modify exported Lists records before importing them again.

Unlike other Biota tables, each record in the Lists table has a special function, and must be *exactly three Lists records in every Biota Data File*.

- **The three Lists records must have consecutive integer values (1, 2, and 3) for the field [Lists] Record Number.**
- **Record 1 of the Lists table specifies values for “Long” Field Aliases** (see “[Renaming Core Fields: Setting Aliases](#)” in Chapter 18). Biota assigns default values for fields in this record when you create a new Data File (see “[Data Files](#)” in Chapter 2). Any Aliases you later assign replace the defaults.
- **Record 2 specifies values for “Short” Field Aliases.** Biota assigns default values for fields in this record when you create a new Data File. Any Aliases you later assign replace the defaults.
- **Record 3 specifies which Core Fields have Entry Choice Lists currently enabled.** A value of 1 means the List is enabled, a value of 0 means that the List is currently disabled (see “[Activating or Deactivating Choice Lists](#)” in Chapter 17). Biota assigns a default value of 0 to fields in this record when you create a new Data File (see “[Data Files](#)” in Chapter 2).

The diagrams below show the fields of the Lists table. All fields are alphanumeric with the exception of Record Number, which is an integer field.

Each alphanumeric field has the same character length as the field with the same name in Core and Peripheral tables shown earlier in this Appendix.

(See the next page.)

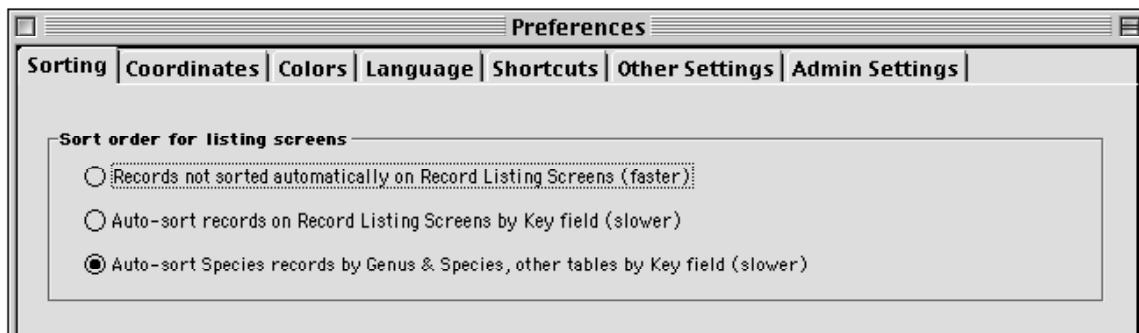
Lists		(Lists table continued)	
SpecimenCode	A20	Superorder	A40
StageSex	A40	Subclass	A40
Medium	A40	OrderCustom1	A40
Storage	A40	OrderCustom2	A40
Deposited	A20	OrderCustom3	A40
CollectionCode	A20	Subphylum	A40
Site	A40	ClassCustom1	A40
Source	A40	ClassCustom2	A40
Method	A40	Subkingdom	A40
CollIXYAccuracy	A20	PhylumCustom1	A40
LocalityCode	A20	PhylumCustom2	A40
LocalityName	A80	Superkingdom	A40
District	A40	KingdomCustom1	A40
StateProvince	A40	KingdomCustom2	A40
Country	A50	RecordNumber	I
LatLongAccuracy	A20	TypeStatus	A20
SpeciesCode	A20	Elevation	A20
SpeciesName	A40	CommonName	A80
SpeciesAuthor	A80	Distribution	A80
Subgenus	A40	TypeLocality	A50
ImageName	A30	TypeDepository	A50
Tribe	A40	SubSpAuthor	A80
Subfamily	A40	VarietyAuthor	A80
GenusCustom1	A40	Section	A40
GenusCustom2	A40	AltCoordinate1	A50
GenusCustom3	A40	AltCoordinate2	A50
Superfamily	A40	AltCoordinate3	A50
Suborder	A40	CollLatLongAccuracy	A20
FamilyCustom1	A40	SpecimenCustom1	A80
FamilyCustom2	A40	SpecimenCustom2	A80
FamilyCustom3	A40		

Appendix B

Setting Preferences

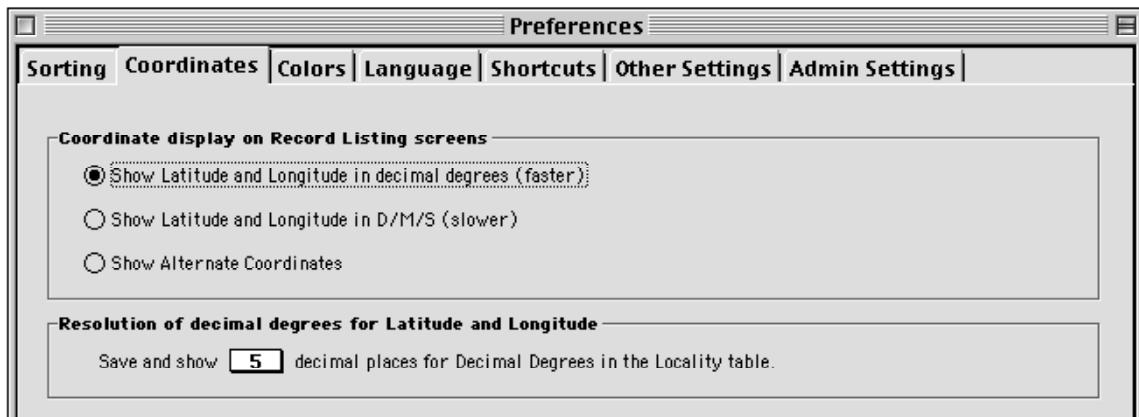
The text and illustrations below direct you to the options you can set using the Preferences screen. You can display this screen by choosing “Preferences” from the Special menu.

The “Sorting” Tab



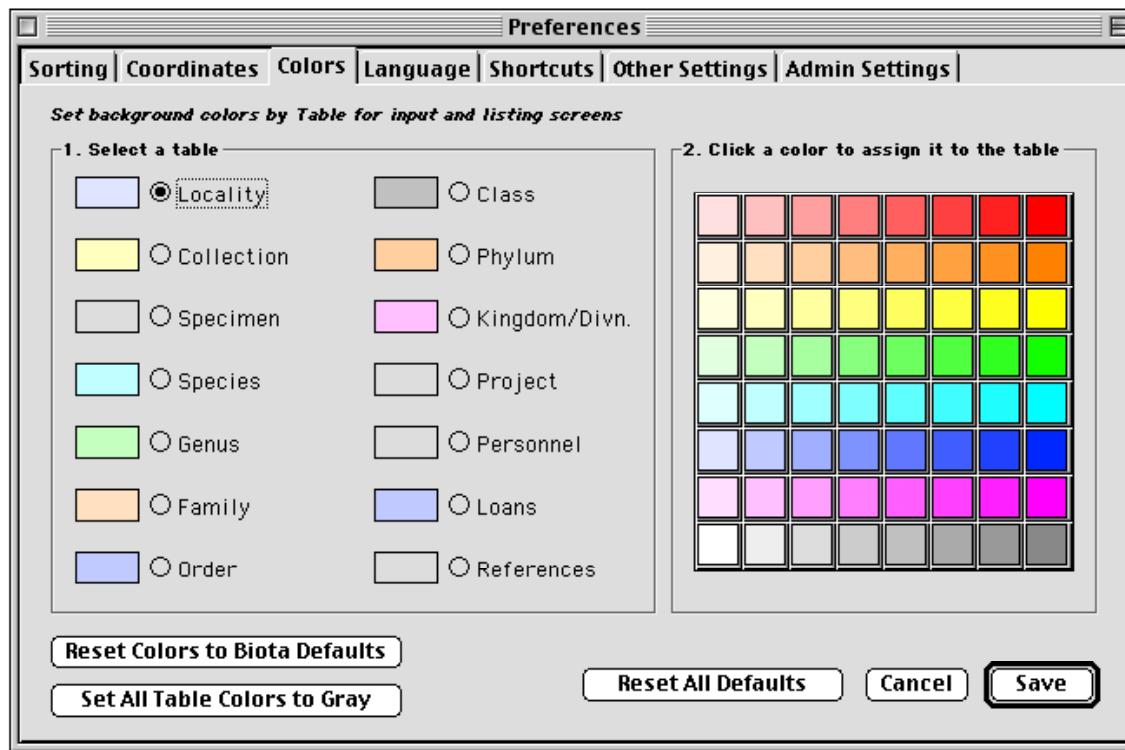
All the options on the “Sorting” tab are discussed in “[Sorting Records by Record Codes](#)” in Chapter 8.

The “Coordinates” Tab



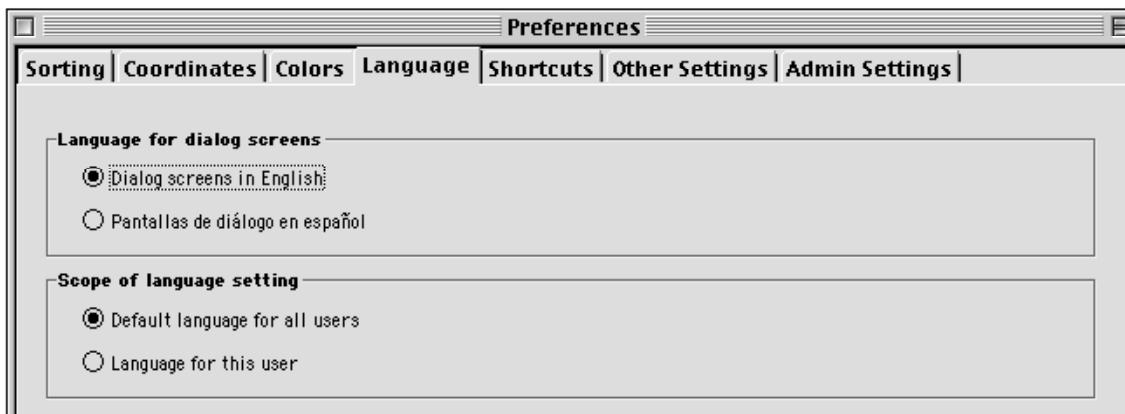
All the options on the “Coordinates” tab are discussed in “[Setting the Display Format and Internal Resolution for Latitude and Longitude](#)” in Chapter 9.

The “Colors” Tab



Use of the “Colors” tab is discussed in the section “[To Change the Screen Color Scheme](#)” in Chapter 7.

The “Language” Tab



Biota is partially bilingual. Spanish language versions are available for all “dialog screens” (instructions, options, warnings, error messages, result reports, and the Preferences screen itself) that are accessible to users with “Read Write Export,” “Read

Export,” or “Read Only” access privileges. (See “[Users, User Names, Passwords, Access Levels, and Privileges](#)” in Chapter 26 for discussion of access levels.)

Biota tools and screens accessible only to users with “Administration” access privileges are available in English only. The justification for this design is that the Administrator needs to be able to read this manual, to use Biota’s most powerful tools safely. All menu bars and menus are in English for all users.

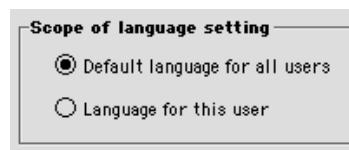
You can enable or disable the Spanish version of the dialog screens in the “Language” tab (illustrated above) or by means of the Startup Procedure assigned to a particular User in the User Password system.

- **Settings in the “Language” tab of the Preference screen**

- ◊ **Use the “Language for dialog screens” options** to set the Language.



- ◊ **Use the “Scope of language setting” options** to control whether the setting on the “Language for dialog screens” applies to all users, or only to the current user.



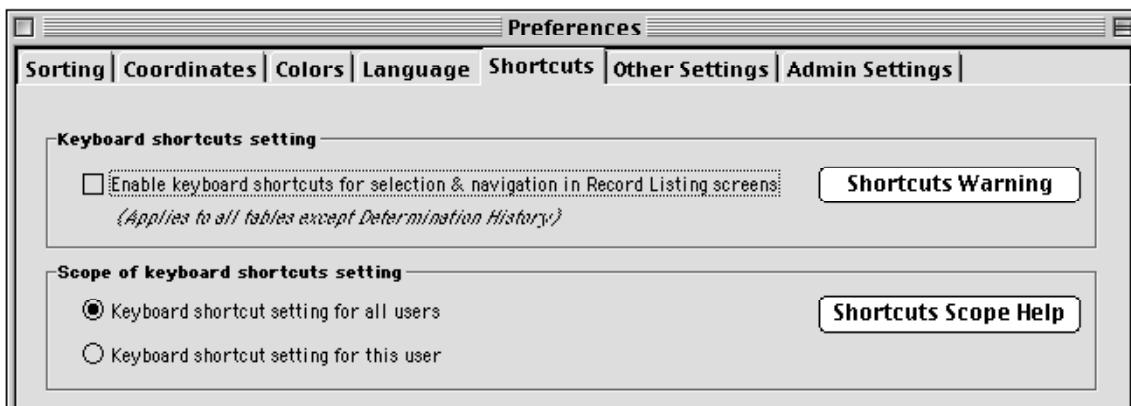
NOTE: See “[The ‘Admin Settings’ tab](#),” later in this appendix, for information on controlling whether Language and other settings are saved between Biota sessions.

- **Using the “Startup Procedure” to control the Language setting for individual users** (See “[Editing a User’s Password and Profile](#)” in Chapter 26 for details.)

Biota has two alternative startup procedures that can be assigned to individual users in the User Password system, *StartupEnglish* and *StartupSpanish*.

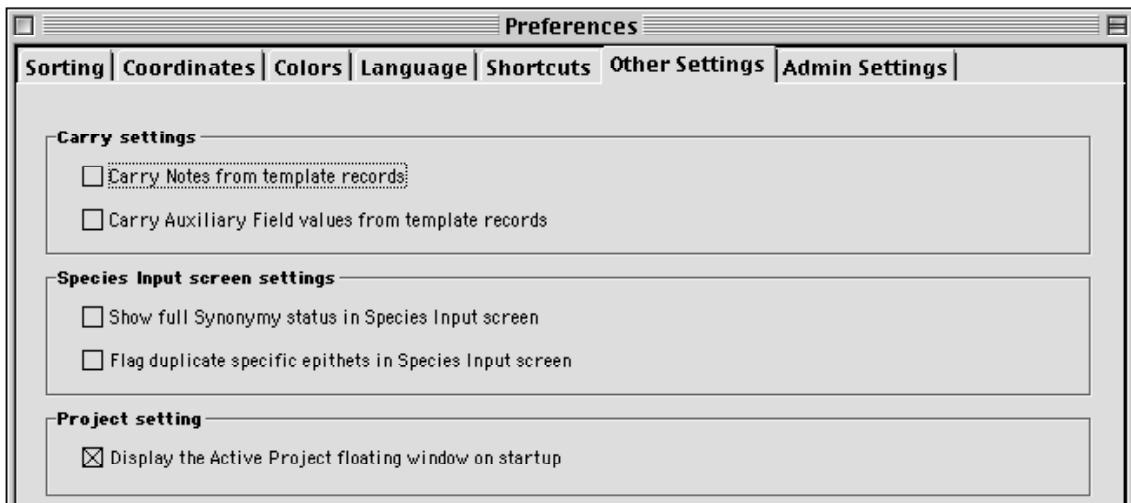
- ◊ **If you assign StartupEnglish** (no spaces) to a particular user, Biota displays the English language version of all dialogue screens for that user, *regardless* of the saved Language setting in the Preferences screen.
- ◊ **If you assign StartupSpanish** (no spaces) to a particular user, Biota displays a Spanish language version of all dialogue screens, *regardless* of the saved Language setting in the Preferences screen.
- ◊ **If you leave the “Startup procedure” blank**, Biota displays dialogue screens in English or Spanish, depending on the saved Language setting in the Preferences screen. If no user is likely to change the Language setting in the Preferences screen, you can leave the Startup procedure setting blank for all users.

The “Shortcuts” Tab



All the options on the “Shortcuts” tab are discussed in “[Optional Keyboard Shortcuts](#)” in Chapter 10.

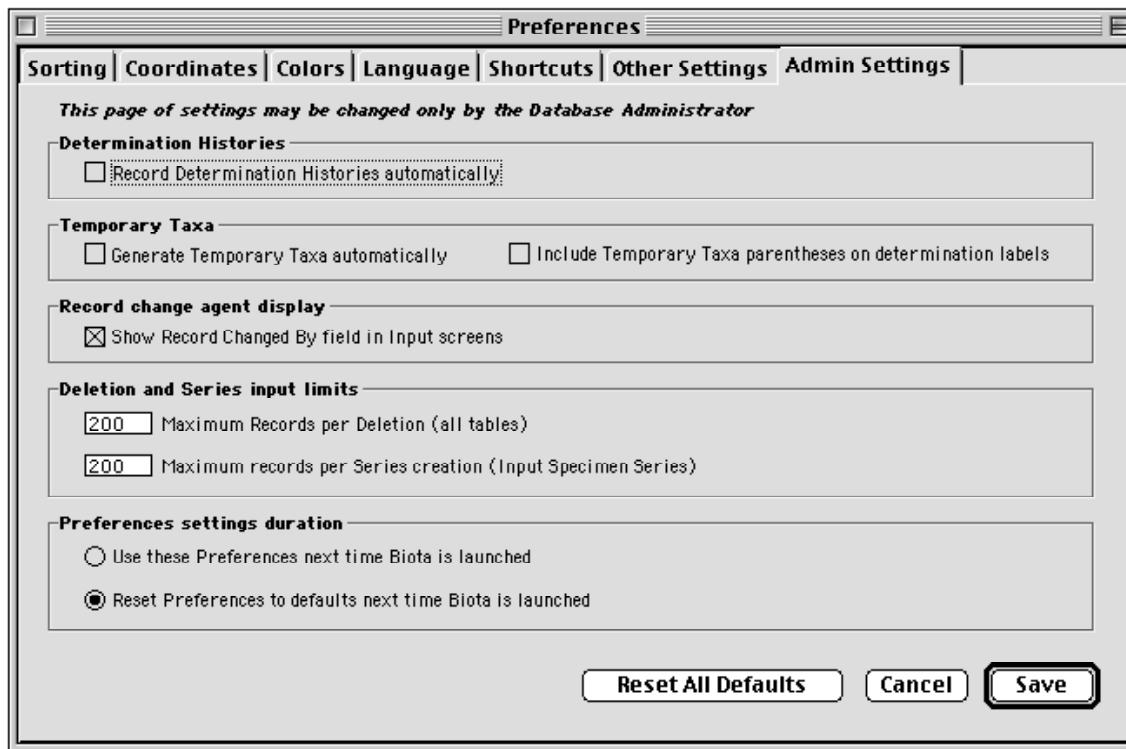
The “Other Settings” Tab



- The “Carry settings” panel.
 - ◊ “**Carry Notes from template records.**” See “[Carrying Notes](#)” in Chapter 11.
 - ◊ “**Carry Auxiliary Field Values from template records.**” See “[Carrying Auxiliary Fields](#)” in Chapter 16.
- The “Species Input screen settings” panel.
 - ◊ “**Show full Synonymy status in Species Input screen.**” See “[To Enable or Disable Full Synonymy Display](#)” in Chapter 23.
 - ◊ “**Flag duplicate specific epithets in Species Input screen.**” See [Step 3 in “Entering Species Data: The ‘Classification’ Tab,”](#) in Chapter 11.

- The “Project Setting” panel.
 - ◊ “Display the Active Project floating window on startup.” See “[Using the Active Project Floating Window](#)” in Chapter 16.

The “Admin Settings” Tab



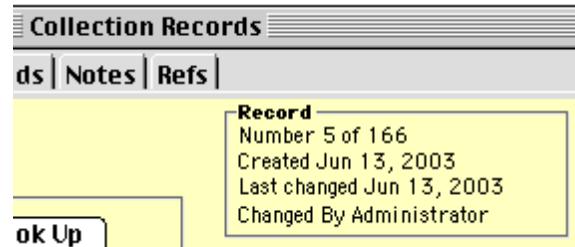
NOTE: This page of settings may be changed only by the Database Administrator, or by another user with Administration privileges.

- The “Determination Histories” panel.
 - ◊ “Record Determination Histories automatically.” See “[Enabling or Disabling the Determination History System](#)” in Chapter 22.
- The “Temporary taxa” panel.
 - ◊ “Generate Temporary Taxa automatically.” See “[Enabling or Disabling Automatic Creation of Temporary Taxon Records](#)” in Chapter 25.
 - ◊ “Include Temporary Taxa parentheses on determination labels.” See “[Temporary Taxa on Determination Labels](#)” in Chapter 25.

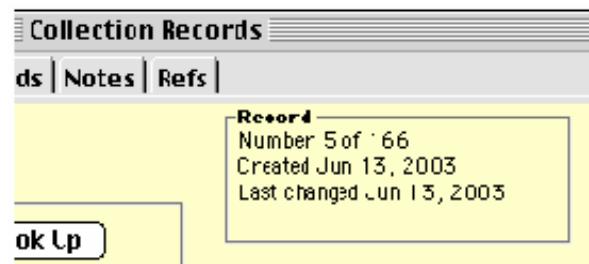
- The “Record change agent display” panel.

- ◊ “Show ‘Record Changed By’ field in Input screens.”

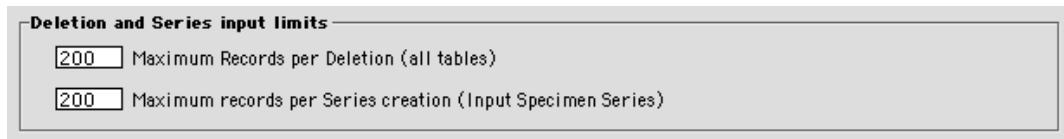
If this option is checked (the default), the Input screen for the Specimen, Species, Collection, Locality, Personnel, Loans, References, and Project tables displays the automatically archived record who last changed each record.



If this option is not checked, this information is hidden.

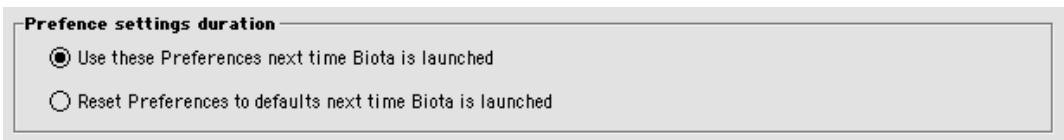


- The “Deletion and Series input limits” panel.



- ◊ “Maximum Records per Deletion (all tables).” The database Administrator can set a limit on the number of records that can be deleted at each use of the “Delete Selection” button on Record Listing screens (see “[Deleting a Group of Records from the Record Listing screen](#)” in Chapter 10), to prevent accidental deletion of large numbers of records. The default is 200.
- ◊ “Maximum records per Series creation (Input Specimen Series).” The database Administrator can set a limit on the number of records that can be created at each use of the “Input Series” tools and “Input and Identify Series” tools (Series menu). See “[Specimen Series Input: Step by Step](#)” in Chapter 13. The default is 200.

- The “Preferences settings duration” panel.



Note: The settings in the “Preferences settings duration” panel are *not* affected by the “Reset All Defaults” button in the Preferences screen.

- ◊ “**Use these Preferences next time Biota is launched.**” The database Administrator can ensure the persistence of all Preference settings (on all tabs) for all users by selecting this option.
- ◊ “**Reset Preferences to defaults next time Biota is launched.**” With this option, Biota resets all Preferences (except for this one) to their default values each time Biota is launched, for all users. Clicking the “Reset All Defaults” button in the Preferences screen produces the same settings, within the current session.

The “Reset All Defaults” Button

Any user can click the “Reset All Defaults” button. If the user lacks “Administration” privileges, however, only the settings on the first six tabs are re-set (all tabs except the “Admin Settings” tab).



Settings on the “Admin Settings” tab can be reset using the “Reset All Defaults” button (or changed manually) only by the database Administrator or another user with “Administration” privileges.

NOTE: The settings in the “Preferences settings duration” panel of the “Admin Settings” tab are *not* affected by the “Reset All Defaults” button in the Preferences screen, even when that button is clicked by the Administrator.

Appendix C

Keyboard Shortcuts

Note: This appendix unites, but duplicates the information in the sections “[Keyboard Shortcuts for Input Screen Tabs](#)” and “[Keyboard Shortcuts for Input Screen Buttons](#)” in Chapter 7, and “[Keyboard Shortcuts for Record Listing Screens](#)” in Chapter 10.

Biota offers many keyboard shortcuts for buttons and tabs in Input screens, and for records in Record Listing screens. This comprehensive set of keyboard shortcuts represents an important feature for people with disabilities, including mouse-related repetitive motion disorders, and to any user who dislikes using the mouse. MS Windows users can also tab between buttons and use the menu shortcuts that Windows automatically provides.

Keyboard Shortcuts for Input Screens

Keyboard Shortcuts for Input Screen Tabs

To avoid using the mouse, you can use keyboard shortcuts to move between tabs in the Input screens for Biota Core tables. The first table below shows the shortcuts that apply to several Core Tables, and the second table below displays shortcuts that apply to only a particular Core Table or Input screen.

FUNCTION	MAC OS	WINDOWS
General tab	COMMAND–G (⌘–G)	CTRL–G
Images tab	COMMAND–I (⌘–I)	CTRL–I
Aux Fields tab	COMMAND–M (⌘–M)	CTRL–M
Notes tab	COMMAND–N (⌘–N)	CTRL–N
Refs tab	COMMAND–R (⌘–R)	CTRL–R

FUNCTION	MAC OS	WINDOWS
<i>Specimen Input screen</i>		
Determination tab	COMMAND–D (⌘–D)	CTRL–D
Preparation tab	COMMAND–B (⌘–B)	CTRL–B
<i>Specimen & Collection (combined) Input screen</i>		
Specimen tab	COMMAND–G (⌘–G)	CTRL–G
Collection tab	COMMAND–H (⌘–H)	CTRL–H
Determination tab	COMMAND–D (⌘–D)	CTRL–D

Preparation tab	COMMAND-B (⌘-B)	CTRL-B
<i>Specimen Series Input screens</i>		
Primary Fields tab	COMMAND-G (⌘-G)	CTRL-G
Other Fields tab	COMMAND-H (⌘-H)	CTRL-H
<i>Species Input screen</i>		
Classification tab	COMMAND-G (⌘-G)	CTRL-G
SubSp/Names tab	COMMAND-H (⌘-H)	CTRL-H
Synonymy tab	COMMAND-B (⌘-B)	CTRL-B
Dist/Types tab	COMMAND-D (⌘-D)	CTRL-D
<i>Collection Input screen</i>		
Host record tab	COMMAND-H (⌘-H)	CTRL-H
Georeference tab	COMMAND-B (⌘-B)	CTRL-B
<i>Locality Input screen</i>		
Georeference tab	COMMAND-B (⌘-B)	CTRL-B

<i>Personnel Input screen</i>		
Create/Edit Group tab	COMMAND-R (⌘-R)	CTRL-R
Create/Edit Note tab	COMMAND-N (⌘-N)	CTRL-N
<i>Project Input screen</i>		
Auxiliary Fields Set tab	COMMAND-M (⌘-R)	CTRL-M
<i>Reference Input screen</i>		
Reference tab	COMMAND-R (⌘-R)	CTRL-R
Links tab	COMMAND-L (⌘-L)	CTRL-L
<i>Loan Input and Loan Return screens</i>		
Loan tab	COMMAND-L (⌘-L)	CTRL-L
Returns tab	COMMAND-R (⌘-R)	CTRL-R

Keyboard Shortcuts for Input Screen Buttons

Keyboard shortcuts are available for most Input screen buttons. (The exceptions are the Delete button and a few others that have far-reaching consequences. These require use of the mouse, for safety's sake.) The table below lists button shortcuts that apply to record Input screens for several tables.

FUNCTION	MAC OS	WINDOWS
Any default button (double border), regardless of function	RETURN (⌘-RETURN)	ENTER
“Cancel” button	COMMAND-RETURN (⌘-RETURN)	CTRL-ENTER

“Save” button	COMMAND–S (⌘–S) or COMMAND–J (⌘–J)	CTRL–S or CTRL–J
“Carry” button	COMMAND–K (⌘–K)	CTRL–K
“Print” button	COMMAND–P (⌘–P)	CTRL–P
Next record button 	COMMAND–RIGHT ARROW (⌘–RIGHT ARROW)	CTRL–RIGHT ARROW
Previous record button 	COMMAND–RIGHT ARROW (⌘–RIGHT ARROW)	CTRL–RIGHT ARROW
Show parent record button (e.g., “Show Genus” Record on the Species Input screen)	COMMAND–UP ARROW (⌘–UP ARROW)	CTRL–UP ARROW
Show child record(s) button (e.g., “Show Specimens” on the Species Input screen)	COMMAND–DOWN ARROW (⌘–DOWN ARROW)	CTRL–DOWN ARROW
First “Assign” button on a screen	COMMAND–EQUALS (⌘–=)	CTRL–EQUALS (=)
Second “Assign” button on same screen	OPTION–EQUALS (OPTION–=)	ALT–EQUALS (=)
Third “Assign” button on same screen	COMMAND–OPTION–EQUALS (⌘–OPTION–=)	CTRL–ALT–EQUALS (=)
First “Look Up” button on a screen	COMMAND–L (⌘–L)	CTRL–L
Second “Look Up” button on same screen	OPTION–L	ALT–L
First “Today” button on a screen	COMMAND–T (⌘–L)	CTRL–T
Second “Today” button on same screen	OPTION–T	ALT–T
Dismiss screen (without saving; same as “Cancel” button, for Input screens)	COMMAND–HYPHEN (⌘–HYPHEN)	CTRL– HYPHEN

The following table lists shortcuts that apply to only a particular Input screen or tab.

FUNCTION	MAC OS	WINDOWS
<i>Image tab (Specimen, Species, Collection, and Locality Input screens)</i>		
“Zoom” (first image) button	COMMAND–E (⌘–E)	CTRL–E
“Zoom 4” (first 4 images) button	COMMAND–F (⌘–F)	CTRL–F
“Save” image button	COMMAND–Y (⌘–Y)	CTRL–Y
<i>Notes tab (Specimen, Species, Collection, Locality and Loans Input screens)</i>		
“New Note” button	COMMAND–T (⌘–T)	CTRL–T
“Save Note” button	COMMAND–Y (⌘–Y)	CTRL–Y
<i>Reference tab (Specimen, Species, Collection, and Locality Input screens)</i>		
“New Reference” button	COMMAND–T (⌘–T)	CTRL–T

“Link Reference” button	COMMAND-L (⌘-L)	CTRL-L
<i>Specimen Input screen</i>		
“Show Species Record” button (first parent record button)	COMMAND-UP ARROW (⌘-UP ARROW)	CTRL-UP ARROW
“Show Collection Record” button (second parent record button)	OPTION-UP ARROW	ALT-UP ARROW
<i>Input & Identify Specimen Series screen</i>		
“Show Species Record” button (first parent record button)	COMMAND-UP ARROW (⌘-UP ARROW)	CTRL-UP ARROW
“Show Collection Record” button (second parent record button)	OPTION-UP ARROW	ALT-UP ARROW
<i>Loan Input and Loan Return screens</i>		
“Add More Specimens” button	COMMAND-J (⌘-J)	CTRL-J
“Reprint Loan Form” button	COMMAND-P (⌘-P)	CTRL-P
“List Specimens” button	COMMAND-DOWN ARROW (⌘-DOWN ARROW)	CTRL-DOWN ARROW

Keyboard Shortcuts for Record Listing Screens

You can use keyboard shortcuts for most functions in Record Listing screens. Some are always available and other must be enabled in the Preferences screen.

Keyboard Shortcuts Always Available

The table below summarizes shortcuts that are always available in Records Listing screens. The following section, “[Optional Keyboard Shortcuts](#),” describes shortcuts available only if you enable them in the Shortcuts tab of the Preferences screen (Special menu).

In the table below, shortcuts for on-screen buttons are indicated with a lavender background, whereas shortcuts that do not correspond to an onscreen button are indicated with a yellow background. Most of the button functions are described in Chapter 10, “[Working With Records in Record Listing and Input Screens](#),” but a few are detailed in other chapters:

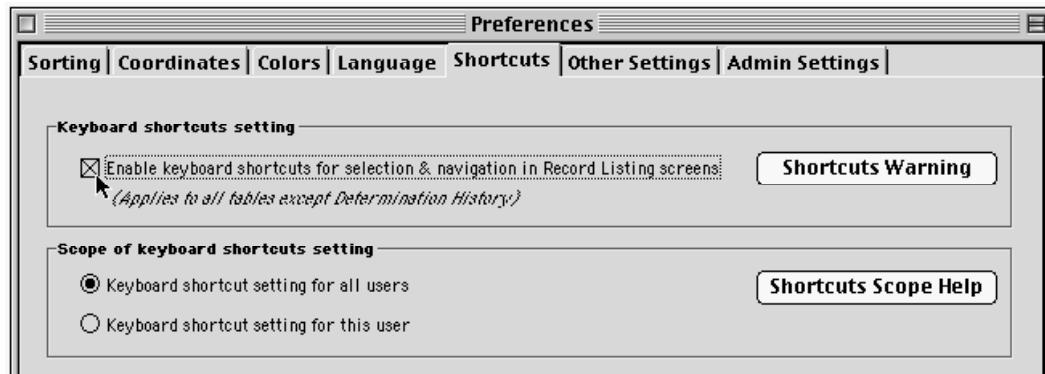
- **The Aux Fields button** is described in Chapter 16, “[User-Defined Auxiliary Fields and the Project System](#).”
- **The Scroll and Page (Display Images) buttons** are described in Chapter 19, “[Images](#).”

FUNCTION	MAC OS	WINDOWS
“Done” button	RETURN	ENTER
“Print” button	COMMAND-P (⌘-P)	CTRL-P
“Sort” button	COMMAND-R (⌘-R)	CTRL-R

“Sub-Selection” button	COMMAND–N (⌘–N)	CTRL–N
Add Record button (e.g., “Add Species”)	COMMAND–J (⌘–J)	CTRL–J
“Aux Fields” button (Core fields screens)	COMMAND–M (⌘–M)	CTRL–M
“Core Fields” button (Auxiliary fields screens)	COMMAND–M (⌘–M)	CTRL–M
“Scroll” (Display Images) button	COMMAND–H (⌘–H)	CTRL–H
“Page” (Display Images) button	COMMAND–I (⌘–I)	CTRL–I
Close screen (with Record Set Query screen; same as “Done” button)	OPTION–W	ALT–W
Dismiss screen (bypassing the Record Set Query screen)	COMMAND–HYPHEN (⌘–HYPHEN)	CTRL–HYPHEN

Optional Keyboard Shortcuts

This section summarizes keyboard shortcuts for Record Listing screens that become available only if you enable them in the Shortcuts tab of the Preferences screen (Special menu), shown below. (See also Appendix B, “[Setting Preferences](#)”).



- In the “Keyboard shortcuts setting” panel, you indicate whether the shortcuts in the table below are to be enabled (checkbox checked) or disabled (checkbox empty).
- In the “Scope of keyboard shortcuts settings” panel, you control the scope of the setting in the “Keyboard shortcuts setting” panel.
 - ◊ If you select the first option, “Keyboard settings for all users” (the default setting), the keyboard shortcuts setting is saved between Biota sessions and affects all users if you are running Biota4D under 4D Server.
 - ◊ If you select the second option, “Keyboard settings for this user,” you must reset your preferred keyboard shortcut setting each time Biota is launched, if it differs from the setting most recently saved under the first option. With the second option, any changes you make in the keyboard shortcuts setting will not affect other users under 4D Server.

- **These optional shortcuts are not enabled** when you first create a new Biota Data File, so if you want to use them you must specifically enable them.
- **These shortcuts do not apply** to the Record Listing screen for the Determination History table.

Function	Mac OS	Windows
Next record	DOWN ARROW	DOWN ARROW
Previous record	UP ARROW	UP ARROW
Last record	PAGE DOWN	PAGE DOWN
First record	PAGE UP	PAGE UP
Select or deselect highlighted record	SPACE BAR	SPACE BAR
Display selected record(s) in the input screen	SEMI-COLON (;)	SEMI-COLON (;)

WARNING: With the optional keyboard shortcuts for Record Listing screens enabled, if you use the mouse or another pointing device to select a record (single click) in the second or higher page of records in the Record Listing screen, the clicked record immediately scrolls to the top the display. (No scrolling occurs with the *first* page of records.)

For this reason, if you use a mouse or another pointing device to *open* a record from the Record Listing screen while the optional shortcuts are enabled, you must first select the record with *one* mouse-click, *wait* for the record to scroll to the top of the list, *then* double-click the record to open it in the Input screen. If you double-click a record without waiting for the scrolling to occur, the second click may open the wrong record. Using the semicolon key to open a selected record or records (details in the next section, “[Using the Optional Keyboard Shortcuts for Record Selection and Revision](#)”) avoids this problem entirely.

A warning regarding this behavior appears when you first enable the optional shortcuts and, as a reminder, each time Biota is launched while the optional shortcuts are enabled. Unfortunately, there is currently no way to alter this 4D behavior with programming.

Using the Optional Keyboard Shortcuts for Record Selection and Revision

With the optional keyboard shortcuts for Record Listing screens enabled (see the previous section, “[Optional Keyboard Shortcuts](#)”), you can select individual records or groups of records in the Record Listing screen for a table without using the mouse or other pointing device, then display the selected group of records in the record Input screen for the table.

- **To highlight a record**, use the up and down arrow keys to move one record at a time
- **To select a highlighted record**, click the keyboard space bar. When you move the highlight to another record, the selected record remains highlighted.

- **To add another record to the highlighted selection**, move to that record and click the keyboard space bar. You can create a highlighted selection including any number of records, whether they are consecutive on the screen or not.
- **To remove a record from the highlighted selection**, move to that record and click the keyboard space bar. No other record in the selection will be affected.
- **To display a highlighted record or a highlighted selection of records in the Input screen**, click the semicolon key on the keyboard. The highlighted record or the first record in a highlighted selection appears in the Input screen for the table.
- **The behavior of the navigation buttons** (“Navigate records”) in the Input screen depends on how many records you highlighted in the Record Listing screen before clicking the semicolon key to display the Input screen.
 - ◊ **If only one record was highlighted**, the navigation buttons operate just as they do when the optional keyboard shortcuts are disabled, and you open a record in the Input screen with a mouse double-click. The navigation buttons in the Input screen access all the records in the selection of records in the Record Listing screen.
 - ◊ **If more than one record was highlighted**, the navigation buttons in the Input screen access only the records that were highlighted in the Record Listing screen. In this case, other records in the full selection in the Record Listing screen are not accessible with the navigation buttons. This behavior is quite useful for viewing or editing a subset of the records in the current selection, without using the Sub-Selection button and thereby losing view of the rest of the full selection.



WARNING: With the optional keyboard shortcuts for Record Listing screens enabled (see the previous section, “[Optional Keyboard Shortcuts](#)”), if you use the mouse or another pointing device to select a record (single click) in the second or higher page of records in the Record Listing screen, the clicked record immediately scrolls to the top of the display. (No scrolling occurs with the *first* page of records.)

For this reason, if you use a mouse or another pointing device to *open* a record from the Record Listing screen while the optional shortcuts are enabled, you must first select the record with *one* mouse-click, *wait* for the record to scroll to the top of the list, *then* double-click the record to open it in the Input screen. If you double-click a record without waiting for the scrolling to occur, the second click may open the wrong record. Using the semicolon key to open a selected record or records (details above in this section) avoids this problem entirely.

A warning regarding this behavior appears when you first enable the optional shortcuts and, as a reminder, each time Biota is launched while the optional shortcuts are enabled. Unfortunately, there is currently no way to alter this 4D behavior with programming.

Appendix D: The 4D Label Wizard

4th Dimension's Label Wizard provides a convenient way to print a wide variety of labels.

With the Label editor, you can do the following:

- Design labels for specimens, file folders and file cards, and for many other needs
- Specify the font, font size, and style to be used for the labels
- Specify the number of labels across and down on each page
- Specify the label page margins
- Load and save label designs
- Print labels

The Label Wizard

You use the Label Wizard to create, format, and print Custom labels in Biota. The Label Wizard contains settings for designing labels and positioning the labels on label paper. For example, when producing mailing labels, you might want a label design that includes the person's first and last name on the first line, the street address on the second line, and so on.

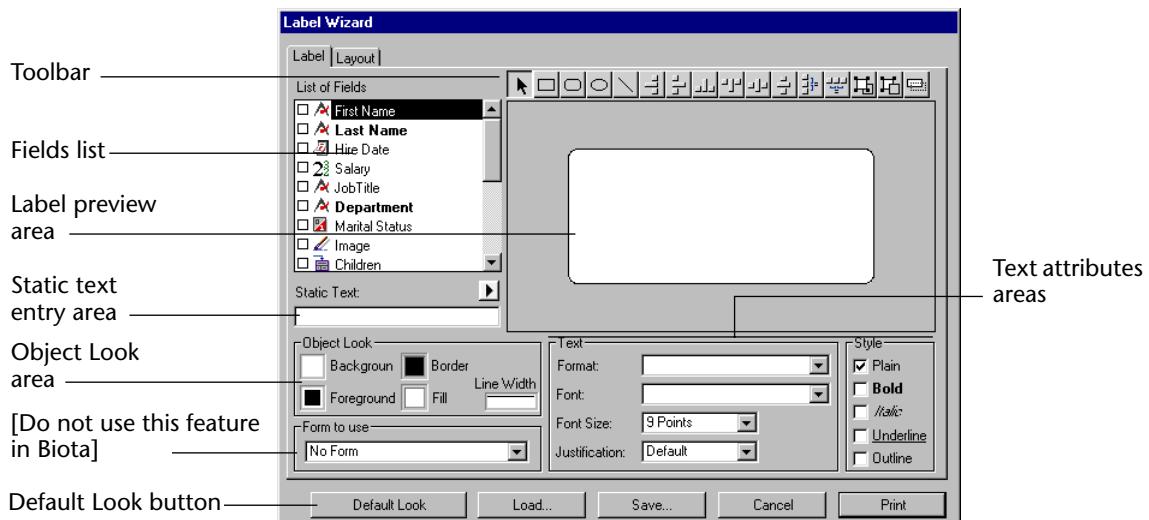
As part of the design, the Label Wizard enables you to specify the number of labels on the page and the margins of the label paper so that the label text is centered within the labels.

The Label Wizard consists of two pages, the Label page and the Layout page, each identified by a tab at the top of the dialog box. You use the Label page to specify the content of the label and the Layout page to define the size and position of the labels on the page. When you create a satisfactory label design, you can save it to disk so that you can reuse it.

Opening the Label Wizard

To open the Label Wizard:

- Choose "Design & Print Custom Labels" from Biota's Labels menu.
(See "[Designing and Printing Custom Labels](#)" in Chapter 15.)



Label Page

The Label page contains settings for designing and formatting labels.

The Label page contains the following elements:

- **Fields list** This area displays the names of the fields in the current table in a hierarchical list. If this table is related to other tables, the foreign key fields have a plus sign (on Windows) or an arrow (on Macintosh). You can display fields from the related table by expanding the relating fields. The fields in the related table are indented.

Note This Appendix has been slightly modified from the the 4D user manual, with permission of 4D Inc. For this reason, the examples *do not refer to Biota tables and fields.*

- **Label preview area** You use this area to design your label.
- **Toolbar** The Label Wizard toolbar contains tools for drawing, selecting, aligning, distributing, layering, and duplicating objects. For complete information on the toolbar, see the section “[The Label Wizard Toolbar](#)” later in this Appendix.
- **Object Look area** These controls let you specify foreground and background colors, fill patterns, and borders for individual objects on the label.
- **Default Look button** This button applies the default set of Object Look attributes to the selected object.
- **Static Text entry area** This area allows you to add static text objects to the label.
- **Text attributes areas** These controls allow you to specify the font, font size, display format, and style of the text.
- **Form to Use drop-down list** This drop-down list has no function in Biota. Do not change the setting from the default, "No Form."

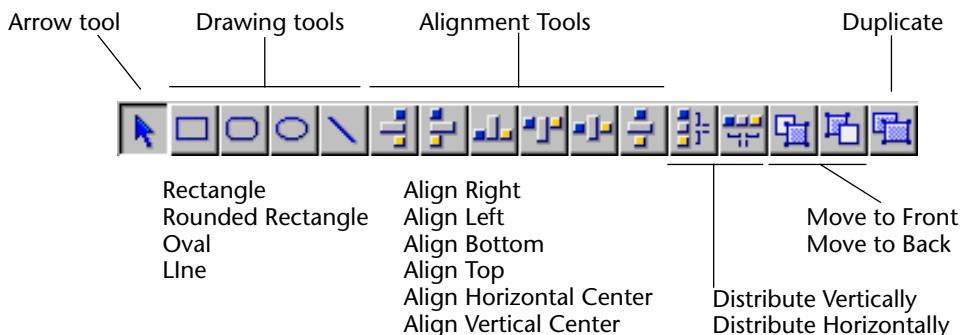
Layout Page

The Layout page contains controls for printing labels based on the requirements of the printer you selected in the Print Manager (Chooser on Macintosh), so that it can format the page accurately.

For complete information on the Layout page, see the section “[Specifying the Label Layout](#)” later in this Appendix.

The Label Wizard Toolbar

The Label Wizard toolbar contains the following tools.



Creating a Label Design

You create a label by dragging field names to the Label Preview area, adding static text, drawing graphic objects using the graphics tools in the toolbar, and pasting graphics from the Clipboard. You can edit the label by distributing, moving, resizing, layering, and aligning objects. With the Object Look and Text attribute areas, you can control the font attributes, foreground and background colors, fill patterns, and borders of individual objects.

The Label Preview area shows the approximate size and shape of the selected label. Before adding elements to the label, you may want to specify your label paper and label dimensions using the Layout page. For information, see the section “[Specifying the Label Layout](#)” later in this Appendix.

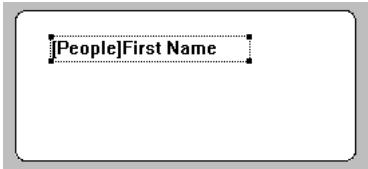
Note You cannot add a formula (a variable) to a label with the Label Wizard.

► To create a label:

- 1 **Drag the first field you want to display in the label from the Fields list to the Label Preview area.**

If the field is in a related table, expand the relating field to display the fields in the related table.

Your field is added to the Label Preview area. Selection handles indicate that it is selected.



- 2 If you want to concatenate a field to this field, drag the new field from the Field list to the existing field.

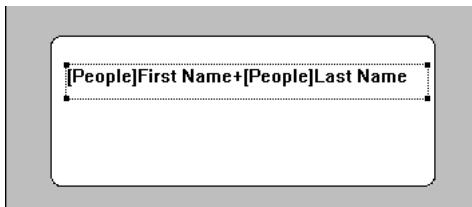
OR

If you want to concatenate two fields using the Return character as the separator, drag the new field by holding down the Shift key.

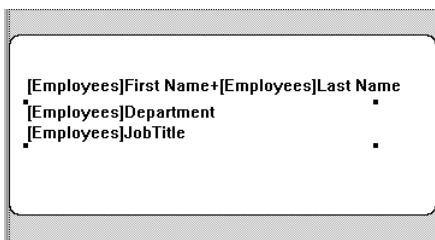
OR

Otherwise, continue dragging fields to the Label Preview area.

- When you concatenate two fields by simply dragging and dropping them, the separator used is the one defined in 4th Dimension's resources. By default, the Space character is used. A “+” between field names in a field object indicates that the fields are concatenated on a single line. When 4th Dimension prints the label, it will insert a space between the fields on the same line. The following illustration shows the concatenation of the First Name and Last Name fields.



- If you concatenate two fields by dragging and dropping the second field while holding down the Shift key, the Return character is used as the separator. When the labels are being printed, if the second field is empty, its position is deleted and is replaced by the next field. If a field contains some text with Return characters, they are taken into account.



For example, this feature allows you to create address labels by using many concatenated fields ([Clients]Address1, [Clients]Address2, etc.) without generating an empty line when a field is blank.

You can automatically resize a group of concatenated fields so that it corresponds to the number of lines that it contains. To do so, **Ctrl+click** (Windows) or **Command+click** (MacOS) on the lower right handle of the group.

As you add fields, you can reposition them by dragging or using the alignment tools in the toolbar.

- 3 **To add a text element to the label, enter the text in the Static Text area and click the arrow ►.**

The static text object is added to the Label Preview area. The following illustration shows a static text element being added to the label.



After you add the element to the label, you can reposition it by dragging and aligning it with other objects.

- 4 **(Optional) Using a drawing tool, draw any graphic objects that you want to add to the label.**

For example, you could add different backgrounds to the "TO:" and "FROM:" sections of the label.

- 5 **(Optional) Paste a graphic from the Clipboard into the Label Preview area.**

For information on adding a graphic to the label, see the section "[Adding a Graphic to the Label](#)" later in this Appendix

After you add all required elements to the Label Preview area, you can use any of the editing tools to modify the label design. For complete information, see the section "[Working with Label Wizard Objects](#)" later in this Appendix.

How the Label Wizard Handles Blank Fields

Some records in your database may not contain entries for every field. When printing labels, the Label Wizard handles blank fields intelligently. Instead of leaving gaps where the data should be, the Label Wizard concatenates the data.

If a field in a line contains no data for a particular record, 4th Dimension concatenates the remaining fields in the line without leaving a blank space for the missing data.

If an entire line contains no data for a particular record, 4th Dimension vertically concatenates the remaining lines in the label without leaving a blank line.

4th Dimension automatically centers the text of the label inside the label area.

Clearing Fields

If you make a mistake, you can remove one or more fields from the label.

- ▶ To remove an object:
- **Select the object and press Backspace (Delete on Macintosh).**

The selected object is removed. If the object is a row of concatenated fields, pressing Backspace removes only the last field in the row. Continue pressing Backspace to remove more fields from the row.

Working with Label Wizard Objects

This section discusses the techniques for editing objects placed on the label. It includes:

- Creating graphic objects,
- Aligning objects,
- Distributing objects,
- Layering objects,
- Duplicating objects,
- Moving objects,
- Resizing objects,
- Adding a border to an object,
- Adding foreground or background fill colors, patterns, and borders,
- Pasting a graphic into the label,
- Deleting objects.

Creating Graphic Objects

You can create a graphic object by drawing.

- To create an object:

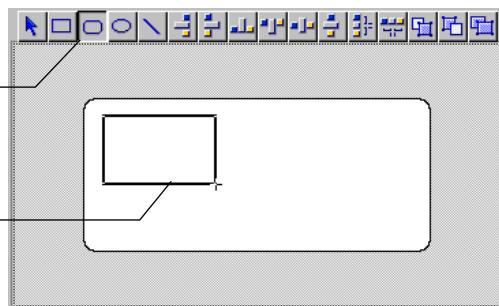
1 Select the type of object you want to draw by clicking its tool in the toolbar.

The pointer becomes a crosshair when it is over the Label Preview area.

2 Drag to create an area for the object.

For two-dimensional objects (ovals, rectangles, and rounded rectangles), drag diagonally.

1 Select the drawing tool you want to use



2 Drag to draw the object

Note Hold down the Shift key as you draw to constrain the object to a regular shape. Lines are constrained to horizontal or vertical, rectangles are constrained to squares, and ovals are constrained to circles.

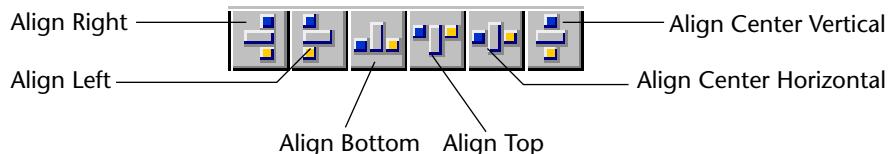
3 When you have finished drawing the object, release the mouse button.

4th Dimension creates the object and makes it the currently selected object. The Arrow tool is automatically selected and the pointer becomes an arrow.

Aligning Objects

The alignment tools let you align objects to each other. When you align one object to another, you can align it to the top, bottom, side, or horizontal or vertical center of the other object.

The following illustration shows the Label Wizard's alignment tools.



The arrangement of lines represents the function of each tool. For example, the Align Right icon shows the lines aligned vertically on the right side of the box. The Align Center Vertical icon shows the lines aligned vertically in the middle.

- ▶ To align a set of objects:
 - 1 **Select the objects that you want to align.**
Shift-click to select several objects.
 - 2 **Click the alignment tool that corresponds to the alignment you want.**
4th Dimension aligns the selected objects according to the alignment you selected.

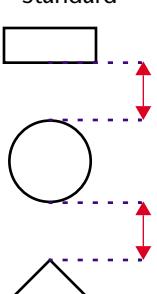
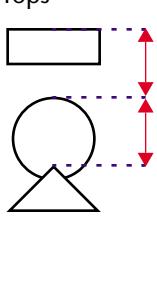
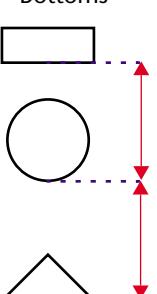
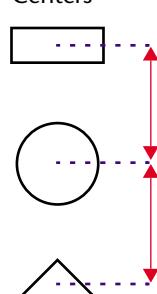
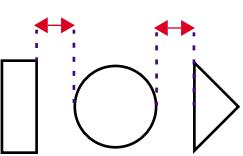
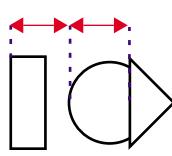
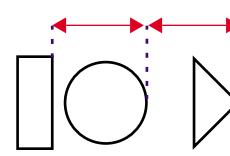
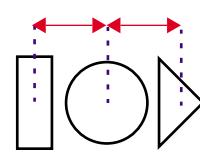
Distributing Objects The toolbar includes two tools that let you distribute three or more objects evenly.



When you use either tool, you can modify its action by holding down the **Shift** or **Alt** keys when you click either tool.

- **Clicking** Distributes the objects from their adjacent sides,
- **Shift+Clicking** Distributes the objects from their left sides (horizontal) or tops (vertical),
- **Alt+Clicking** Distributes the objects from their right sides (horizontal) or bottoms (vertical),
- **Shift+Alt Clicking** Distributes the objects from their centers.

These rules are illustrated in the following diagram.

Action	Click	Shift+Click	Alt+Click (Windows) Option+Click (MacOS)	Shift+Alt+Click (Windows) Shift+Option+Click (MacOS)
Distribute Vertically	Standard 	Tops 	Bottoms 	Centers 
Distribute Horizontally	Standard 	Left Sides 	Right Sides 	Centers 

► To distribute a set of objects:

1 **Select the objects that you want to distribute.**

You must select at least three objects. Hold down Shift and click to select several objects.

2 **If desired, hold down a modification key or key combination and click the Distribute Horizontally or Distribute Vertically tool.**

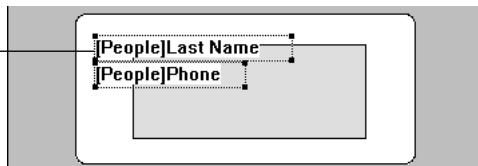
4th Dimension distributes the selected objects according to the rules you selected.

Layering Objects

You may want to create a design that uses objects in different layers. For example, you may want to place a shaded rectangle behind the fields on a label. The Label Wizard provides the **Move to Back** and

Move to Front, tools that let you layer objects on the label. The following illustration shows objects in front of other objects.

Fields in front of shaded rectangle



Clicking the **Move to Front** or **Move to Back** tools moves the selected objects to the top or bottom layer. If you want to move the object only one layer toward the front or back, hold down the **Shift** key when you click **Move to Front** or **Move to Back**.

- ▶ To move an object to the front or back:
 - 1 **Select the object or objects that you want to move to the back.**
Hold down **Shift** and click to select several objects.
 - 2 **Click the Move to Front or Move to Back tool in the toolbar.**
4th Dimension moves the selected object or objects to the front of or behind all the other objects.

Note When you move an object to the back, it may be hidden by objects in front of it. To see the object, select the object in front and send it to the back.

Duplicating Objects You can duplicate any object in the label. Copies of active objects retain all the properties of the original, including foreground and background colors and fill patterns, text attributes, and display format.

- ▶ To duplicate an object:
 - 1 **Select one or more objects.**
Hold down **Shift** and click to select several objects.
 - 2 **Click the Duplicate tool in the toolbar.**
4th Dimension duplicates the selected object or objects.

Moving Objects You can move objects by selecting them and dragging with the mouse. You can also use the arrow keys to move the object one or ten pixels at a time.

- To move an object one pixel at a time, select the object and press an arrow key.

-
- To move an object ten pixels at a time, select the object, hold down the **Ctrl** key (on Windows) or **Command** key (on Macintosh), and press an arrow key.

Resizing Objects

You can resize any object on the label by selecting it and dragging a selection handle.

- To resize an object by dragging:

- 1 **Select the object you want to resize.**
- 2 **Move the pointer over one of the four handles that appear on the selected object.**

The pointer changes into a multi-directional arrow  and the handles disappear.

- 3 **Drag the handle toward the center of the object to shrink it.**

OR

Drag the handle away from the object's center to enlarge it.

4th Dimension resizes the object.

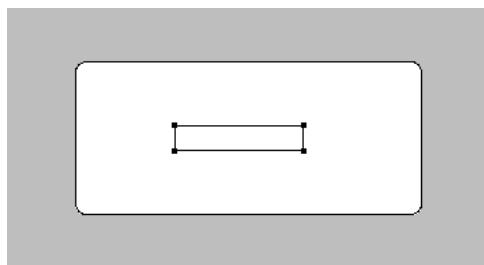
Adding a Border to an Object

You can add a one-pixel border to an object. The border can be from one to nine pixels from the object.

- To add a border:

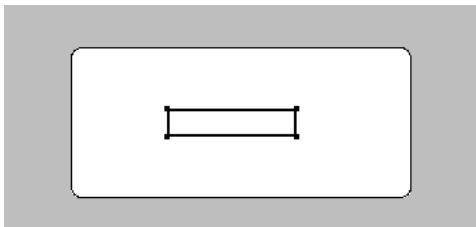
- 1 **Select the object.**

The selected object is indicated by selection handles.



- 2 **Hold down the **Ctrl** key (Command key on Macintosh) and press a number from 1 to 9.**

A border is added to the object. The distance from the object (in pixels) is controlled by the number you pressed. The following illustration shows the results of pressing Ctrl+1.



Adding Foreground or Background Colors

4th Dimension lets you add colors to objects for display on a color monitor or (if your printer supports color) for color printing. By combining selected colors with fill patterns, you can display thousands of different color shadings.

Note Colors appear black and white on a black and white monitor. They appear as shades of gray on a gray-scale monitor. The color palettes display shades on a gray scale monitor.

You can specify different colors for foreground pixels (pixels that appear black on a black-and-white monitor) and background pixels (pixels that appear white on a black-and-white monitor). If the object is a field or static text, the foreground color controls the color of the text and the background color controls the color of the object's rectangle.

You set foreground and background colors using the **Background** and **Foreground** picture menus in the Object Look area of the Label Wizard.

If your monitor supports 16 colors, choose the colors from the first 16 colors on each palette. If your monitor supports 256 colors (or more), any colors you choose will display properly.

Setting Fill Patterns

You can apply a fill pattern to any two-dimensional graphic object in the form such as an oval, a rectangle, a line, the enclosed area of a field or static text object, and a two-dimensional object's border.

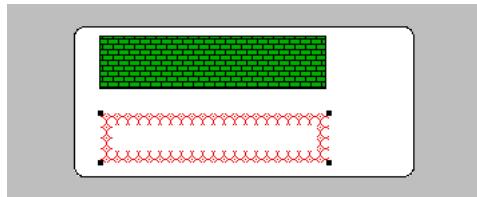
The **Fill** picture menu controls the fill pattern for the selected object. The **Border** picture menu controls the fill pattern for the border.

Setting Border Patterns

You can set patterns for the borders of any object in the form that has a border such as an oval, a rectangle, and a grid object. The border patterns available are the same as the fill patterns. The appearance of

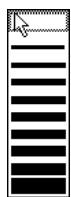
the border also depends on the line width you have specified for the border.

The following illustration shows a fill pattern applied to the upper rectangle and a border fill pattern applied to the bottom rectangle.



Setting Line Width

The **Line Width** pop-up menu controls the width of a line or the width of the border of a two-dimensional object.



To set a line width, select the object and choose a line width from the **Line Width** pop-up menu.

Restoring the Default Look

When you add an object to the label, it takes on the Object Look attributes of the most recently created object. If you want to assign the default Object Look attributes to this object (or any object), select the object and click **Default Look**. The foreground and background colors, fill patterns, and border width are reset to the default settings.

Adding a Graphic to the Label

In addition to the drawing tools in the toolbar, you can paste a graphic from the Clipboard into the label.

- To paste a graphic into the label:

1 **Place the graphic on the Clipboard.**

2 **Choose Paste from the 4th Dimension Edit menu or press Ctrl+V (Command-V on Macintosh).**

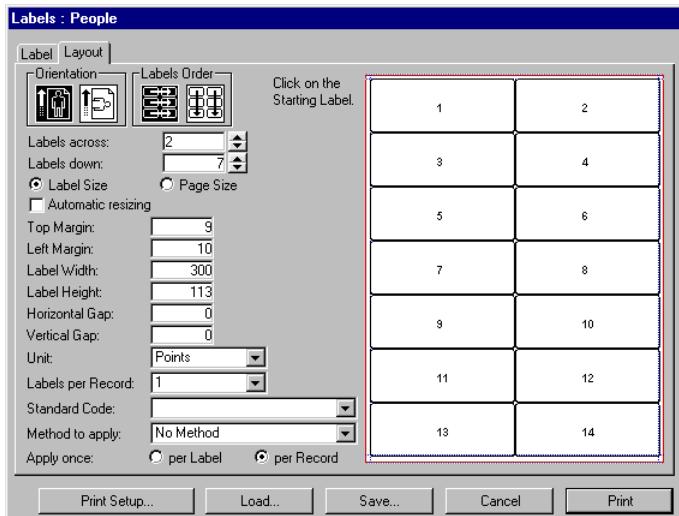
The graphic appears in the Label Preview area with selection handles. You can then move, align, distribute, or resize the object like any other object.

Deleting Objects

You can delete the selected object by pressing the **Backspace** key (**Delete** key on Macintosh). If the selected object contains concatenated fields, the last field is removed is removed from the object. If you want to delete the entire object, continue pressing the **Backspace** or **Delete** key.

Specifying the Label Layout

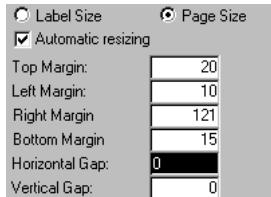
You specify the label layout with the Layout page of the Label Wizard. You can display the Layout page at any time by clicking its tab.



The Layout page contains the following elements:

- **Orientation and Labels Order buttons** These buttons enable you to specify the page orientation and the order in which information is assigned to labels.
- **Labels across and down boxes** These boxes are used to control the size of labels by specifying the number of labels that appear on your label paper.
- **Layout preview area** This area provides a reduced view of how an entire page of labels will look, based on the dimensions you enter in the Label Wizard. The page preview also reflects the paper size selected in the Print Setup dialog box. You can also select the first label on the page to be printed. The red border indicates the size of the physical page and the blue border indicates the size of the printable area.

-
- **Label Size and Page Size radio buttons** These buttons are used to select the label or the page for setting label and page dimensions. If you click Label Size, you can enter the label width and label height in the appropriate areas. If you click Page Size, you can enter values for right margin and bottom margin, as shown below.

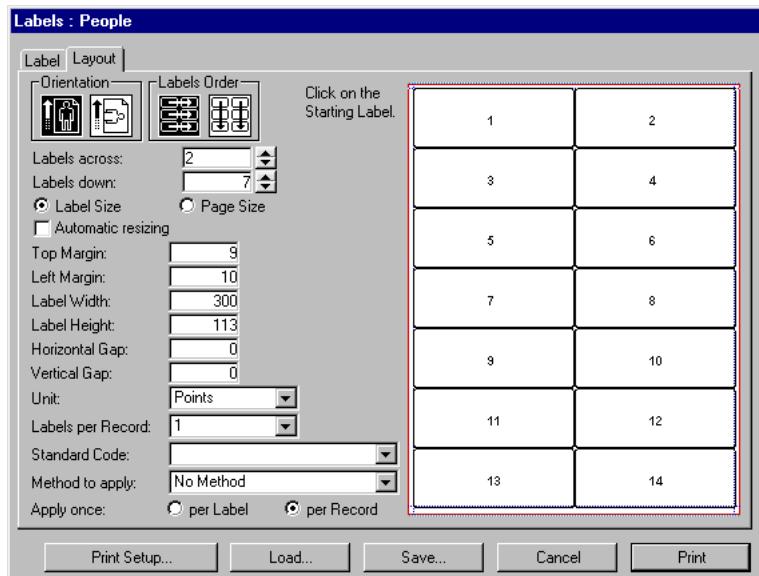


- **Margin boxes** These boxes are used to specify the dimensions of the label and the page size, depending on the radio button you select. After you have entered the margins of your label paper, you may need to make some additional adjustments so that the label text is centered in the labels. You can use both positive and negative numbers in the Margin boxes to increase and decrease the margins.
- **Automatic Resizing** If Automatic Resizing is checked, the values in the Label Width and Label Height entry areas are set automatically.
- **Horizontal Gap** This area controls the amount of space between label columns.
- **Vertical Gap** This area controls the amount of space between label rows.
- **Unit drop-down list** This drop-down list allows you to change the units in which you specify your label and label page measurements. You can use pixels, millimeters, centimeters, or inches.
- **Labels per record drop-down list** This control lets you print more than one copy of each label. If you print more than one copy, 4th Dimension prints the copies consecutively rather than making copies of the label pages.
- **Standard Code drop-down list** This control lets you specify the label, page dimensions, and margins by choosing a standard commercial label paper from the drop-down list.
- **Method to apply** This control lets you choose a method that will be run at print time. For example, you can execute a method that posts the date and time that each label was printed.

- **Apply Once radio buttons** These radio buttons are used to specify whether to run the method once per label or once per record. this control has meaning only if you are printing more than one copy of each label and you are also executing a method at print time.
- **File buttons** These buttons provide options for page setup, printing, saving, and loading label designs.
- To specify the layout of the label paper you are using:

- 1 **Click the Layout page tab.**

The Layout page of the Label Wizard appears.



You can specify the design of the label paper using the entry areas on the Layout page or choose a standard design from the Standard Code drop-down list. This drop-down list contains specifications for a wide variety of standard commercial label sheets.

- 2 **Click the Print Setup button.**

The Print Setup dialog box for your operating system appears.

- 3 **Choose the desired printer and click OK.**

If necessary, the Label Preview area changes to reflect your selection.

- 4 **If appropriate, choose the type of label paper you are using from the Standard Code drop-down list.**

The remaining entry areas on the page change to reflect the selected label paper's characteristics. If necessary, you can modify these specifications.

5 Click the appropriate Orientation and Labels Order radio pictures.

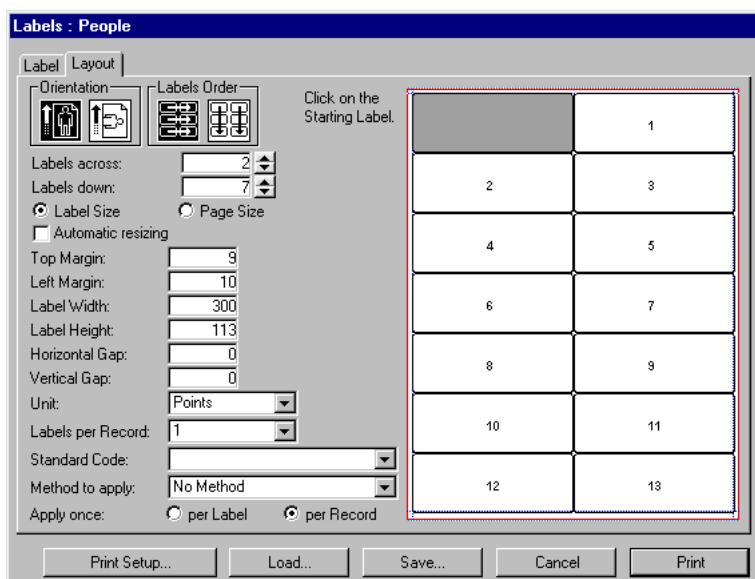
You can choose between portrait and landscape orientation and horizontal or vertical order.

6 Enter the number of labels in each row of your label sheet in the Labels Across box and the number of labels in each column in the Labels Down box.

The Label Preview area adjusts to display the appearance of the labels on a printed page.

7 If the first sheet of label paper is partially used, click on the first blank label in the Label Preview area.

4th Dimension will begin printing labels on the label you indicated. The following illustration shows the Preview area after clicking on the second label area.



8 If desired, choose a unit of measurement from the Unit drop-down list to use for entering margin sizes.

9 Enter values to reflect the margins on your label paper.

Use the Label Size and Page Size radio buttons to control whether you use the entry area for the size of the label or the size of the page.

The size of the individual labels in the label page preview will adjust to accommodate the margins. For example, if you increase the size of your margins to two inches, top and bottom, the size of the individual labels will shrink to maintain the same number of labels that you specified earlier.

Because some printers use portions of the margin to hold the label sheet in place, the printer may not take the full margins into account when printing your labels. In this case, you may need to adjust the margin settings so the label text is properly centered in each label.

Since the printer uses part of the margins, the printer begins measuring the margins from a point that is not precisely at the edge of the label paper. When the labels are printed, the label text may appear skewed to the right or to the bottom of the label paper.

To compensate for this lost margin space, you can use negative numbers in some of the margin boxes. When placed in the Right margin box, negative numbers pull the label text to the right. When entered in the Top margin box, negative numbers pull the label text toward the top of the page.

Note As a rule, using a negative number in a margin box moves the label text toward the margin you are setting.

- 10 **(Optional)** If you want to print more than one copy of each label, use the Labels per Record drop-down list to choose the number of copies to print.

The copies are printed consecutively on the label paper. 4th Dimension does not duplicate the entire label page.

- 11 **(Optional)** If you want to run a method when the labels are printed, choose the method from the Method to Apply drop-down list.

- 12 **(Optional)** If you are running a method and printing more than one copy of each label, click either the Once Per Record or Once Per Label radio button in the Apply Once area.

This control has no meaning unless you are using both the multiple copies and method features.

Saving and Loading Label Designs

4th Dimension lets you save each label design as a file that you can open from the Label Wizard. By saving label designs, you can maintain a library of labels that you can use according to your needs.

Saving a Label Design

To save a label design:

- 1 **Click the Save button.**

4th Dimension displays a dialog box where you can enter a file name for the label design.

Note Label files on Windows are denoted by the file extension .4LB.

- 2 Enter a filename for the label design and click OK (on Macintosh, click the Save button).

Loading a Label Design

You can load the label design whenever the Label Wizard is active.

- To load a label design:

- **Click the Load button.**

4th Dimension displays an open-file dialog box where you can select the filename of a label design. Double-click the filename or select the filename and click OK. (On Macintosh, choose a filename and click Open).

4th Dimension replaces the current label design with the design you selected.

Printing Labels

After you have completed your label design, you can preview or print the labels. You may want to print first on regular paper so that you can check the placement of text before you use the more expensive label paper.

- To print your labels:

- 1 **Click the Print button.**

The Print dialog box appears for the printer you selected in the Print Manager. If you check the **Print Preview** check box before clicking OK, the labels are previewed to screen.

If you are printing using a form, 4th Dimension will use the selected form to print the labels. 4th Dimension assumes that the form was designed to print labels.

After the labels are printed, 4th Dimension closes the Label Wizard and returns you to the form you were using when you opened the Label Wizard.

Appendix E: The 4D Quick Report Editor

With the Quick Report editor, you can:

- Produce lists of records
- Create break areas
- Compute summary calculations
- Use fonts and styles in the report
- Save quick report designs to disk

The Quick Report editor produces reports from the current selection of records. Before you print a report, set the current selection to the records you want to include in your report, using one of the methods described in Chapter 12, "[Finding and Updating Records](#)."

First Name	Last Name	Department Name	Salary
Biff	Davis	Accounting	43780
Smeldorf	Garbando		19610
Alan	Hull		41460
Bryan	Pfaff		26440
Shirley	Ransome		36040
Marlys	Wilson		36500
		Sum for Department : Accounting	203830
Kathy	Forbes	Engineering	18840
Dennis	Hanson		40520
Mary	Smith		55000
Andy	Venable		43520
Lance	Wolfram		27300
		Sum for Department : Engineering	185180

Quick Report Basics

This section describes basic operations used when working with the Quick Report editor to design a report.

Creating a New Quick Report

To open the Quick Report Editor, follow the instructions in the section "[Designing & Printing Reports with the Quick Report Editor](#)" in Chapter 14.

Loading and Saving a Quick Report Design

4th Dimension displays the Quick Report editor. If an existing report design is displayed, choose **New** from the **File** menu to begin a new Quick Report design.

You can save a quick report design as a file that you can open from the Quick Report editor. The quick report design includes all of your specifications for the report, but not the data. By saving report designs, you can maintain a library of quick report designs that you can use depending on your needs.

Note If you do not save your design, it is displayed the next time you open the Quick Report editor in that worksession only.

- ▶ To save a quick report design:

1 Choose Save from the File menu.

4th Dimension displays a create-file dialog box in which you can name the quick report design.

Note Quick report files in 4th Dimension for Windows are denoted by the file extension **.4QR**.

2 Enter a filename for the quick report and click OK.

4th Dimension saves the report as a file that you can open with the Quick Report editor. You can save the file on any available hard disk.

Saving a previously saved or loaded report replaces the old report.

Loading a Quick Report Design

When the Quick Report editor is open, you can load a saved design and use it to print a new report. You can use the same quick report design repeatedly to print different selections of records.

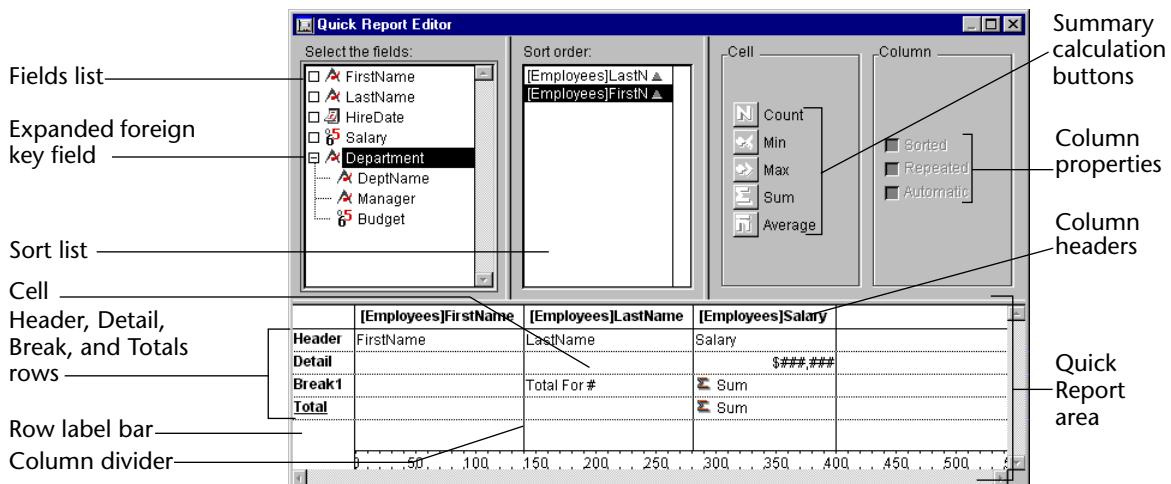
-
- To load a report design:
 - 1 Choose Open from the File menu.**
4th Dimension displays an open-file dialog box displaying a list of available quick report designs.
 - 2 Double-click a filename or select a filename from the list and click OK.**
4th Dimension replaces the current report design with the design you opened.

The Quick Report Editor

When you create a quick report, you can specify the following:

- Columns that display fields or formulas, either from the current table or from related tables
- Sort levels and order
- Break levels
- Summary calculations
- Text for labels
- Formats for numeric and Boolean data
- Font, font size, style, and justification for labels, summary calculations, and data
- Page headers and footers

The following illustration shows the major elements of the Quick Report editor.



The Quick Report editor contains the following elements:

- **Fields list** This list displays fields in the current table. You can view the names of fields in related tables by expanding the foreign key fields. A foreign key field has a plus sign (on Windows) or an arrow (on Macintosh) to its left.

Note This Appendix has been slightly modified from the the 4D user manual, with permission of 4D Inc. For this reason, the examples *do not refer to Biota tables and fields*.

- **Sort list** This list displays the sort order assigned to the report and indicates whether each sort level is ascending or descending. If your report will contain summary calculations from groups of records, you must sort the current selection on one or more fields.

Note You can change the order of fields in the Sort list by dragging the field name vertically to the desired position in the list.

- **Quick Report area** You use this area to design the report by dragging fields, adding formulas, adjusting column widths, and adding or deleting breaks.

- **Summary calculation buttons** You use these buttons to place summary calculations in the Break and Total areas of the report.

-
- **Column properties** You use these check boxes to set the following characteristics for each column in the report:
 - **Sorted** Click this check box if you want the records to be sorted on the selected column.
 - **Repeated Values** You use this check box to tell the Quick Report editor to repeat the values in a Break column. If you do not select the **Repeated Values** check box, each Break value is displayed only once.
 - **Automatic Width** Click this check box to request that the Quick Report editor compute the width of the selected column based on the maximum length of the contents of the column. The sizing is done only at the time the report is printed. You can check this option for each column individually. The check box does not refer to the entire report. If the Automatic Width check box is not checked for a column, you can modify that column's width by dragging column dividers.
 - **Column dividers** These lines indicate the boundaries between columns of the report.
 - **Right margin marker** This marker indicates the right margin of the report. The right margin marker is meaningful only when no columns have the Automatic Width check box selected. You may have to scroll horizontally to view the right margin marker.
 - **Column header** The column header displays the names of fields or formulas added to the report.
 - **Row label bar** This bar shows the different areas of the report: the Header, Detail, Break, and Total rows.
 - **Header row** This row contains information that appears in the printed report above the records. The Quick Report editor automatically places field names in the Header row, but you can modify its contents.
 - **Detail row** This row prints information from individual records and will be repeated in the printed report for each break.
 - **Break and Totals rows** These rows display summary calculations and any associated labeling. The Break row displays summary calculations for each subgroup in the report and the Totals row displays summary calculations obtained from all records in the current selection.
 - **Cells** A cell is the intersection of a row and a column.
 - **Scroll bars** You use the scroll bars to view parts of the quick report design that extend beyond the area of the quick report form.

The following figure shows a completed quick report design and the relationship between the specifications in the design and the printed output.

	Department Name	C2	Title	Salary
H	Department Name	Name	Title	Salary
D				\$ ###,###
B1		Statistics for Department: #	Average Count	(R) Average count (N)
I		Statistics for all Departments	Average Count	(R) Average Count (N)

Department Name	Name	Title	Salary
Accounts Payable	Flake, Peggy Fredrickson, Anna Garbondo, Smeldorf Lindsay, Susy Swenson, Marcy Statistics for Department: Accounts Payable	Accountant Manager Accountant Secretary Accountant Average Count	\$26,650 \$28,324 \$23,500 \$18,750 \$31,200 \$27,987 5
Accounts Receivable	Irving, Samuel C. Kane, Karyn Base, Jud Rosner, Alice Statistics for Department: Accounts Receivable	Accountant Manager Accountant Secretary Average Count	\$35,567 \$38,550 \$27,000 \$17,500 \$29,261 4
	Statistics for all Departments	Average Count	\$30,616 77

Resizing Areas in the Editor You can resize the various list and display areas in the Quick Report editor. Areas that can be resized are bordered by a raised line.

- To resize an area in the editor:
 - 1 Move the pointer over the area border to change the pointer into a resizing pointer or .
 - 2 Drag the border up or down, or left or right to resize the area.

The Quick Report Contextual Menus

The Quick Report editor has “hidden” contextual menus that make it easy to access certain row, column, and cell operations. Instead of making menu selections or working with the Cell or Column properties areas, you can perform certain operations by displaying a Quick Report contextual menu.

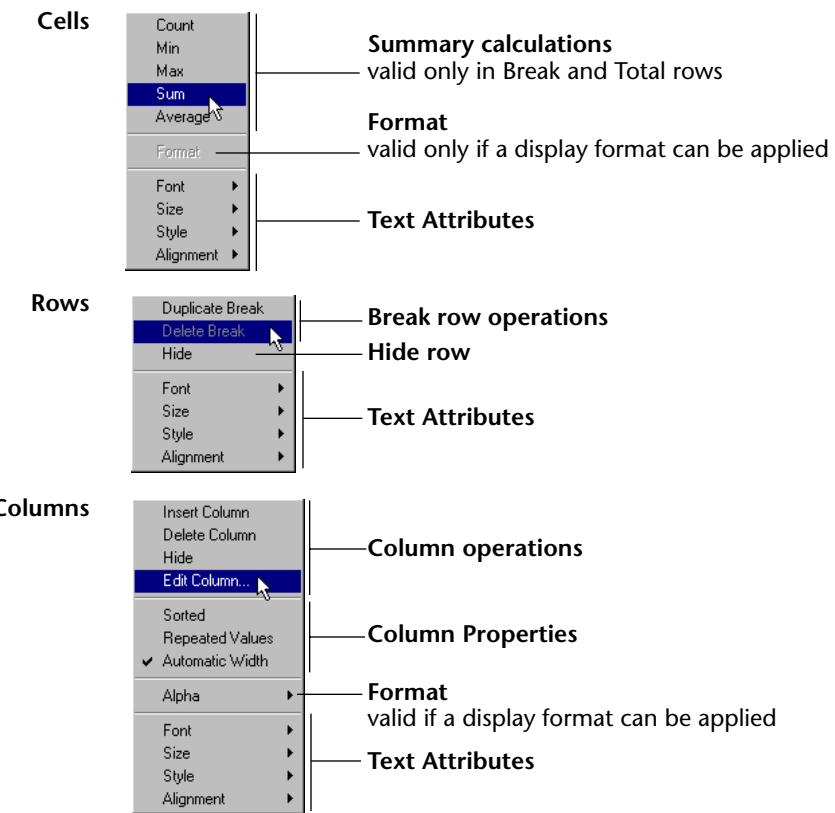
There are separate contextual menus for row, column, and cell operations.

- To use a contextual menu:

1 Position the pointer in a cell, a row label, or a column heading and hold down the mouse button.

A contextual menu appears. The commands in the contextual menu depend on where your pointer is (i.e., a row label, column heading, or cell). Also, menu commands that are inappropriate for the particular row, column, or cell are disabled.

The following illustration shows the three Quick Report contextual menus.



2 Choose the desired menu command.

Working with the Quick Report Editor

This section describes the basic operations that you can perform in the Quick Report editor.

Selecting Rows, Columns, and Cells

When designing a quick report, you need to select rows, columns, and cells in the quick report form. A cell is the intersection of a row and a column.

- ▶ To select a row:
 - Click on the Header, Detail, Break, or Total markers on the row label bar to the left of the Quick Report form.
OR
Click in a row to the right of all columns in the Quick Report form.
- ▶ To select a column:
 - Click above the Header row of a column.
- ▶ To select a cell:
 - Click the cell.

Adding and Modifying Text

You can add or modify text in the quick report form to label parts of the report. For example, if you requested summary calculations, you can label them by adding text to other cells in the Break and Total rows.

You can add and modify text as follows:

- Edit the text that 4th Dimension automatically adds to the Header row of the report
- Insert text in empty cells of the Break and Totals rows
- Insert the value of a Break field in the Break rows
- Specify the font, font size, justification, and style for any text that appears in the report

Adding Text

To add text in a report cell:

- 1 Click twice on an empty cell in the quick report form.

A text insertion point appears in the cell.

If you are entering a label for a summary calculation, select a cell in the same row as the cell containing the calculation icons. You cannot enter text into the same cell that contains summary calculations.

2 Type the text in the cell.

Modifying Text

To modify text in a cell:

1 Double-click in a cell to get an insertion point and drag across the text in the cell you want to modify.

4th Dimension highlights the selected text.

2 Type the new text in the cell.

Specifying Font Attributes

While designing your quick report, you can specify different fonts, font sizes, justification, and styles. You can then apply these specifications to text, data, and summary calculations within rows, columns, or cells in the quick report.

If you assign specifications to the Detail row of the report, you will not see the results until you preview or print the report.

You can specify font attributes using either the Quick Report menu commands or the Quick Report contextual menu.

► To specify font attributes using the Quick Report menus:

1 Select the column, row, or cell where you want to apply the font.

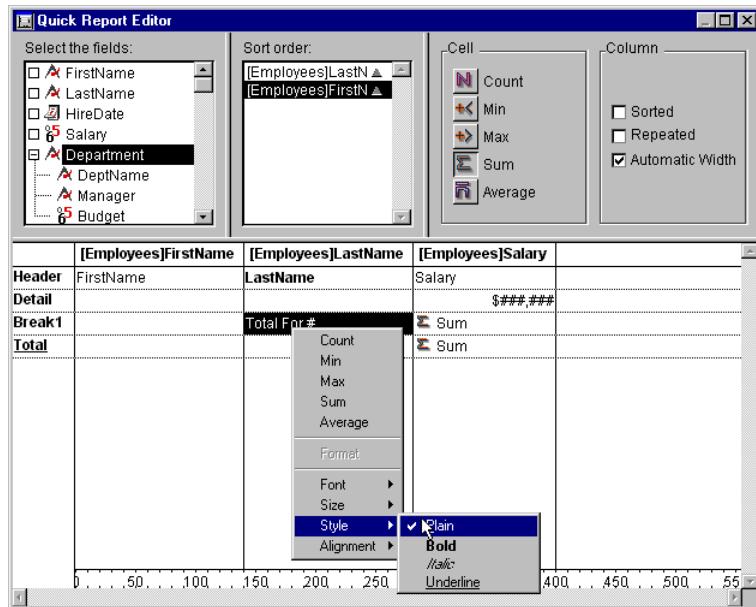
2 Choose a font from the Font menu or choose a font size, style, or justification from the Style menu.

4th Dimension applies the font to any text, data, or summary calculations that appear in the selected area.

► To specify font attributes using the Quick Report contextual menu:

1 Hold down the mouse button on the row label, column header, or cell to which you want to apply the font attributes.

A contextual menu appears.



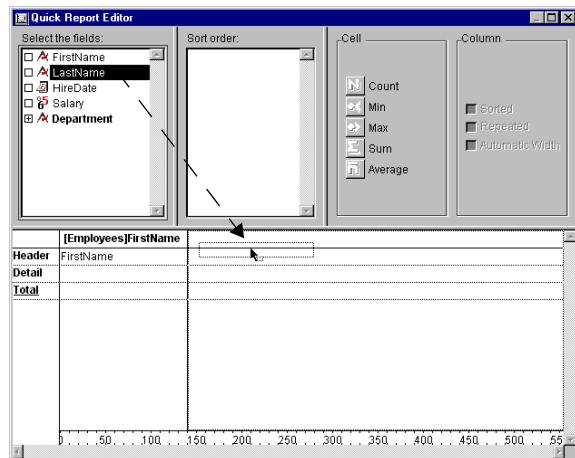
- 2 Use the Font, Size, Style, or Alignment hierarchical menus to change the font attributes as desired.**

Adding Columns to the Report

You create columns by dragging field names from the Fields list in the to the quick report area. If you want to add a field from a related table, expand the foreign key field in the hierarchical list of fields to display the fields in the related table. You can add fields from related tables, provided that the relationship is automatic.

- To add a field:
 - Drag the name of a field to the right of existing columns in the Quick Report area and release the mouse button.
4th Dimension creates a column for the field and places the field name in both the column header and the cell in the Header row.

The following figure shows the Last Name field being added as a column to the Quick Report area.



By default, 4th Dimension prints the field names as column heads at the top of each page in the quick report.

Note If you use a subfield in a quick report design, the report will list all values of the subfield for each parent record. You cannot sort on a subfield.

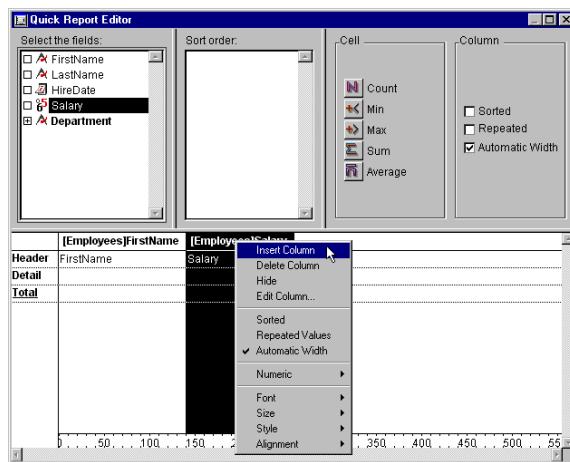
Inserting Columns

You can insert an empty column in a quick report. After you insert the column you can assign a field or a formula to the column.

- To insert a column:
 - 1 Select a column.
 - 2 Choose Insert Column from the Edit menu.
OR



Hold down the mouse button to display the Quick Report contextual menu and choose Insert Column.

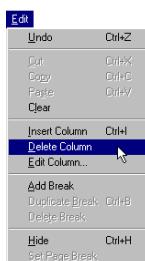


4th Dimension inserts a blank column to the left of the column you selected. To assign a field to the empty column, drag a field name to it. To assign a formula to the column, see the section "[Adding Formulas to a Quick Report](#)".

Deleting Columns

As you specify fields for your quick report, you may want to remove some columns to place them elsewhere. Or, you might want to delete the column from the report.

- To delete a column using the Quick Report menu bar:
 - 1 Select the column you want to delete.
 - 2 Choose Delete Column from the Edit menu.
4th Dimension removes the selected column from the quick report form.
- To delete a column using the Quick Report contextual menu:
 - 1 Hold down the mouse button on the column header. The Quick Report contextual menu appears.
 - 2 Choose Delete Column from the contextual menu.



Replacing Columns

You can replace a column in the quick report by dragging another field over it. You can also replace a field with a formula.

- To replace a column:

1 Drag a field from the Fields list to the column you want to replace.

OR

Select the column you want to replace and choose Edit Column from the Edit menu.

OR

Hold down the mouse button on the column header to display the Quick Report contextual menu and choose Edit Column.

The Formula editor appears.

2 If you displayed the Formula editor, enter a formula for the column.

If you want to assign a field to the column, you can simply use the field name as the formula.

When you print the quick report, 4th Dimension prints the results of the formula for each record that appears in the Detail row.

See the section “[Adding Formulas to a Quick Report](#)” for information about adding a formula to a quick report.

Sizing Columns

By default, the Quick Report editor sizes columns automatically (as reflected in the **Automatic Width** check box). It sizes each column based on the maximum length of data displayed in the column and any labels typed into the column. The Quick Report editor sizes columns at the time the report is printed.

To view the widths of each column, preview the report to the screen. See “[Printing a Quick Report](#)” for more information about previewing the report.

Because selecting the **Automatic Width** check box changes the width of a column based on the maximum width of data in the records being printed, selecting different records can change the size of the columns.

You can resize a column manually after deselecting the **Automatic Width** check box. When a column is set manually, text in the column wraps within the specified area.

- To manually resize a column:

1 Select the column you want to resize.

2 Deselect Automatic Width¹.

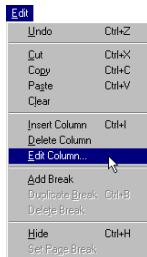


-
- 3 Move the pointer over the column divider in the quick report to change the pointer into a column width cursor .
 - 4 Drag the column divider to the left or right to resize the column.

Adding Formulas to a Quick Report

You can add a formula to a column in a quick report. For example, you can add a formula that computes employees' monthly salaries from an Annual Salary field.

- To add a formula:



- 1 Insert an empty column or click an existing column and choose Edit Column from the Edit menu.

OR

Double-click an existing column.

OR

Hold down the mouse button on an existing column header to display the Quick Report contextual menu and choose Edit Column.

4th Dimension displays the Formula editor, in which you can build a formula. If you selected an existing column, the formula you create will replace the previous contents of the column.

Warning: There are hundreds of 4D commands and nearly 2000 Biota methods listed in the “Commands by Themes” list that appears in the Formula editor. *Under no circumstances attempt to use any of the italicized Biota methods in a formula. You may do irreparable damage to your Data File if you do so.*

- 2 Build the formula.

OR

Click the Load button to retrieve an existing formula from disk.

For information about using the Formula editor, refer to "[Using Formulas to Sort Dates by Day, Month, or Year](#)" in Chapter 10.

To save the formula as a file that you can retrieve and use in another column or in another report, click the Save button and enter a filename in the dialog box.

If you click the Load button, 4th Dimension displays an open-file dialog box and asks you to select a file. When you load a file, it replaces any formula that currently appears in the Formula editor. After you load a formula, you can modify it in the editing area.

-
1. You can deselect Automatic Width using either the check box in the Column Properties area or the Quick Report contextual menu for that column.

3 Click OK to assign the formula to the column.

4th Dimension adds a new label to the column that identifies it as a formula. You can relabel the column by typing a label into the header cell for that column.

Formulas are labeled *C1* through *Cn*. The labels are the names of variables that contain the column's value. You can use these variables in other formulas.

Click the **Cancel** button to close the editor and return to the Quick Report editor without adding the formula.

Sorting Records and Creating Breaks

An important feature of the Quick Report editor is the ability to sort the records in your report. You sort records for two reasons:

- To view records in a particular order,
- To create groups of records and Break areas in the report for the purpose of reporting summary calculations for groups.

See the section “[Setting Break Levels](#)” later in this Appendix for information about summary calculations.

Specifying a Sort Order

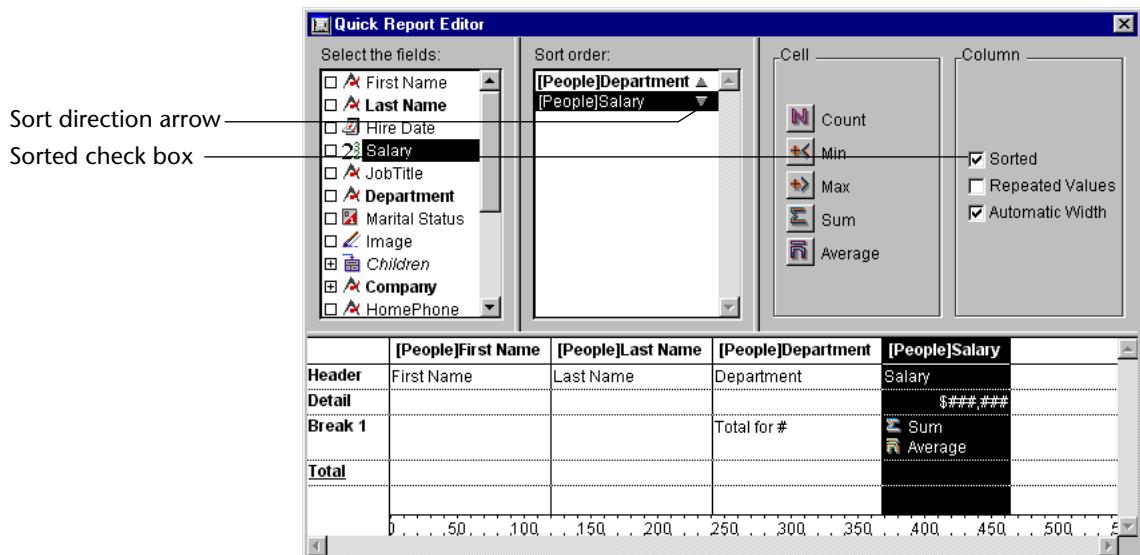
You can specify a sort order at any time. For example, if you wanted to sort the records of salespeople by the Sales Region field, you would select the Sales Region column, and then set the **Sorted** property.

You can also sort on a formula by selecting the column that contains the formula and then clicking the **Sorted** check box or choosing **Sorted** from the Quick Report contextual menu for that column. See the section “[Adding Formulas to a Quick Report](#)” earlier in this Appendix for more information about adding formulas to quick reports.

- ▶ To specify the sort order using the **Sorted** check box:
 - 1 Select the column that contains the field or formula you want to specify as the first sort level.
 - 2 Click the **Sorted** check box.
- ▶ To specify the sort order by dragging:
 - Drag a field from the Fields list to the Sort order list.

If the field is not already in the quick report design, 4th Dimension adds it as the last field in the design.

- To specify a sort order using the Quick Report contextual menu:
 - 1 Hold down the mouse button on the column header belonging to the column you want to sort.
The Quick Report contextual menu appears.
 - 2 Choose Sorted from the contextual menu.
4th Dimension displays the name of the field in the Sort list. To the right of the name is an arrow, indicating an ascending sort order. By default, all sorts are performed in ascending sort order.
 - 3 If necessary, click the sort direction arrow  to sort the column in descending order.



- 4 If desired, select additional fields or formula columns and add the Sorted property using either the Sorted check box or contextual menu command.

You can specify ascending or descending sort order for any additional fields or formulas you specify.

When you specify multiple sort levels, 4th Dimension sorts the records on the first field in the Sort field list, then on other fields in the order that they appear in the list. For example, if you specify the Department Name field as the first sort level and Last Name as the second sort level, your design might look like the quick report design shown in step 3.

-
- ▶ To change the level of a Sort field:
 - Drag the name of a field or formula up or down within the Sort list to the desired sort level.

Deleting a Field or Formula from the Sort List

- ▶ To delete a field or formula from the sort order:
- Select the column and deselect the Sorted check box.
OR
Hold down the mouse button on the column header to display the Quick Report contextual menu and deselect the Sorted menu command.
4th Dimension removes the field or formula in the Sort field list. It does not delete the column itself from the report. When you print the report, 4th Dimension will no longer use that field or formula to sort the records.

Setting Break Levels

In a quick report, you set break levels to separate or “break” records into groups according to values in one or more sort fields. A Break area is printed at each break level. You can print summary calculations in the Break area. The summary calculations — sum, average, minimum, maximum, and count — are calculated for each group of records.

Break levels are determined by the sort levels and Break rows. For example, if you sort records by Sales Region and create a Break row, 4th Dimension inserts a break between each group of records that have the same sales region.

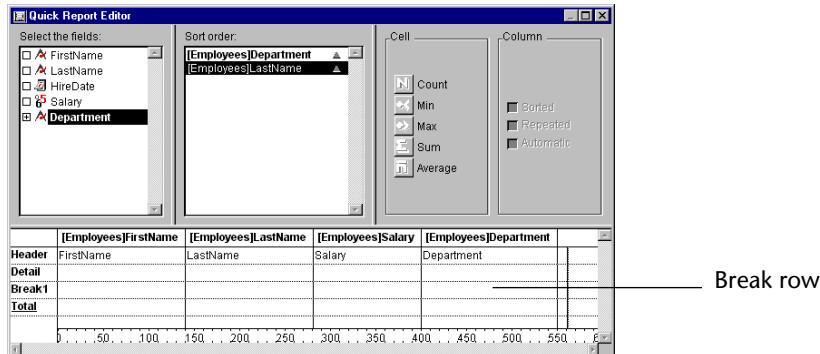
After you add a Break row to the quick report, you can request summary calculations on each break. For example, you can insert a summary calculation in a Break row to display subtotals for sales from each state in a marketing region. Refer to the section “[Adding Summary Calculations](#)” later in this Appendix for more information about adding summary calculations to Break and Total rows.

- ▶ To insert a Break row:
- 1 Choose Add Break from the Edit menu.
OR



Hold down the mouse button on the Total row label in the Row label bar and choose the Duplicate Break menu command.

4th Dimension adds a Break row. The figure shows a Break row in a quick report design.



2 If desired, add additional Break rows by repeating step 1¹.

There should be at least as many sort levels as break levels.

4th Dimension adds a sequential number to each new break label in the row label bar, for example, Break1, Break2, Break3, and so forth.

Using the Values of Break Fields in Labels

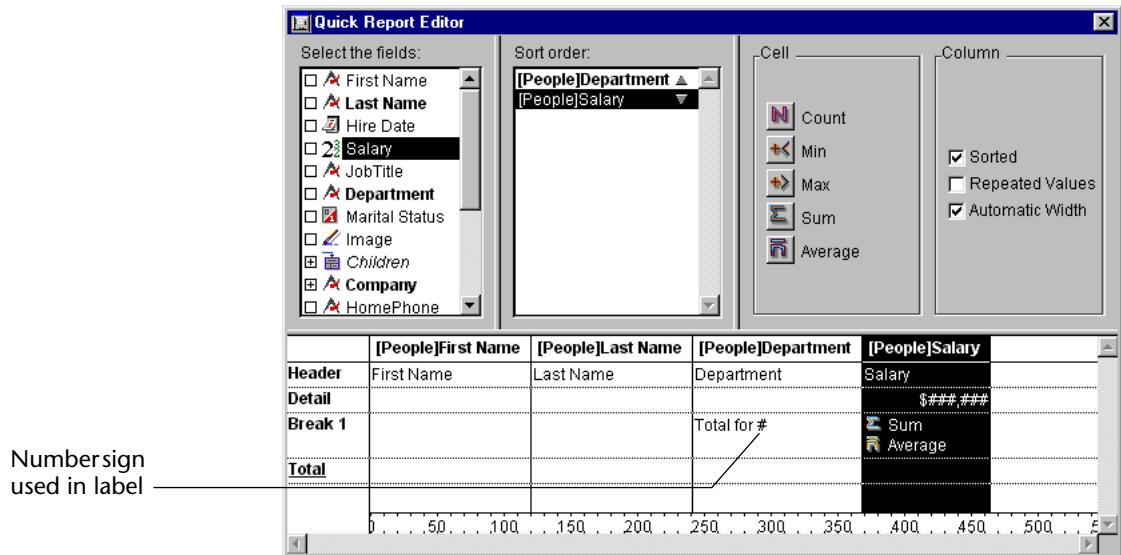
You can improve the appearance and comprehensibility of your reports by labeling each Break row using the value of the Break field.

To request that the value of a Break field be printed in a label placed in the Break area, use the number sign (#) in the label. For example, the text "Total salaries for department #" will insert the department name (in this case, the value of the Department field) in place of the number sign when the report is printed.

The number sign does not need to be placed in the same column as the Break field. It will display the value of the Break field in any cell in the Break row.

1. After you have created a Break row, you can also display the Quick Report contextual menu by holding down the mouse button on the new Break row label.

The following figure illustrates the use of the number sign in a label in the Break row.



Adding Summary Calculations

You can add summary calculations on the contents of fields and formulas to each Break row and to the Totals row.

The check boxes in the Cell area of the Quick Report editor identify the summary calculation options available for quick reports. The following summary calculations are available.

- **Sum** totals the values in the report or break.
- **Minimum** displays the lowest value in the report or break.
- **Maximum** displays the highest value in the report or break.
- **Average** calculates the average of the values in the report or break.
- **Count** calculates the number of records in the report or break.

These options also appear in the Quick Report contextual menu for cells in the Break and Total rows.

When you place a summary calculation in the Totals row, the calculation is done for all records in the report. If you place the summary calculation in a Break row, separate calculations are done for the records in each break.

- To add a summary calculation:
- 1 Select a cell in a Break row or in the Totals row where you want to insert the summary calculation.
- The Sum, Minimum, Maximum, and Average calculations work only on a numeric field or formula.
- 2 Click as many summary calculation check boxes as you like.
Or
Hold down the mouse button and choose the desired summary calculations from the Quick Report contextual menu for cells.
- 4th Dimension displays a calculation icon in the selected cell for each type of summary calculation you request. The following figure shows calculation icons in the Break and Total rows.

The screenshot shows the 'Quick Report Editor' window. On the left, under 'Select the fields:', 'Salary' is selected. In the 'Sort order:' section, '[People]Department' is at the top, followed by '[People]Salary'. The 'Cell' section contains icons for Count, Min, Max, Sum, and Average. The 'Column' section has checkboxes for 'Sorted', 'Repeated Values', and 'Automatic Width', with 'Sorted' checked. The main area shows a report grid with columns: [People]First Name, [People]Last Name, [People]Department, and [People]Salary. The 'Header' row has 'First Name', 'Last Name', 'Department', and 'Salary'. The 'Detail' row is empty. The 'Break 1' row has an empty cell under 'First Name', 'Last Name', and 'Department', and 'Total for #' under 'Salary'. The 'Total' row has an empty cell under 'First Name', 'Last Name', and 'Department', and 'Grand Total' under 'Salary'. The 'Salary' column for 'Break 1' and 'Total' rows has a '\$######' mask. The 'Salary' column for 'Header' and 'Detail' rows has a '#,##' mask. A legend at the bottom indicates that blue icons represent Sum and Average, while red icons represent Count, Min, and Max.

Calculation icons in Break and Totals rows

If you add more than one summary calculation to a cell, 4th Dimension stacks the calculation icons on top of each other, as shown above.

Displaying Repeated Values for Break Columns

In a report with breaks, the columns which are used to group records so that summary calculations can be done are called *Break columns*. In the report shown above, the Department field is a Break column since the records in the report are grouped by department.

When a report like this is printed, the values for the Break column are printed only once per break. In other words, a department name is

printed only for the first record in the group and is not repeated until the department changes.

First Name	Last Name	Department Name	Salary
Biff	Davis	Accounting	43780
Smeldorf	Garbando		19610
Alan	Hull		41460
Bryan	Pfaff		26440
Shirley	Ransome		36040
Marlys	Wilson		36500
Sum for Department : Accounting			203830
Kathy	Forbes	Engineering	18840
Dennis	Hanson		40520
Mary	Smith		55000
Andy	Venable		43520
Lance	Wolfram		27300
Sum for Department : Engineering			185180

Nonrepeating
break values

In some cases, you may want to repeat the values for the Break columns so that they appear for every record in the Break area. You do so by selecting the **Repeated Values** column property. You can do so either by clicking the **Repeated Values** check box in the Column Properties area or by choosing the **Repeated Values** menu command in the Quick Reports contextual menu for that column.

- To display repeated values for fields in Break columns:

- 1 Select the Break column by clicking above the Header row for that column and click the Repeated Values check box.
OR
Hold down the mouse button on the Header row of the Break column and choose Repeated Values from the Quick Reports contextual menu.
- The following figure shows the report at the top of this page after the Repeated Values check box has been checked for the Department Name column.

First Name	Last Name	Department Name	Salary
Biff	Davis	Accounting	43780
Smeldorf	Garbando		19610
Alan	Hull		41460
Bryan	Pfaff		26440
Shirley	Ransome		36040
Marlys	Wilson		36500
Sum for Department : Accounting			203830
Kathy	Forbes	Engineering	18840
Dennis	Hanson		40520
Mary	Smith		55000
Andy	Venable		43520
Lance	Wolfram		27300
Sum for Department : Engineering			185180

Setting Display Formats

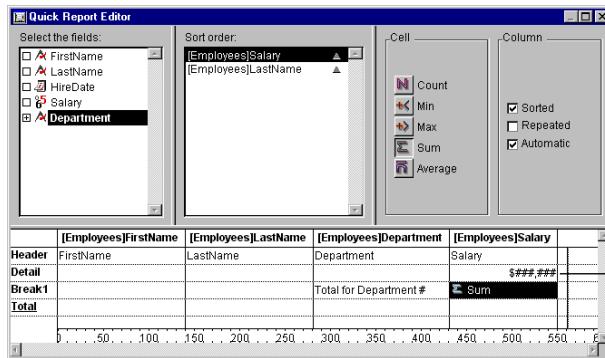
You can specify display formats for columns that contain numeric or alphanumeric (Alpha) data. For example, if you are displaying salaries in a column, you can add a numeric format to the Detail cell for the Salary field. If your report includes Alpha fields such as a telephone number or Social Security number, you can use an Alpha format.

Numeric Formats

The following format places a dollar sign to the left of the number and allows up to 6 digits:

\$###,###

This format can display dollar amounts up to \$999,999.



Alpha Formats

You can use an Alpha format for fields that contain string information. For example, Social Security number or telephone number fields can be formatted with an Alpha format.

For example, the following format would be used to format Social Security numbers:

###-##-####

Entering the Display Format for a Field

You enter a display format or custom format by choosing it from the Quick Report contextual menu for the cell or by typing it into a cell.

- ▶ To enter a display format for a numeric or Alpha field:

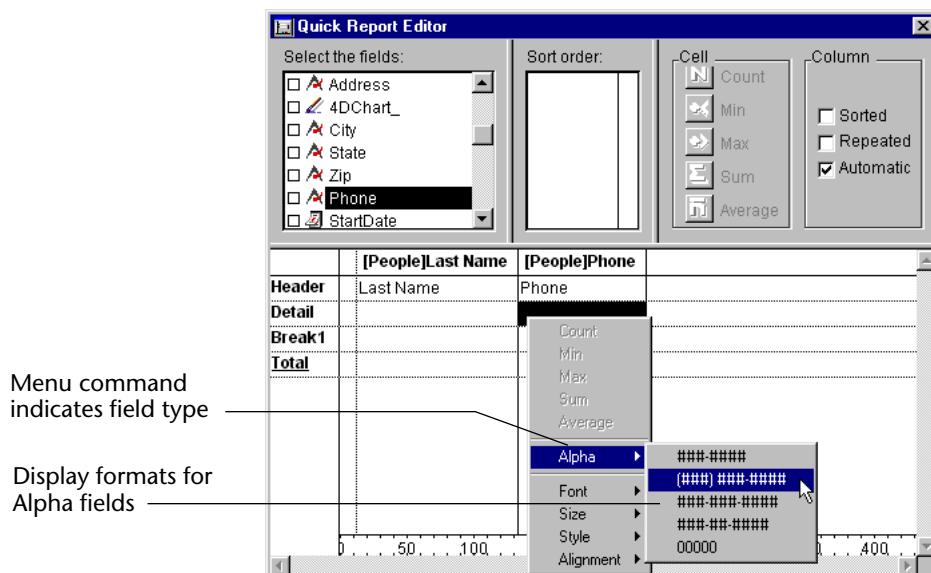
1 Click twice in the Detail cell for a numeric or Alpha column.

2 Type a display format or the name of a style that you want to use as the display format.

The names of styles are preceded by a vertical bar (|).

- ▶ To choose a display format from the Quick Report contextual menu:

1 Position the pointer over the Detail cell for a column and hold down the mouse button and choose a display format from the hierarchical menu.



The hierarchical menu will show display formats that are appropriate for the data type of the column. For example, if the field was a numeric format, the menu command would be “Numeric” instead of “Alpha” and the submenu would list only numeric formats.

After you make your selection, you can edit the format normally.

If you have also requested summary calculations for that column, the format specified in the Detail cell will automatically be applied to the summary calculations. Regardless of the display format, the count is

always displayed as an integer without formatting symbols such as the dollar sign.

Different formats can be applied to different columns in the report.

Hiding and Showing Rows and Columns

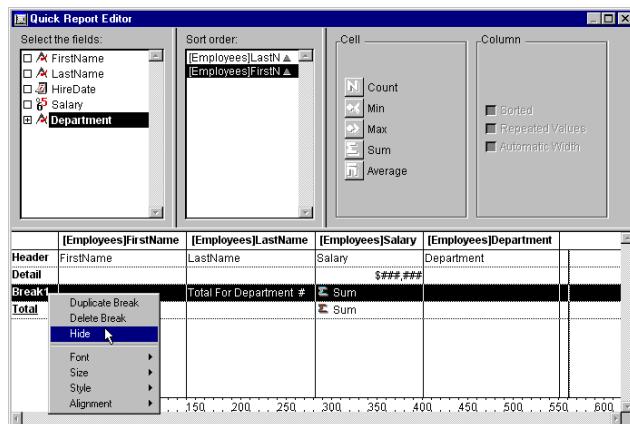
4th Dimension lets you hide rows or columns when printing a quick report. If desired, you can show a hidden column or row.

Hiding rows is useful when you want the report to include only summary calculations. For example, hide the Detail row if you want to display only the summary calculations that appear in the Totals and Break rows. You can also use this feature to hide a Break row or the Totals row.

You can hide a column if you need to use the column as a sort column, but do not want the report to display the column.

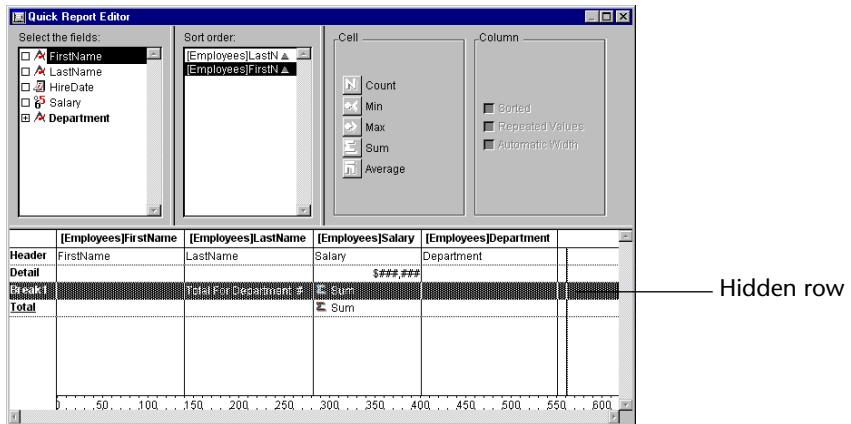
You can hide a row using either a Quick Report menu command or the Quick Reports contextual menu.

- To hide a row using the menu command:
 - 1 Select the row you want to hide.
 - 2 Choose Hide from the Edit menu.
- To hide a row using the contextual menu:
 - 1 Hold down the mouse button over the row label in the Row label bar. The Quick Reports contextual menu appears.



2 Choose Hide from the contextual menu.

4th Dimension displays the column in gray to remind you that the row will not appear when you print or preview the quick report.



You can also use a menu command or the Quick Reports contextual menu to hide a column.

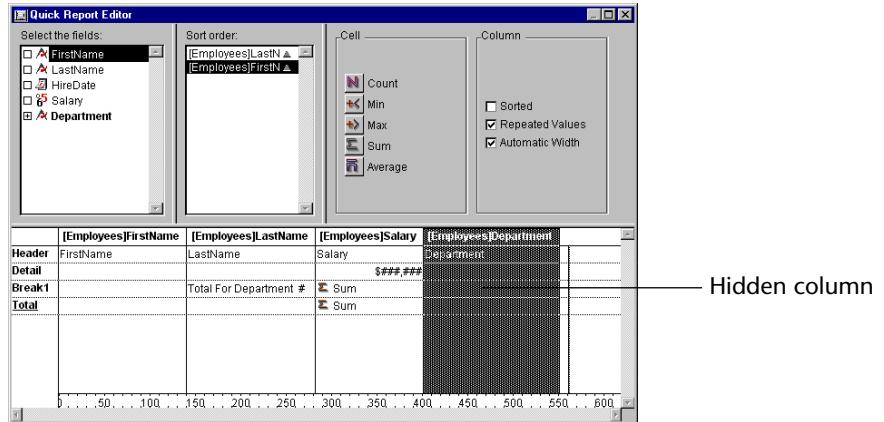
- To hide a column using the menu command:

- 1 Select the column you want to hide.**
- 2 Choose Hide from the Edit menu.**

- To hide a column using the Quick Reports contextual menu:

- 1 Hold down the mouse button over the column header.**
The Quick Reports contextual menu appears.
- 2 Choose Hide from the contextual menu.**

4th Dimension displays the column in gray to remind you that it will not appear in the printed report.



Showing a Hidden Row or Column

When a row or column is hidden, the **Hide** menu command in the **Edit** menu and Quick Report contextual menu becomes **Show**. You can display a hidden row or column choosing **Show** from either the **Edit** or contextual menu. When you do so, the row or column is displayed normally in the Quick Report area.

Adding Page Headers and Footers

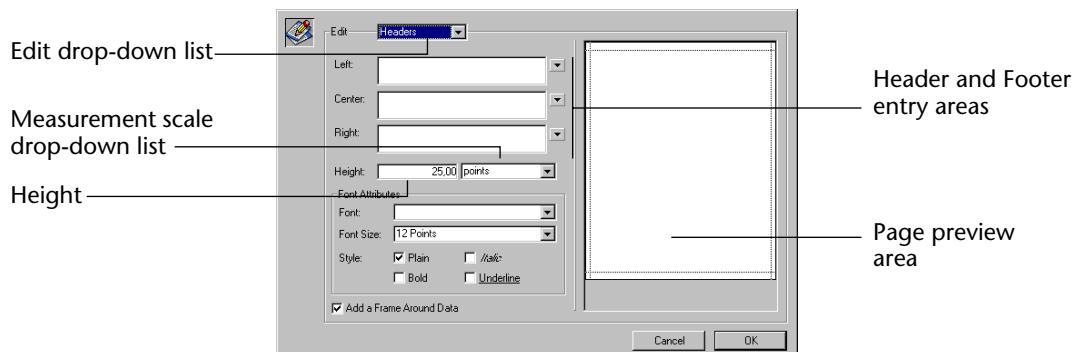
Before printing a quick report, you can add page headers and footers. You specify page headers and footers in the Headers and Footers dialog box. Use this dialog box to do the following:

- Add page header and footer text,
- Specify the size of the page header and footer areas,
- Specify fonts, font sizes, and font styles for page header and footer text,
- Insert codes that add page numbers and the date and time to your reports.

You can only specify page headers when printing to a printer. See the section "[Printing a Quick Report](#)" for more information about alternate output devices.

- To add page headers and footers:
 - 1 Choose Headers and Footers from the File menu.

The Headers and Footers dialog box appears.



The Header and Footers dialog box lets you specify both headers and footers from the same screen. You use the **Edit** drop-down list to specify either the header or footer.

2 Choose Header or Footer from the Edit menu.

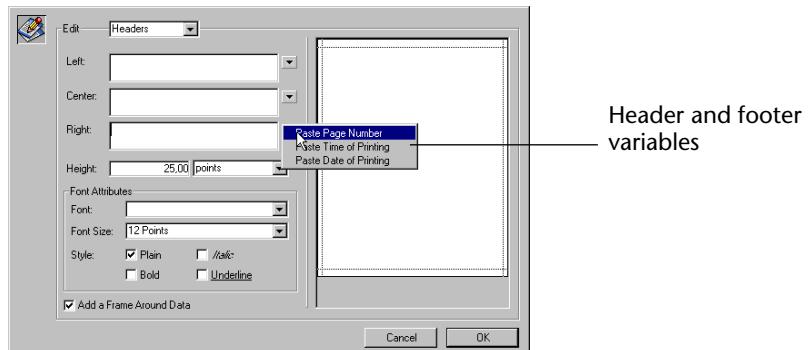
3 Enter the header or footer height in the Height area.

When you first enter the dialog box, the header and footer heights are set to 25 points each. You can change values for the height and can change measurement scale to enter values in inches or centimeters.

As you enter the header and footer height, the dotted lines on the page preview area change to indicate the size of the header and footer as they will appear on the printed report.

4 Select an entry area and type the header or footer text.

To the right of each entry area is a contextual menu that lets you insert variables into the entry area.



You can insert the current page number, time of printing, or date of printing.

To insert a variable, choose it from the contextual menu. 4th Dimension inserts the variable in the entry area at the insertion point. You can combine variables with text.

Specifying Font, Attributes

You can specify different fonts, font sizes, justification, and styles for page headers and footers.

- ▶ To specify font attributes:
 - Choose a font and font size from the drop-down lists and click one or more Style check boxes.

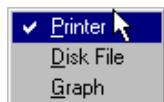
Your specifications are applied to all three entry areas. You cannot apply different font attributes to different areas of the header or footer. Some Style combinations are not valid. For example, you can choose Bold and Italic, but you cannot choose both Plain and Bold.

Printing a Quick Report

After you have completed your report design, you can print the quick report. You can print a quick report to a variety of output devices:

- On the standard printer selected in the Print Manager (the Chooser on Macintosh)
- To disk
- To a graph
- ▶ To select an output device:
 - Choose Print Destination from the File menu.

The Print Destination hierarchical menu contains three items.



Printer

This option uses the printer you have chosen in the Print Manager (Chooser on Macintosh). You can print to a printer without using the Print Destination item by choosing **Print** from the **File** menu. If you are printing to a printer, you can preview the report before printing it.

- ▶ To print to a printer:
 - 1 Choose Print from the File menu.

2 Click the OK button and follow the standard 4th Dimension procedure for previewing and printing your report.

3 Choose the settings that are appropriate for your report and click the OK button.

Disk File

This option saves your quick report to a tab-delimited disk file that can edit with other applications, including text editors and spreadsheets.

When you use this option, 4th Dimension automatically uses the column headings as the first “record” that is exported.

► To print to a disk file:

1 Choose Disk File from the Print Destination hierarchical menu.

1 Choose Print from the File menu.

4th Dimension displays a standard create-file dialog box and asks you to enter a filename.

2 Enter a filename and click the OK button.

4th Dimension displays a dialog box that keeps you informed of the progress of the operation. Click the **Stop Printing** button to cancel the operation.

After the report is printed to a file, 4th Dimension returns you to the Quick Report editor. Remember to change the output device if you want to resume sending a quick report to a standard printer.

Print to Graph

This option is not supported in Biota. If you wish to create a graph from a Quick Report, export the report as a flatfile, then use another application (e.g. Microsoft Excel) to create the graph.

Appendix F

Updating Biota 1.x Data Files to Biota 2 Format

WARNING: Once a Data File is converted to Biota 2 format, you will not be able to open the file under Biota 1 anymore.

Biota Data Files created under Biota 1 (any version) must be converted to a new format to run under Biota 2 (any version). In most cases, Data File conversion goes quickly and smoothly. This section provides instructions for straightforward cases as well as those few that require extra steps.

The steps needed for conversion depend on whether your Biota 1 Data File has any hidden problems, so you may need several copies of the original Data File before you are through. For this reason, be sure to always keep at least one full backup of each *original* Biota 1 Data File that you intend to convert, in case of difficulties with the conversion.

Tools for Data File Conversion

Depending on your Data File, you will need to use some or all of the following software tools for the conversion. Their use is described in more detail in later sections of this Appendix.

- **Biota 2.** Whether you are using BiotaApp (the stand-alone version of Biota) or Biota4D (the client/server version), Biota 2 itself actually does the final conversion to the new format, simply by opening the Biota 1.x Data with Biota 2. You can find Biota 2 in the installation folder on the Biota CD.
- **BiotaApp 1XFR.** Sometimes, Biota 1 Data Files with images do not convert properly to Biota 2. BiotaApp 1XFR is a final version of Biota 1 that includes a special tool (Export Images to Biota2, in the Im/Export menu) that exports images from a Biota 1 Data File to external image files, deletes the images from the Biota 1 file, and creates a log file to guide automated image import to the corresponding Biota 2 Data File. You can find BiotaApp 1XFR in the Biota Tools folder on the Biota CD.
- **4D Tools Version 3.5.4.** This version of 4D Tools is used with Biota 1.x and Biota 1 Data Files. It is recommended that you use 4D Tools to compress (and repair, if necessary) your Biota 1 Data Files before converting them to Biota 2 format. You can find 4D Tools Version 3.5.4 in the Biota Tools folder on the Biota CD.
- **4D Tools Version 6.7 (or later).** This version of 4D Tools is used with Biota 2.x and Biota 2 Data Files. You can use it to compress (and repair, if necessary) your Biota 2 Data Files after conversion from Biota 1 format. You can find 4D Tools Version 6.7 (or later) in the Biota Tools folder on the Biota CD.

Data File Conversion: Step by Step

A. Decide on a Conversion Strategy

- **If your Biota 1 Data File contains no images or only very small images,** skip Section B and follow the steps in [Section C](#). Then continue with Sections D (if necessary), and E, below; skip Section F.
- **If your Biota 1 Data File contains many images or any large images,** it is highly recommended that you begin with the steps in [Section B](#), then proceed with Sections C, D (if necessary), E, and F.

B. Export All Images from the Biota 1 Data File

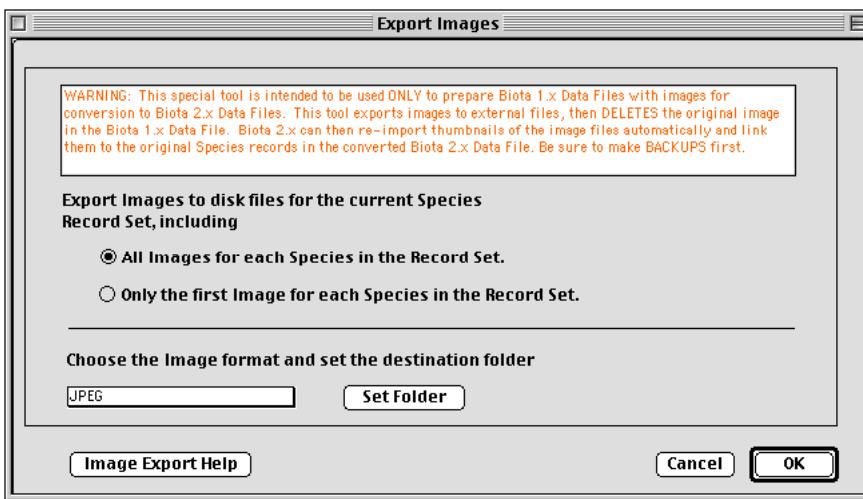
1. **Make a backup copy of the Biota Data File you intend to convert.**
2. **Locate the appropriate version of BiotaApp 1XFR for your platform** (Windows or Mac OS) in the Biota Tools folder on the Biota CD. BiotaApp 1XFR includes a special tool that exports images from a Biota 1 Data File to external image files, deletes the images from the Biota 1 file, and creates a log file to guide automated image import of the corresponding Biota 2 Data File.

NOTE: Biota 1.6.1 and earlier versions do not include this tool.

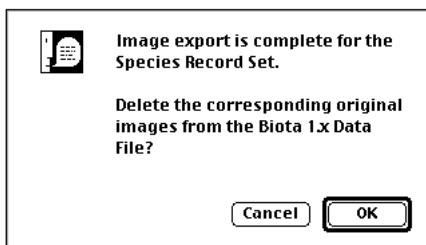
3. **Install BiotaApp 1XFR on your hard-drive.**
4. **Press and hold the ALT key (Windows) or OPTION key (MacOS) while launching BiotaApp 1XFR.** The file navigation window opens.
5. **Locate and open the Biota Data File you intend to convert.**
6. **Using Biota search tools** (Chapter 12, “[Finding and Updating Records](#)”), **create a Species Record Set** representing the Species records for which you will export Image files.

NOTE: Ultimately, you will need to export all the images in your Data File and delete the images from the Data File. If you have a large number, however, try it out first with a smaller group of Species records to understand the process or to test image formats. Biota exports the images first and then asks you to confirm or cancel deletion of the Data File Image records, so you can wait to delete until you are sure it is working properly and then export and delete all Image records at once.

7. From the Im/Export menu in BiotaApp 1XFR, choose Export Images to Biota 2. Biota presents an options screen.



- **Either:** Choose “All Images for each Species in the Record Set,” when you are ready for the final export.
 - **Or:** Choose “Only the first Image for each Species in the Record Set,” if you wish to perform preliminary tests.
8. Choose an image format for the exported image files from the popup list.
9. Click the Set Folder button and confirm or enter the name of the Image Folder that Biota will create to hold the exported image files. *Be sure you have plenty of space on the drive you choose to hold the exported image files.*
10. Click the OK button to launch the image file export. A progress indicator appears. When the export process is complete, Biota asks if you wish to delete the Image records in the Biota Data File.



- **Either:** Click OK to permanently delete the Image records in the Biota Data File that were exported to image files.
 - **Or:** Click Cancel to leave the Image records untouched. The exported image files will not be affected.
11. Once external image files have been created for all Image records and the Image records deleted from the Biota 1 Data File, carry out the steps in Parts C, D (if necessary), and E, below. You will then follow the instructions in Part F to create

thumbnail images in the Biota 2 Data File, each linked to an exported image file. A special log file guides this process.

WHAT BIOTAPP 1XFR EXPORTS. File names for the exported image files are assigned automatically, in the form SpeciesCode_ImageName.Extension, where the Extension identifies the image format that you specify in the popup list in [Step 8](#), above. If the total length of the file name, including the extension, exceeds 31 characters, it is truncated to 31 characters. If a proposed file name would duplicate an existing one in the Image Folder, a numerical suffix is automatically added after the Image Name component of the file name.

Two log documents are automatically created and placed in the Image Folder. Both are plain text documents, which can be read with any text editor. The initial exclamation point, which is part of the file name, forces the log files to appear first in the image folder.

1. **!ImageExportErrors.txt** lists any Image records that could not be exported to image files, with an error code for each failure. If you get errors, try to figure out why by looking at the offending Image record in BiotaApp 1XFR. (The most common errors involve corrupted image records.) If you cannot figure out the problem, try manually exporting the image from within BiotaApp 1XFR to an image file, then delete it from the Data File. If all else fails, write to: colwell@uconn.edu for help, and send the **!ImageExportErrors.txt** file as an attachment.
2. **!ImageFileList.txt** lists all images exported and the file names assigned. When you import the image files into the converted Biota 2 Data File, as detailed in [Section F](#), Biota will use this list to link the external image files with corresponding thumbnail images that it creates in the Biota 2 Data File. (You may choose, instead, to import the full images in the Biota 2 Data File.)

The format for the Image File List is as follows:

Column 1: The name of the parent table in Biota (all exported image files exported by BiotaApp 1XFR belong to the Species table).

Column 2: The Species Code for the parent record.

Column 3: The Image Name for this Image.

Column 4: The full name (including extension) of the external image file created.

C. Compact the Biota 1.x Data File

1. **Make sure space is available on your hard drive** for a duplicate copy of the Biota 1 Data File to be compacted. The process of compacting creates a new copy of the Data File.
2. **Locate 4D Tools Version 3.5.4 for your platform** (Windows or Mac OS) in the Biota Tools folder on the Biota CD. (You do *not* want 4D Tools Version 6.7 or a later version at this point.)
3. **Copy 4D Tools to your hard drive.**

WARNING: 4D Tools does not allow you to use any other application while it is running.

4. **Launch 4D Tools.** A file navigation window appears.

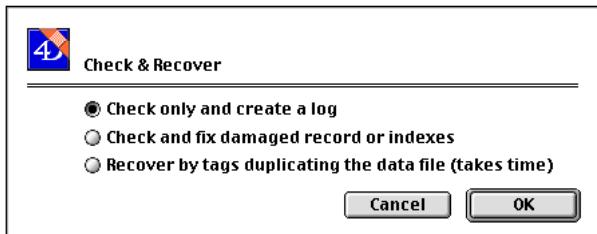
- **Windows:** The window instruction reads “Open.” Make sure the File Type option selected is “All Files (*.*)”.
 - **Mac OS:** The window instruction reads “Select the Structure File to Open.”
5. **Locate your installed copy of Biota 1.x.** You can use BiotaApp 1.6.1, BiotaApp 1XFR, Biota4D 1.6.1, or an earlier 1.x version of BiotaApp or Biota4D if you did not update to 1.6.1. Select the file, but follow the next step before opening it.
 6. **Press and hold the ALT key (Windows) or OPTION key (Mac OS) while clicking Open** in the navigation window. 4D Tools now requests you open a data file.
 - **Windows:** The window instruction reads “Open which datafile.”
 - **MacOS:** The window instruction reads “Open Data File.”
 7. **Locate and open the Biota 1.x Data File that you want to compact** for conversion to Biota 2 format. 4D Tools completes its launch but opens no windows.
 8. **From the Utilities menu in 4D Tools, select Compact.** 4D Tools asks you to “Create a data file.” This will be a compacted copy of the Biota Data File you selected in Step 7.
 9. **Give the compacted Data File a distinctive name and click the Save button.** 4D Tools compacts the Biota Data File, displaying a series of progress indicators. Depending upon the size of your Data File, this process will take from a few seconds to a few hours. The process is complete when the final progress indicator finishes.
 - **If no error messages appear during the compacting process,** proceed to the next section, “[Convert the Data File to Biota 2 Format](#).”
 - **If one or more error messages appear,** you will need to take other steps, then try compacting the Data File again.
 - ◊ **If you get the message: “Out of memory. Quit the program as soon as possible”** while compacting the Image Archive Table, follow the directions in Section B, “[Export All Images from the Biota 1 Data File](#),” above, then try compacting the Data File again.
 - ◊ **If you get the “Out of memory...” error message at any other stage, or if other errors occur,** follow the instructions in Section D, “[If Necessary, Repair the Biota 1.x Data File](#),” immediately below.

D. If Necessary, Repair the Biota 1.x Data File

1. **Make sure space is available on your hard drive** for a duplicate copy of the Biota 1 Data File to be compacted. The repair process creates a new copy of the Data File.
2. **Locate 4D Tools Version 3.5.4 for your platform** (Windows or Mac OS) in the Biota Tools folder on the Biota CD. (You do not want 4D Tools Version 6.7 or a later version at this point.)
3. **Copy 4D Tools to your hard drive,** if you have not already done so.

WARNING: 4D Tools does not allow you to use any other application while it is running.

4. **Launch 4D Tools.** A file navigation window appears, asking you to “Select the Structure File to Open.”
5. **Locate your installed copy of Biota 1.x.** You can use BiotaApp 1.6.1, BiotaApp 1XFR, Biota4D 1.6.1, or an earlier 1.x version of BiotaApp or Biota4D if you did not update to 1.6.1. Select the file, but follow the next step before opening it.
6. **Press and hold the ALT key (Windows) or OPTION key (Mac OS) while clicking Open** in the navigation window. 4D Tools now requests you to “Open Data File.”
7. **Locate and open the Biota 1.x DataFile that you want to compact** for conversion to Biota 2 format. 4D Tools completes its launch but opens no windows.
8. **From the Utility menu in 4D Tools, choose Check & Recover.** An option screen appears.



9. **Choose an option.**
 - **Check only and create a log.** If you choose this option (the default), 4D Tools will check the Data File for damage. A text file called “Journal,” in the same folder with the Data File, describes any damage found. The Biota Data File is not modified.
 - **Check and fix damaged records or indexes.** If you choose this option, 4D Tools will attempt to repair any damage it finds. If it cannot do so successfully, a message appears recommending the next option.
 - **Recover by tags, duplicating the Data File.** With this option selected, 4D Tools attempts to build an entirely new copy of the Data File (named DataFilename.temp, where DataFilename is the name of your original Data File) based on “tags” stored with each record when it was created.

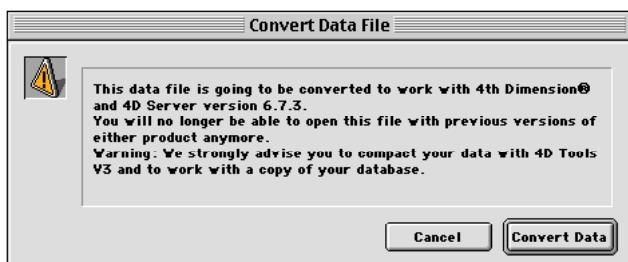
WARNINGS:

- a. Use the recover-by-tags option only if the previous option fails.
 - b. Recovery by tags may take several hours for a large Data File.
 - c. If you choose to recover by tags, you must have a single mounted volume with at least enough space available to duplicate the Data File.
 - d. A Data File that has been recovered by tags may contain records that were previously deleted.
-

10. Once the Date File is repaired, you should compact it, before conversion to Biota 2 format. Follow the steps in Section C, “[Compact the Biota 1.x Data File](#),” above.

E. Convert the Data File to Biota 2 Format

1. **Make sure the Biota 1 Data File is ready.** You should have successfully compacted (or repaired and compacted it), as described in [Section C](#) and [Section D](#), above.
2. **Press and hold the ALT key (Windows) or OPTION key (Mac OS) while launching BiotaApp 2.x or Biota4D 2.x.** The file navigation window opens.
3. **Locate and open the Biota Data File to be converted.** A 4D warning message appears.

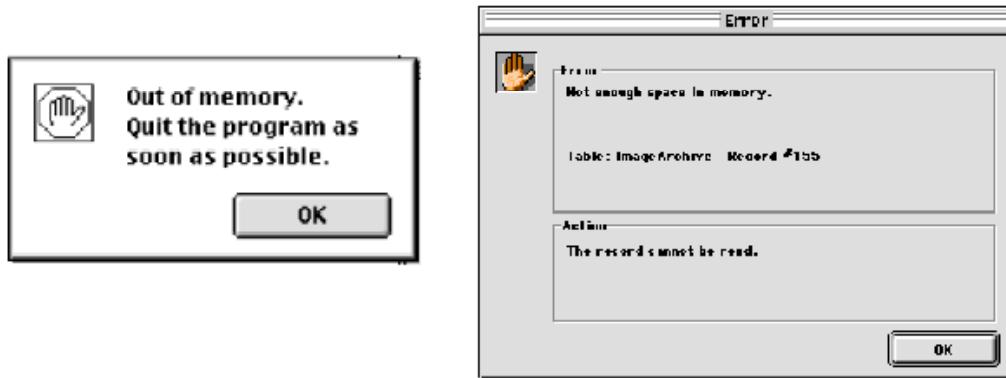


4. **Click the Convert Data button.** Biota presents a series of progress indicators as each table and index is converted.



- **If no error message appears** during the conversion process, the conversion is complete. You can begin to use the converted Biota Data File, but keep your backups of the unconverted Biota 1 Data File until you are sure there are no hidden problems. If you have images in your Data File, be sure to verify that they were properly converted and perform normally. If you exported Images to external files, now is the time to re-import them as linked thumbnails, following the instructions in [Section F](#), below.

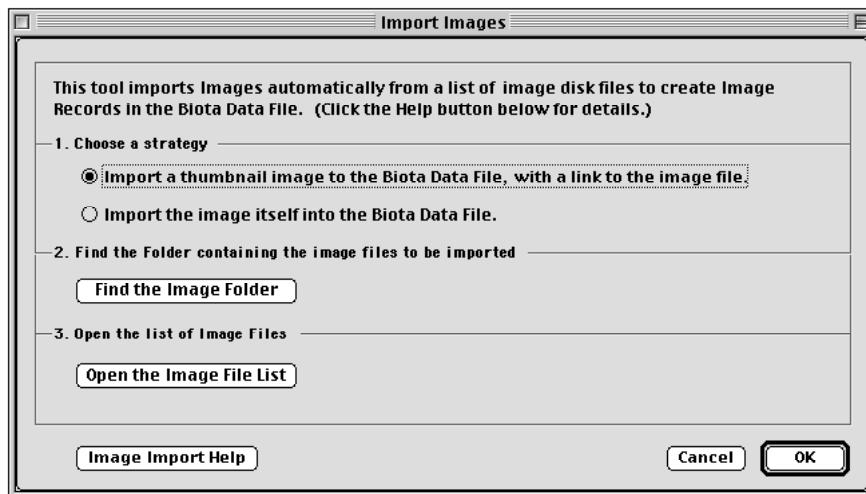
- If an error message appears, you will need to repair the Biota 1 Data File ([Section D](#), above), compact it ([Section C](#), above), and then try converting it again (this section). The most common error messages are these:



- If 4D Tools cannot repair the Data File, all is not lost! You can export all text information and images from your Biota 1.x Data File, create an empty Biota 2 Data File, and import the information and images, table by table. This process is described in detail in Appendix G, "[Merging Two Biota Data Files](#)."

F. Import Linked Thumbnails or Full Images Into the Biota 2 Data File

1. Make a backup copy of the Biota 2 Data File that you have successfully converted from Biota 1 format.
2. Press and hold the ALT key (Windows) or OPTION key (Mac OS) while launching BiotaApp 2.x or Biota4D 2.x. The file navigation window opens.
3. Locate and open the Biota 2 Data File that you converted from Biota 1 format.
4. From the Im/Export menu in Biota 2, choose Import Images. Biota presents a setup screen.



5. Choose an import strategy.

- ***Either: Import a thumbnail image to the Biota Data File, with a link to the image file.*** This option creates a thumbnail image in your Biota Data File for each external image file in the **!ImageFileList.txt** log, with a persistent link to the external image file. The external image file remains unchanged. (When you use the image zoom tools in Biota 2, the link is used to display the full image from the file.)

NOTE: This option is highly recommended for any Biota Data File that has more than a few images or any large images.

- ***Or: Import the image itself into the Biota Data File.*** In this case, a full copy of the image is imported to the Biota Data File for each image file in the **!ImageFileList.txt** log file. The external image file remains unchanged.

6. **Find the folder containing the image files to be imported.** Click the “Find the Image Folder” button and locate the folder that contains your exported Biota 1 images and the **!ImageFileList.txt** log file.

WARNING: Do not change the name of the **!ImageFileList.txt** document.

7. **Find and open the list of image files.** Click the “Open the Image File List” button and locate the **!ImageFileList.txt** log file.

8. **Click OK to launch the import.** While displaying a progress indicator, Biota automatically reads the file names, Image Names, and Species Codes from the log file.

If you chose the thumbnail option, Biota creates and saves a thumbnail image in the Biota 2 Data File, for each external image file, with the same placement and Image Name it had in the Biota 1 Data File. The path to the external image file is also saved in the Biota 2 Data File, allowing the full image from the external file to be transparently displayed in zoomed views or edited within Biota 2. See Chapter 19, [“Images”](#)

9. **Test the images when the process is complete.**

Appendix G

Merging Two Biota Data Files

Once in a while, you may need to merge all or part of the contents one Biota Data File with another. You and a colleague or an assistant might work separately for a while, then merge records in a single Data File. Or you might decide to combine two Data Files of your own. Or, as a last resort when a Data File is damaged and cannot be repaired with 4D Tools (see Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#)”) you might need to rescue all the data you can from the damaged file and import it into an empty, new one.

Biota users sometimes ask why there is no “Merge Files” tool in Biota. Such a tool is certainly possible, theoretically, but extremely complex to develop and maintain, because of the extensive integrity-checking required in a complex relational structure such as Biota’s. For a start, the problem of non-unique Record Codes (if it arises) is one best solved by you, not by an algorithm.

Note: This appendix assumes that you are thoroughly familiar with Biota’s Export Editor (see “[Exporting Data by Tables and Fields](#)” in Chapter 27) and Import Editor (see Chapter 28, “[Importing Data](#)”). If you will be moving Images from one Data File to another, you must also be familiar with “[Exporting and Importing Images](#)” in Chapter 19. You will also need to understand the tools of the Find menu (see Chapter 12, “[Finding and Updating Records](#)”).

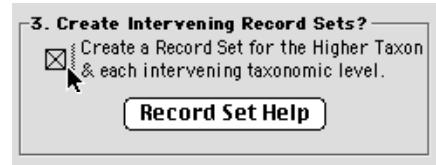
You must first determine which Data File is the *Donor Data File*, and which is to be the *Recipient Data File*. Make a *backup* of each file before beginning.

In the Donor Data File

1. In the Donor Data File, find all the Specimen records that you want to transfer.
2. Save this Specimen Record Set as a Record Set Pointer file so you can find them again easily (see “[Record Set Pointer Files](#)” in Chapter 3).
3. From the Find menu, choose “Higher Taxa for Lower Taxa.” You want to find *all higher* taxon records that are linked to the Specimen Record Set.
4. In the “Higher Taxa for Lower Taxa” window, set up the Query: “Find All Kingdoms for the Specimen Record Set.”



5. Check the option box that creates Record Sets for intervening taxon levels.



6. Click the “Find” button to launch the query.

- **If you get a message that “No Kingdom Records were found for the Specimen Record Set,”** it means that none of the Specimen records is linked through all intermediate taxon tables to any Kingdom record, or that there are no Kingdom records.

In this case, click the “Try Again” button, and try the query “Find All Phyla/Divisions for the Specimen Record Set.”

If that query fails, continue on down the taxonomic hierarchy until you get a successful query result.

- **If the Kingdom Record Listing screen appears,** dismiss it and continue with the next step.

7. Using the Export Editor (“Export by Tables and Fields” from the Im/Export menu), export the Record Set for each level of the taxon hierarchy, each to a separate text file, clearly named. In each case use the “All” button to select all fields for export, in their default (alphabetical) order. (There is no need to include a header row, but you may do so if you wish.)

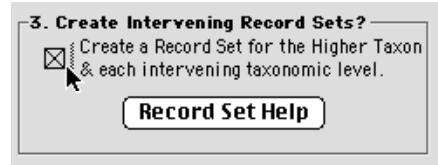


NOTE: If you did not find any linked records above a certain taxon level, export only up to that level.

8. **Using the Export Editor, export the Specimen Record Set** to a text file, clearly named. Use the “All” button to select all fields for export, in their default (alphabetical) order.
9. **From the Find menu, choose “Places for Specimen or Species.”** You want to find all Collection and Locality that are linked to the Specimen Record Set.
10. **In the “Places for Specimen or Species” window, set up the Query: “Find All Localities for the Specimen Record Set.”**



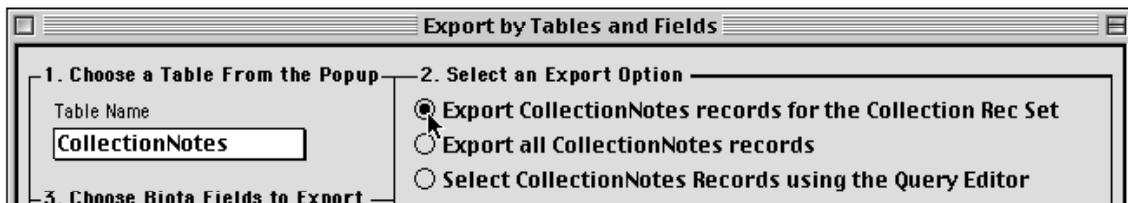
11. **Check the option box that creates Record Sets for intervening taxon levels.**



12. **Click the “Find” button to launch the query.**

13. **Dismiss the Locality Record Listing screen.** (If you get an error message instead, set up the query “Find all Collections for the Specimen Record Set” instead.)
14. **Using the Export Editor, export the Locality and Collection Record Sets**, each to a separate text file, clearly named. In each case use the “All” button to select all fields for export, in their default (alphabetical) order.
15. **If you want to transfer any Loans records**, set up the Loans Record Set to include only those Loan records that you want to transfer, and export them using the Export Editor.
16. **If there are Notes attached to any of the records to be transferred**, use the Export Editor (*not* the “Export Note” tool to export them to text files, using the option “Export [Parent table]Notes records for the [Parent table] Rec Set.” See the example below for the CollectionNotes table.

The Notes tables are: SpeciesNotes, SpecimenNotes, CollectionNotes, LocalityNotes, and LoansNotes.



17. If you have created Auxiliary Fields:

- a. **Using the Export Editor, export all FieldName records** for each parent table (Species, Specimen, Collection, or Locality). The option setup for CollFieldNames is shown below.



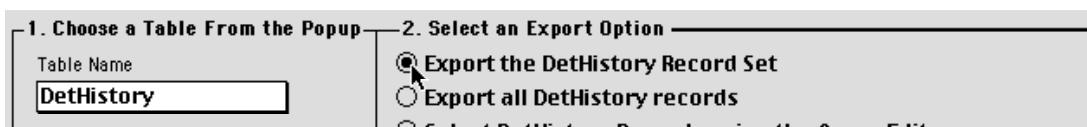
- b. **Using the Export Editor, export allFieldValue records linked to each parent table Record Set** (Species, Specimen, Collection, or Locality Record Set). The option setup for CollFieldValues is shown below.



- c. **Using the Export Editor, export all Project Records.** (Unwanted Projects can be deleted later.)
- d. **Using the Export Editor, export all AuxIndex Records.**

18. If you want to transfer Determination History records:

- From the Special menu, choose “Det Hists for the Spcm Rec Set.”**
- Using the Export Editor, export the Determination History Record Set.**



- Using the Export Editor, export *all* Personnel records (if any) and *all* Group records (if any). (Unneeded records will be deleted later in the recipient Data File.)**
- Using the Export Editor, export *all* Reference records and *all* ReferenceLinks records (if any). (Unneeded records will be deleted later in the recipient Data File.)**
- Using the Export Editor, export *all* ListItems records (if any).**

NOTE: Do *not* export the records of the *Lists* table.

- If you need to transfer ImageArchive records (*Images*), follow the instructions in “[Exporting and Importing Images](#)” in Chapter 19.**

In the Recipient Data File

The biggest headache with transferring records is dealing with Record Codes and other Key fields that must be unique for each record—taking *both* the Donor and the Recipient Data File into account. It is well worthwhile to examine this issue before importing the files you exported from the Donor file.

NOTES:

- You will use the Import Editor (“Import by Tables and Fields” from the Im/Export menu) for importing all text files. Be careful to follow directions regarding the “Import new records” versus the “Merge imported records” options in the Import Editor.
 - In every case, in the instructions below, use the “All” button to select all fields for import, in their default (alphabetical) order.
 - If you included a header row in the exported files, be sure to check the box for it in the Import Editor.
 - Import all Record sets *in the order specified*. Otherwise you will have orphan record errors.
-

1. Using the “Import new records” option, import the text files for the following tables.

- Specimen
- Species
- Collection
- Locality
- Species
- Loans

NOTE: Unless you have planned very carefully, it is likely that you will get duplicate Key errors while importing these records (see “[Duplicate Key Errors](#)” in Chapter 3). You will have to correct the duplications and try again. Alternatively, you could use the “Merge Imported Records” import option, but any records for which the Record Code in the Donor File matches a Record Code in the Recipient File will not be imported.

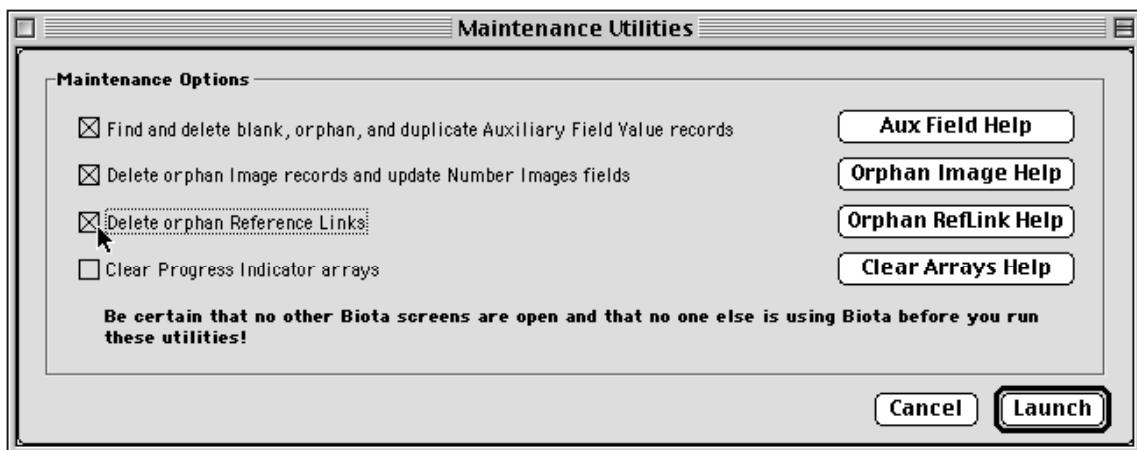
If the two Data Files *intentionally* share Species Codes, Collection Codes, or Locality Codes, then use the “Merge” option instead of the “New Records” option for such tables.

2. Using the “Import new records” option, import the text files for the following tables.
 - SpeciesNotes, SpecimenNotes, CollectionNotes, LocalityNotes
 - LoansNotes
 - DetHistory
3. Using the “Merge imported records” option, import the text files for the following tables.
 - Genus, Family, Order, Class, Phylum, Kingdom
 - Personnel
 - Group

NOTE: The reason for using the Merge option is that the two Data Files may very well legitimately share higher taxa and Personnel records, making the “New Records” option inappropriate. If you want to check for duplications, then use the “New Records” option.

4. If you are importing Auxiliary Fields, use the “Import new records” option to import the text files for the following tables.
 - SppFieldName, SpcmFieldName, CollFieldName, LocFieldName
 - SppFieldValue, SpcmFieldValue, CollFieldValue, LocFieldValue
 - Project (use the Merge option if you know that Projects are shared)
 - AuxIndex

5. If you are importing Reference records, use the “Import new records” option to import the text files for the following tables.
 - Reference
 - ReferenceLinks
6. If you are importing ImageArchive records, now is the time to do so, following the instructions in “[Exporting and Importing Images](#)” in Chapter 19
7. From the Special menu, choose “Maintenance Utilities.”
The utilities option screen appears.



8. Enable the first three options, then click the “Launch” button.
A series of report screens appear as the utilities are run. If you get many errors, you may have made mistakes in exporting or importing.
9. Check the imported data thoroughly.

Appendix H

Using Biota4D with 4D Server or 4th Dimension

If you need to provide direct, simultaneous, desktop-level access to a Biota Data File for two or more users, you can run Biota4D under 4D Server. The 4D Server software, Biota4D, and your Data File all reside on a *server* computer, which can be either a Window or Mac OS machine.

The server computer must be networked with one or more *client* computers. Any network that can run the TCP/IP protocol, including local networks or even the Internet can be used.

4D Server/Client has a true client-server architecture (i. e., not simply file-sharing), with direct, “homogeneous” communications between server and client (no inter-application driver to slow things down) and local object caching on the client machine. The server performs all computationally intensive tasks and uses sophisticated data-caching techniques to minimize disk access delays.

Overview of Biota and 4D Architecture

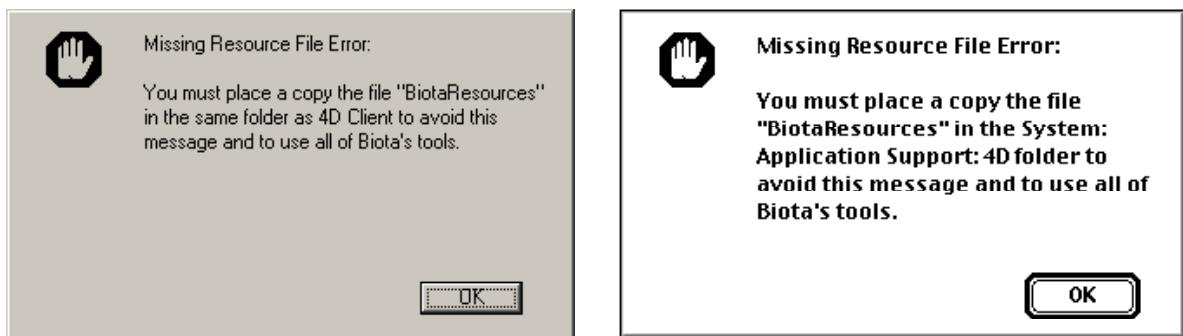
- **Biota4D** is the core Biota application. You can run Biota 4D under 4D Server (the client/server version of 4D) or under 4th Dimension (the single-user version of 4D).
- **BiotaApp** consists of Biota4D merged (invisibly to the user) with 4D Engine; 4D Engine takes the place of 4D Server or 4th Dimension.
- **BiotaApp and Biota4D** are based on precisely the same compiled code (plus 4D Engine in the case of BiotaApp) and have the same features (with the exception of client/server).
- **Biota Data Files are universal.**
 - ◊ **Regardless of whether you use BiotaApp or Biota4D**, the data reside in a Biota Data File (which is just a particular instance of a 4D Data File). You can open and work with the same Biota Data File using Biota4D running under 4D Server or 4th Dimension, or with BiotaApp, running transparently under 4D Engine.
 - ◊ **You can work with the same Biota Data File under Windows or Mac OS** using BiotaApp, or access the Data File from clients of *both platforms simultaneously* running Biota4D under 4D Server.
- **You can run the onboard Biota Web Server** from either BiotaApp or Biota4D. See Chapter 29, “[Internet Strategies](#).”

How to Get Started With 4D Server

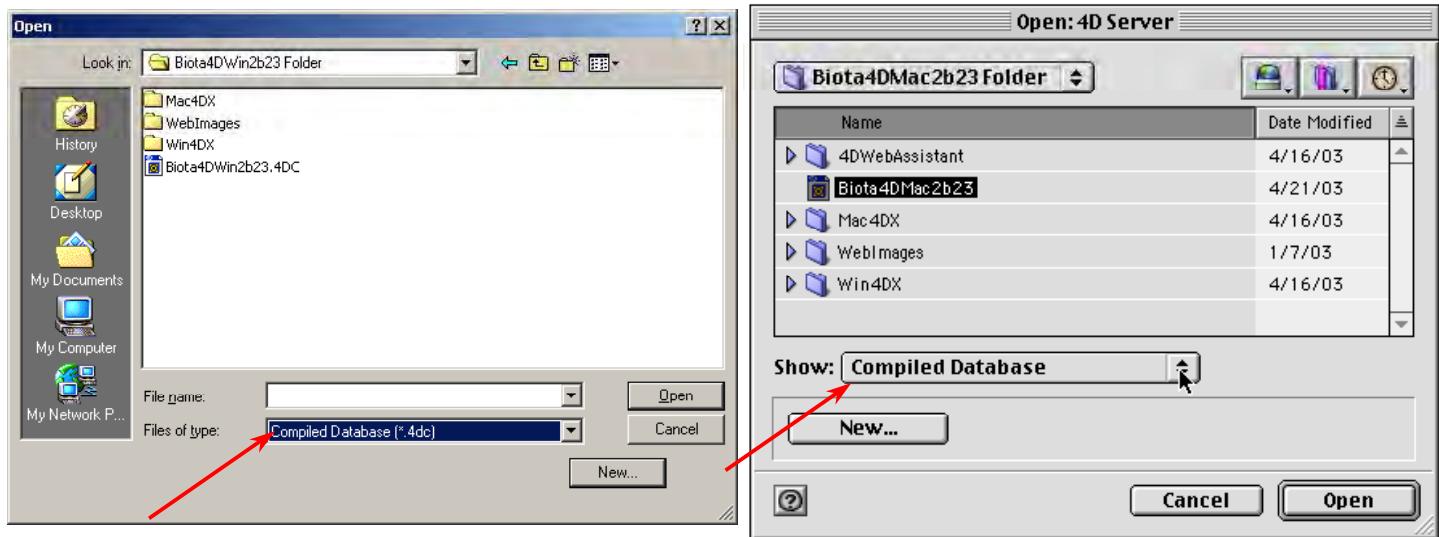
1. **Install the 4D Server application, Biota4D, and your Biota Data File** on whatever computer you designate as the server, following instructions that came with each component.

2. **On each client machine, install 4D Client** following instructions that came with 4D Client. (Do *not* install Biota4D or the Biota Data File on Client machines.)
3. **On each client machine, place a copy of the “BiotaResources” file** that is installed with Biota4D.
 - **Windows Client:** Place the copy of the “BiotaResources.rsr” file in the 4D Client folder.
 - **Mac OS X Client:** Place the copy of the “BiotaResources” file in the Library: Application Support: 4D folder.
 - **Mac OS 9 Client:** Place the copy of the “BiotaResources” file in the System: Application Support: 4D folder.

If the “BiotaResources” file is not present or is in the wrong place, Biota posts an error screen when you launch 4D Client.



4. **Launch 4D Server on the server machine.** The Open file window for your operating system appears.

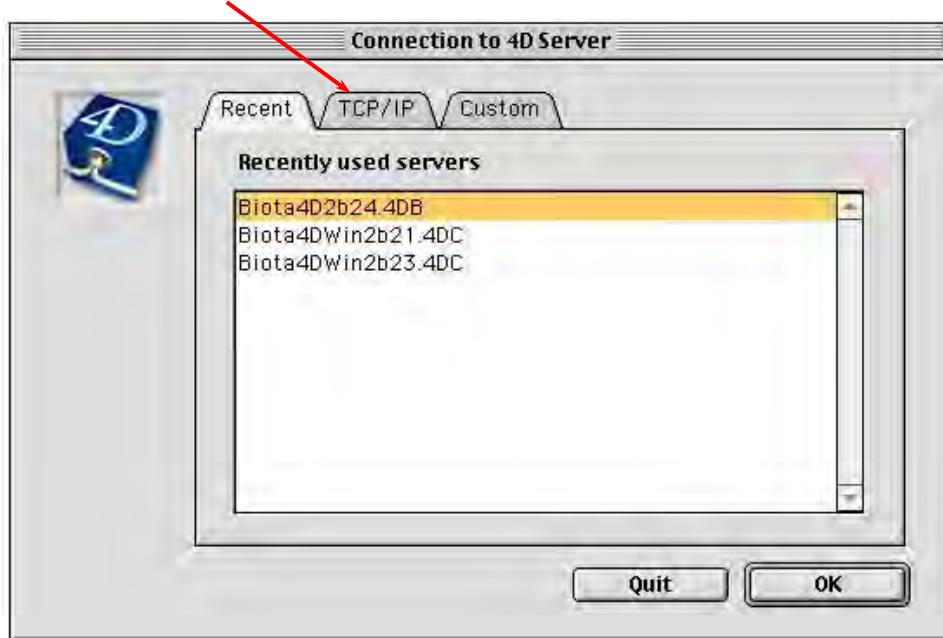


5. **Set the window to display files of type “Compiled Database”** (which is *not* the default). See illustrations above.

- **Windows Client:** The popup is labeled “Files of type.”
 - **Mac OS Client:** The popup is labeled “Show.”
6. **Open the Biota4D application.**
- **Windows Client:** Depress the ALT key while you open Biota4D to force 4D Server to allow you to choose the appropriate Biota Data File.
 - **Mac OS Client:** Depress the OPTION key while you open Biota4D to force 4D Server to allow you to choose the appropriate Biota Data File.
7. **Open the Biota Data File** you want to work with. The 4D Server monitor window appears.

NOTE: If you see a message concerning either a Biota or a QPix licensing issue, please consult “[Licensing for 4D Server/Client, Biota 4D, QPix, and the Web Server](#)” later in this appendix.

8. **Launch 4D Client on a client machine.** The 4D Client selection screen appears, with a list of “Recently used servers” open.



9. **Choose the correct server, or click the TCP/IP tab to show a list of currently available servers.** (Unless there someone else running 4D Server in your local domain, yours will be the *only* database listed.)
- When you select Biota4D from 4D Client on client machine, 4D Server transparently sends all the forms and data that you need on the client machine. To the user, it is exactly like using BiotaApp (although a bit slower, depending on network speed).

Licensing for 4D Server/Client, Biota 4D, QPix, and the Web Server

- **4D Server/Client licensing.**

- ◊ **You must purchase a basic license for 4D Server/4D Client.**

The basic 4D Server license allows 2 simultaneous 4D Client connections. With this license, you receive the software for 4D Server for Windows or for Mac OS, 4D Client for both Windows and Mac OS, and some 4D Utilities (4D Backup, 4D Tools, 4D ODBC, etc.).

In other words, you buy 4D Server to run on *either* a Windows server or a Mac server machine, but in either case, you get 4D Client for both platforms. You can get a version of 4D Server that just runs 4D programs like Biota, or (for more money) one that does that and also allows programming. (But Biota4D is compiled, so no program changes can be made in Biota4D.)

- ◊ **If you want to connect from more than 2 clients,** you must purchase a 4D Client Expansion license or licenses (you can add as many as you need), which come in "packs" of 2, 5, or 10, or 100.
- ◊ **You can download 4D software from www.4d.com.**

WARNING: Before downloading 4D Server/Client and before purchasing a license to use it, be sure to check the [Biota Website](#) to verify *which version of 4D Server* you need to use with the current version of Biota4D.

- ◊ **You can purchase 4D Server/Client licenses** either directly from www.4d.com, or from an authorized 4D reseller.

NOTE: If you work in an academic or non-profit institution, be sure to look for "academic pricing" at www.4D.com.

- ◊ **For information on installing 4D Server/Client licenses,** please see the instructions that come with the 4D software.
- **Biota4D licensing.**
 - ◊ **You must purchase a license for Biota4D** for the same total number of clients that you purchase for 4D Server. Like 4D Server, the Biota4D application comes with a license for two simultaneous Client connections.
 - ◊ **If you want to connect from more than 2 clients,** you must purchase a Biota4D Expansion license or licenses (you can add as many as you need), which (like 4D Server) come in "packs" of 2, 5, or 10, or 100.
 - ◊ **You can download Biota4D software from the [Biota Website](#),** or install the version on the distribution CD.
 - ◊ **You must purchase Biota4D Expansion licenses** directly from Biota's publisher, www.sinauer.com.
 - ◊ **For information on installing Biota4D licenses,** you can use the same procedure described in "[Installing a Biota Web License in Biota4D](#)" in Chapter 30.

- **QPix licensing for Biota4D.** QPix is the image handling plug-in in Biota.
 - ◊ **You must purchase a QPix license for Biota4D** for the same total number of clients that you purchase for 4D Server. Like 4D Server and Biota4D, a QPix license for two client connections come with the basic Biota4D application.
 - ◊ **If you want to connect from more than 2 clients**, you must purchase a QPix Expansion license or licenses (you can add as many as you need), which (like 4D Server) come in "packs" of 2, 5, or 10, or 100.
 - ◊ **QPix software is installed internally in Biota4D.** There is nothing more to install.
 - ◊ **You may purchase QPix Expansion licenses** directly from the developer, www.escape.gr, or at a substantial discount by writing colwell@uconn.edu (the author of Biota, who makes no profit on QPix resales).
 - ◊ **To install a QPix Expansion license**, launch Biota4D under 4D Server, and chose "Licences" from the "Escape" menu on the server machine.
- **Biota's Onboard Web server** runs for one hour (with unlimited connections) each time you launch Biota. To enable the Onboard Web server for unlimited (non-stop) service, you must buy a 4D "Web Extension License" from Sinauer Associates and install it on your computer.
 - ◊ **To place an order with Sinauer**, go to the [Biota Page at the Sinauer Website](http://www.sinauer.com) (www.sinauer.com), telephone (413) 549-4300 (USA), or send a fax to (413) 549-1118 (USA).
 - ◊ **For 4D Web Extension License installation instructions**, see the section "[Installing a 4D Web Extension License](#)" in Chapter 30. If you move Biota to another computer, you can install the same number again.

4D Server: Caveats and Recommendations

- **Do not expect to use the same machine to run both 4D Server and 4D Client.** Although the 4D Server/Client software permits you to set up 4D Server so that you can use 4D Client on the server machine (while running 4D Client on other machines on the network as well, if you wish), communication between Client and Server on the same machine is many times slower than between Client on one machine and Server on another—however counterintuitive that may seem.
- On the other hand, the server machine need not be dedicated solely to running 4D Server. You can use other applications on the server machine while 4D Server operates in the background. Of course, sharing the server CPU in this way will slow down access by clients, and it increases the risk that the server will crash, since something may go wrong with the other applications you are using.
- **Biota always runs faster in single-user mode**—either as BiotaApp or as Biota4D under 4th Dimension—than it runs under 4D Server, accessed only from Client machines. (This comparison assumes that the single-user machine and the server machine are either the same machine or equally fast machines.)

For this reason, you may wish to own either BiotaApp or 4th Dimension for intensive, single-user access to a Biota Data File when it is not being used under 4D Server. (If you own 4th Dimension, you can use it with your copy of Biota4D in single-user mode, as explained below.)

- **Running under 4D Client, Biota speeds up as you use it.** When you first launch 4D Client on a client machine, each “object” (for example, a form) that the client requests is saved in the client machine in “.RES” or “REX” files (see the 4D Server documentation for technical details). The next time the object is needed by that client, whether in the current session or any future one, it is loaded from the local file, rather than over the network from the server.

Further, a second request for the same records (or subsets of records), within a session, is filled faster than the first request, thanks to data caching on the server machine.

Note: Whenever you install an updated version of Biota4D, you can delete all existing.RES and.REX files on each client machine, since new ones are created for the new version.

Running Biota4D under 4th Dimension (Single User)

If you own 4th Dimension (www.4D.com), you can run Biota4D in single-user mode.

The tools, features, and performance of Biota4D under 4th Dimension are identical with BiotaApp. There is no functional advantage to running Biota4D under 4th Dimension, compared with BiotaApp, but if you own 4th Dimension and Biota4D, there is no functional reason not to do so.

Appendix I

Data File Backup, Recovery, Compacting, Indexing, and Segmenting

Backup Strategies for Data Files

It is absolutely essential to back up Biota Data Files on a regular basis.

If a power failure or hardware failure occurs, your Data File may be damaged. Records may be accidentally deleted, in spite of warnings and safeguards built into Biota, or an entire Data File might be accidentally deleted from your hard disk.

The simplest way to back up a Data File is to copy it (or each of its segments, if it is a segmented file) regularly to backup media that can be stored in a different building from the original Data File, or to a backup machine elsewhere. A voltage spike, lightening strike, fire, or flood might easily destroy all disks connected to your computer or even all disks in the same building.

If your Biota Data File is linked to external image files, don't forget to back up the image files on the same schedule.

Of course, you can also use commercial backup software to facilitate record-keeping for multiple backups.

If you use 4D Server (see Appendix H, “[Using Biota4D with 4D Server or 4th Dimension](#)”), an integrated backup system (4D Backup) comes with the server software.

Using 4D Tools to Check, Recover, Compact or Index a Biota Data File

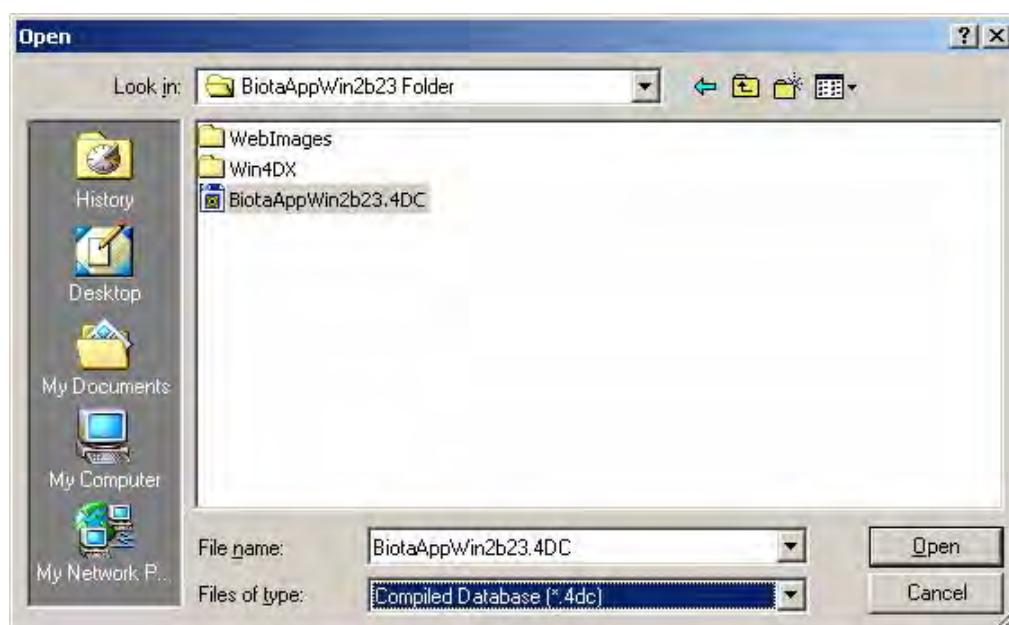
4D Tools is a separate 4th Dimension utility that you will find on the Biota distribution CD. Alternatively, you can download 4D Tools at no cost from www.4d.com. (Be sure to download the correct version. See the [Biota WebSite](#) for information.)

- **Checking and repairing a damaged Data File.** If you see a 4D error message that a Data File is damaged and cannot be opened, try using 4D Tools to repair the Data File. Start with the next section, “[Opening a Biota Data File With 4D Tools](#),” then go to “[Checking and Repairing a Data File](#),” later in this chapter.
- **Compacting or re-indexing a Data File.** 4D Tools can also be used to compact or re-index a Biota Data File that is not damaged. Start with the next section, “[Opening a Biota Data File With 4D Tools](#),” then go to “[Compacting or Re-indexing a Data File](#),” later in this chapter.

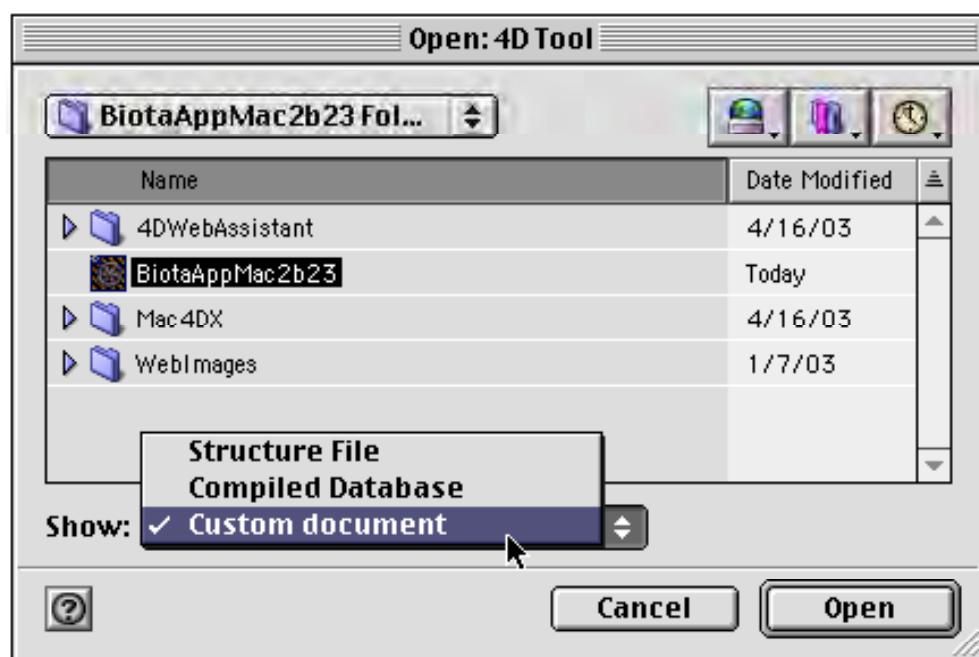
NOTE: If the user Password system has been activated (see Chapter 26, “[Security: Passwords and Access Privileges](#)”), only the Administrator can use 4D Tools to repair Biota Data Files.

Opening a Biota Data File With 4D Tools

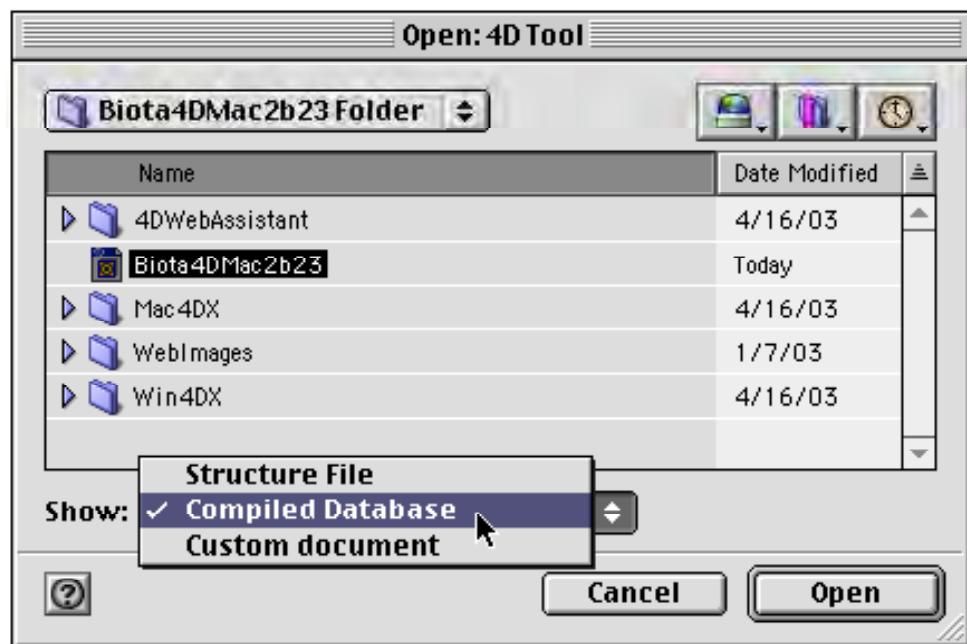
1. **Make a backup of the Data File**, preferably on a different disk. Make sure you have space on your hard-disk for yet another copy, which 4D Tools creates.
2. **Find and launch 4D Tools**. An Open File window for your operating system appears.
3. **Find and open the Biota application** (not the Data File yet) with 4D Tools:
 - **Windows: For BiotaApp or Biota4D, select “Compiled Database” from the “Files of type” popup at the bottom of the “Open” screen, then select the Biota application.**



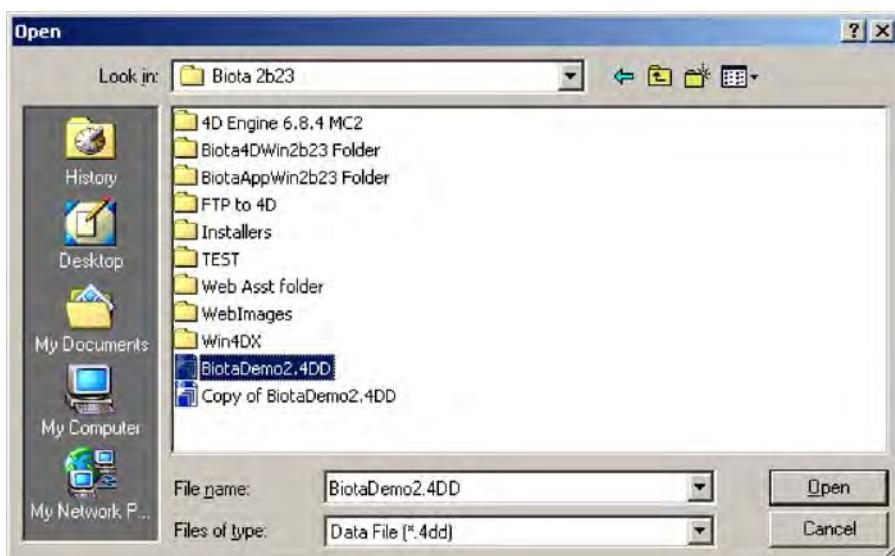
- **For BiotaApp under Mac OS, select “Custom Document” from the “Show” popup at the bottom of the “Open” screen, then select BiotaApp.**



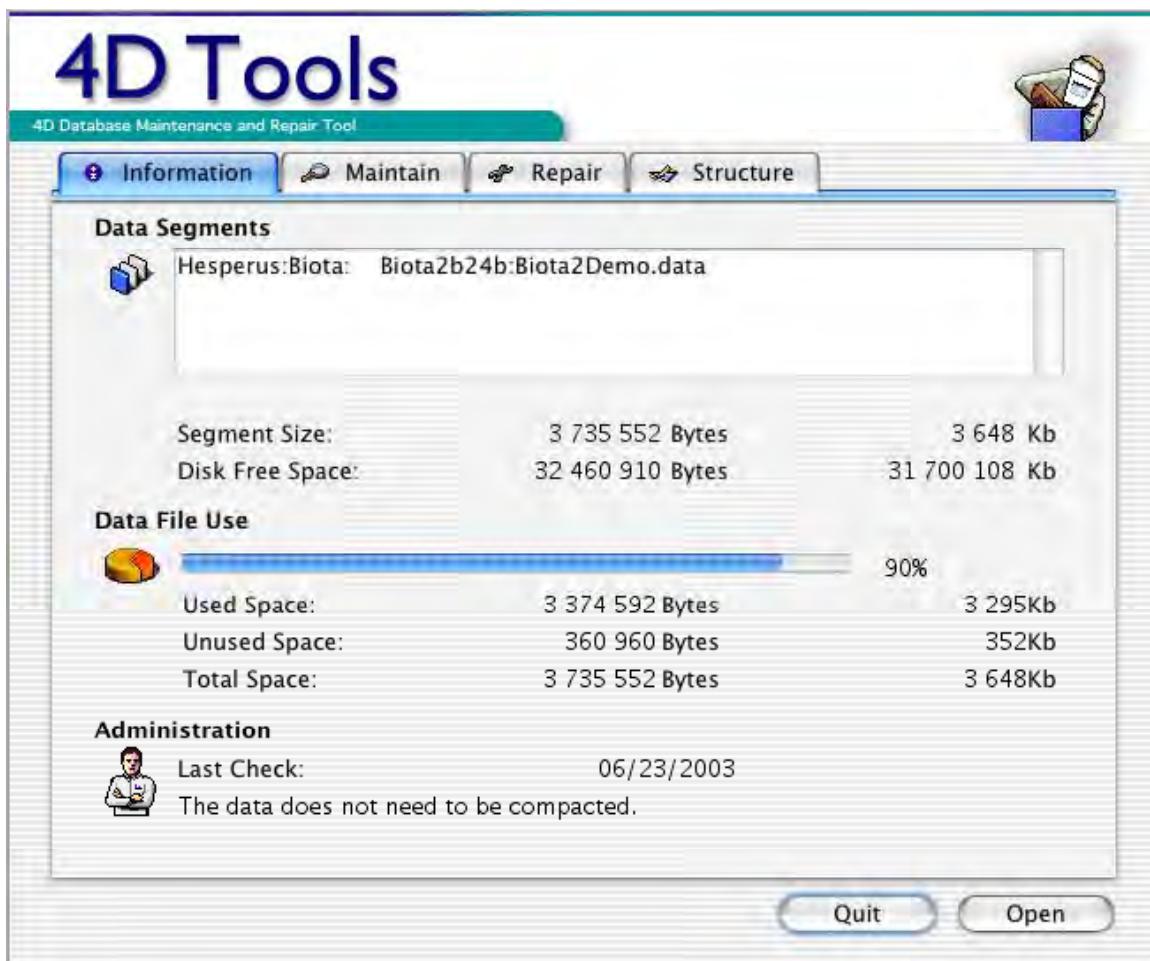
- For Biota4D (the client/server version of Biota) under Mac OS, select “Compiled Database” from the “Show” popup at the bottom of the Open file screen, then select Biota4D.



- Press and hold the ALT key (Windows) or the OPTION key (Macintosh) while you click the “Open” button in the “Open” window.
 - If the User Password system has been activated, the Password window appears.
Enter the Administrator’s user name and password and click the “Connect” button while continuing to press the ALT or OPTION key. An “Open data file” window appears (below).
 - If the user password system has not been activated, an “Open” window appears.



5. Find and open the Biota Data File. The 4D Tools screen appears.



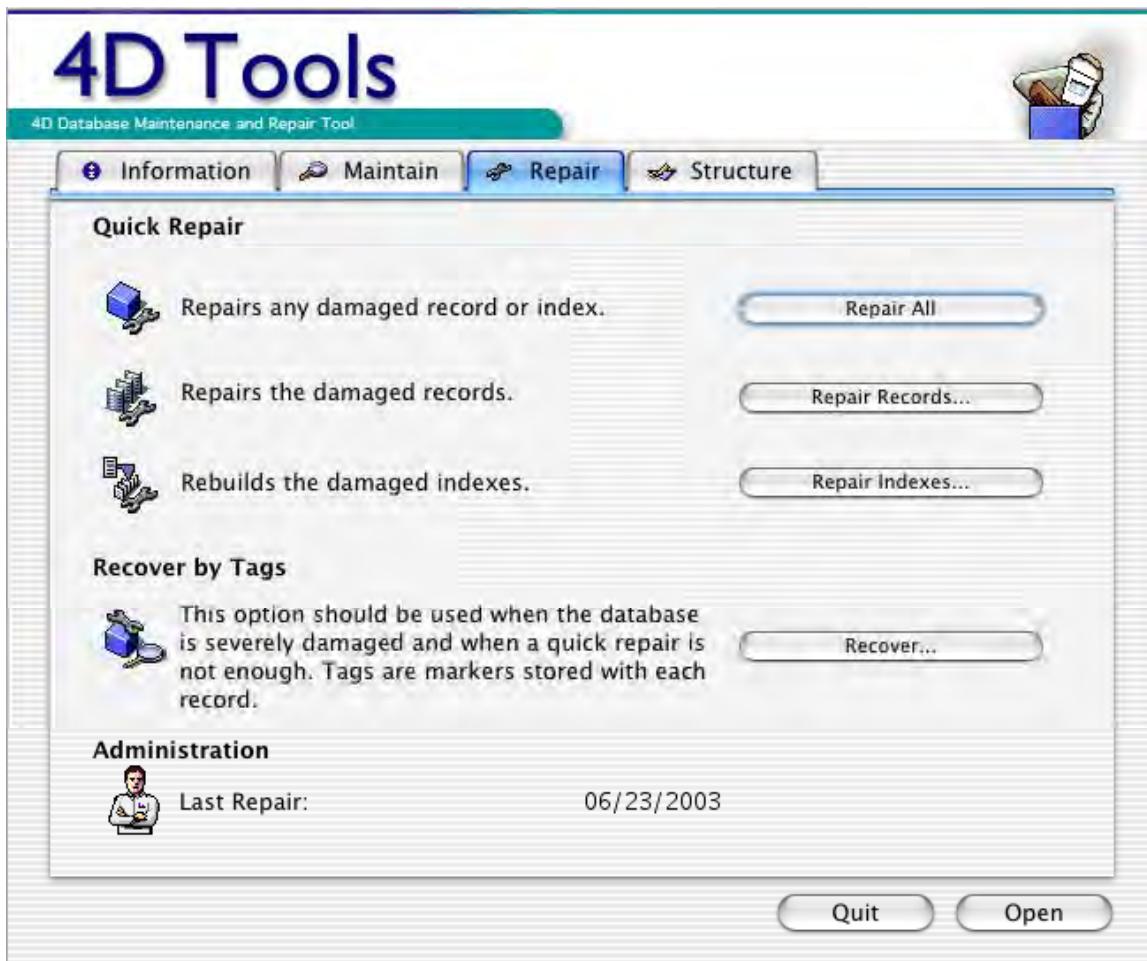
Checking and Repairing a Data File

1. Using 4D Tools, find and open the Data File to be checked and repaired, following the instructions in the preceding section of this chapter, "[Opening a Biota Data File With 4D Tools](#)."
2. Click the "Maintain" tab in the 4D Tools window.



The "Maintain" tab screen appears.

3. Click the “Check All” button. 4D Tools checks records and indexes, and displays a report onscreen.
4. If 4D Tools reports any damage to the Data File, click the “Repair” tab. The Repair tab screen appears.



5. Click the “Repair All” button.

Repair All

4D Tools checks records and indexes, and displays a report onscreen.

6. If 4D Tools was unable to repair the Data File with the “Repair All” tool, click the “Recover” button to attempt to recover the Data File “by tags.”

Recover...

If this approach also fails, you will either have to go back to a previous, undamaged backup of your Data File, or try exporting all records from the damaged Data File to a new, clean Data File (see “[Moving All Records To a New Data File](#)” later in this appendix).

Compacting or Re-indexing a Data File

- **Compacting a Data File.** When you delete records, Biota re-uses the “holes” for new records. Until “holes” are re-used, however, the Data File stays the same size

on the disk. If you want to compact a Data File after deleting many records, you can use 4D Tools to do so.

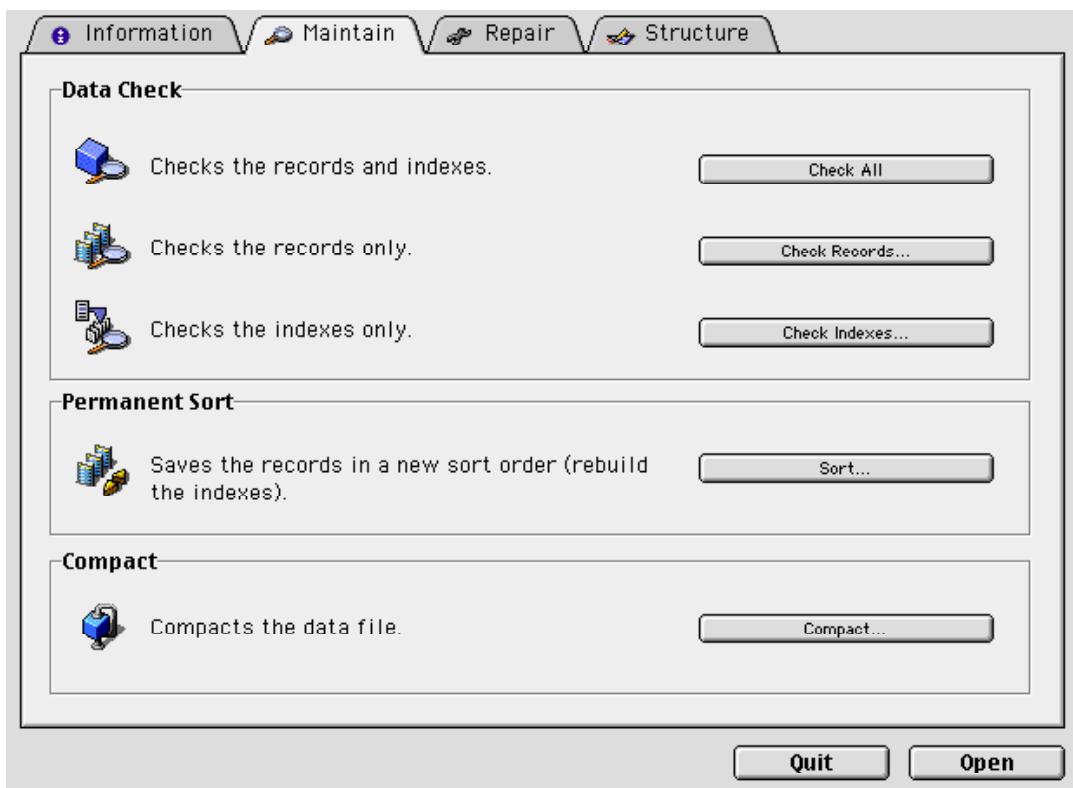
- **Re-indexing a Data File.** When you add new records to a Biota Data File, they are indexed in the order you add them. You can always sort records in a different way using the Sort button in a Biota Record Listing screen (see “[Sorting Records in Record Listing Screens](#)” in Chapter 10), but the Index remains unchanged by such sorts. To change to an index to a particular sorting preference (which will be followed when the “Records not sorted automatically” option is set in the Biota Preferences screen), you can use 4D Tools. Indexing can speed up the display of records in the default (indexed) order, especially for very large databases.

The procedures for compacting or re-indexing a Data File share most steps:

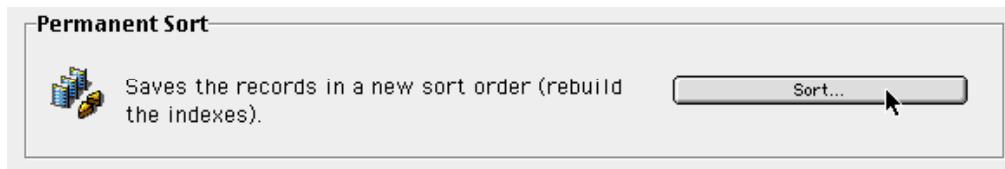
1. **Using 4D Tools, find and open the Data File to be checked and repaired,** following the instructions in the preceding section of this chapter, “[Opening a Biota Data File With 4D Tools](#).”
2. **Click the “Maintain” tab in the 4D Tools window.**



The “Maintain” tab screen appears.

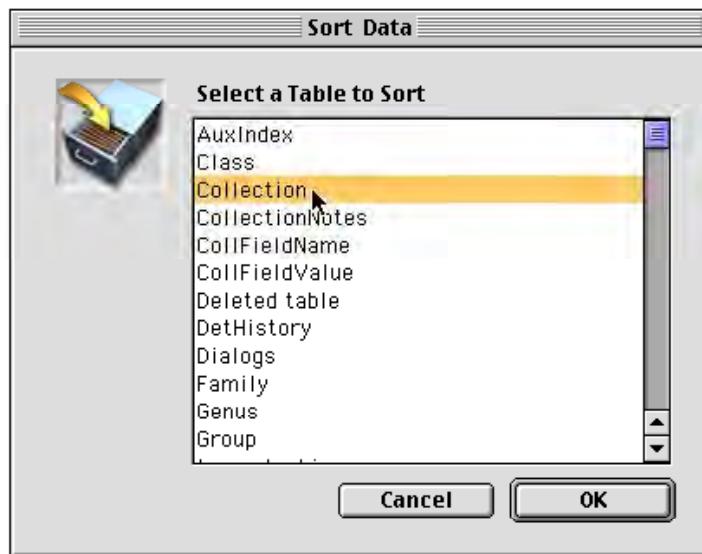


3. To create a new index, take these steps.



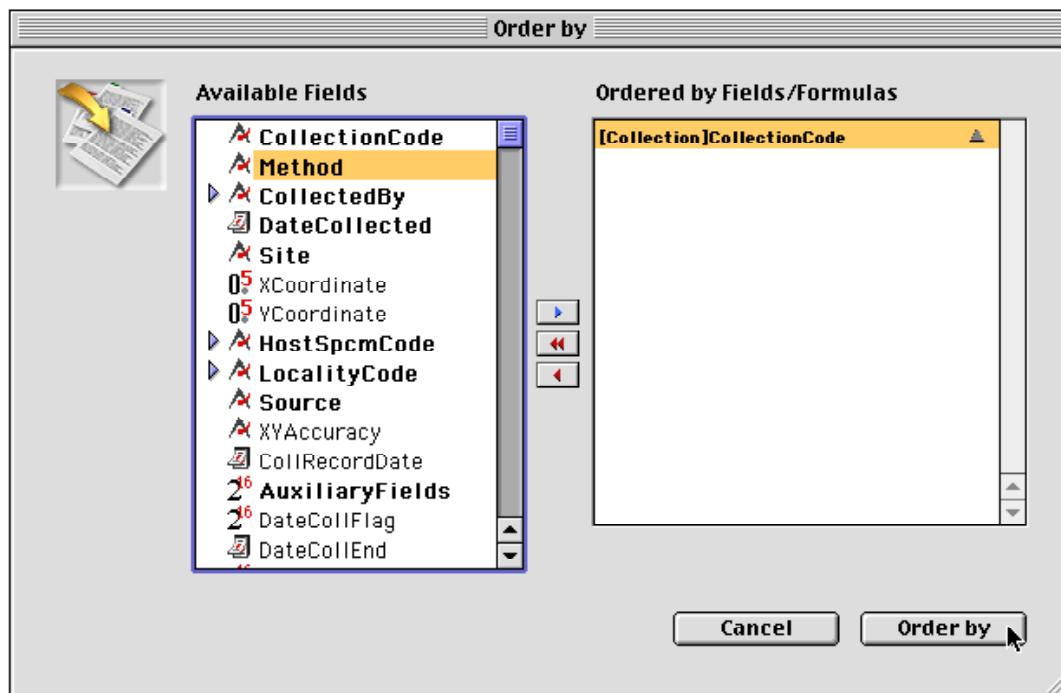
a. Click the “Sort” button.

4D Tools presents a scrolling list of Biota tables.



b. Select a table to index from the scrolling list of tables and click the “OK” button in the list window.

4D Tools presents the standard 4D (Biota) Sort (“Order by”) Editor.

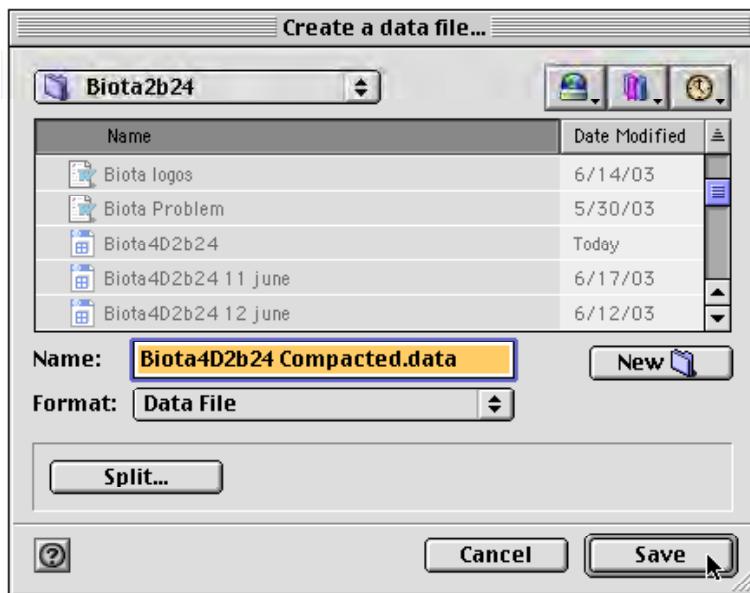


- c. **Set up the sort criteria**, following the instructions in “[Sorting Records in Record Listing Screens](#)” in Chapter 10, then click the “Order by” button.
- d. **Repeat Steps a. through c.**, above, for any other tables you want to re-index.
4. **To compact the Data File**, click the Compact button in the 4D Tools window.

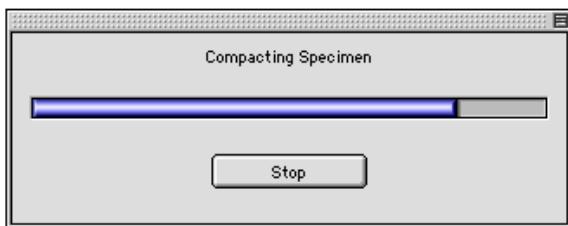


Biota presents the “Create a data file” screen.

5. **Name and Save the compacted Data File.**



Biota presents a series of progress screens as it compacts tables and indexes.



Moving All Records To a New Data File

As a last resort when a Data File is damaged and cannot be repaired with 4D Tools (see “[Checking and Repairing a Data File](#)” earlier in this appendix) you might need to rescue all the data you can from the damaged file and import it into an empty, new one.

For full instructions on these operations, see Appendix G, “[Merging Two Biota Data Files](#).”

Segmenting Data Files

Biota Data Files can be “segmented” to allow expansion beyond the capacity of a single disk drive or simply to partition a Data File into smaller units. Biota (4D) allows you to segment each Data File into a maximum of 64 segments of up to two gigabytes each. Thus, the maximum size of a single Biota Data File is 128 gigabytes.

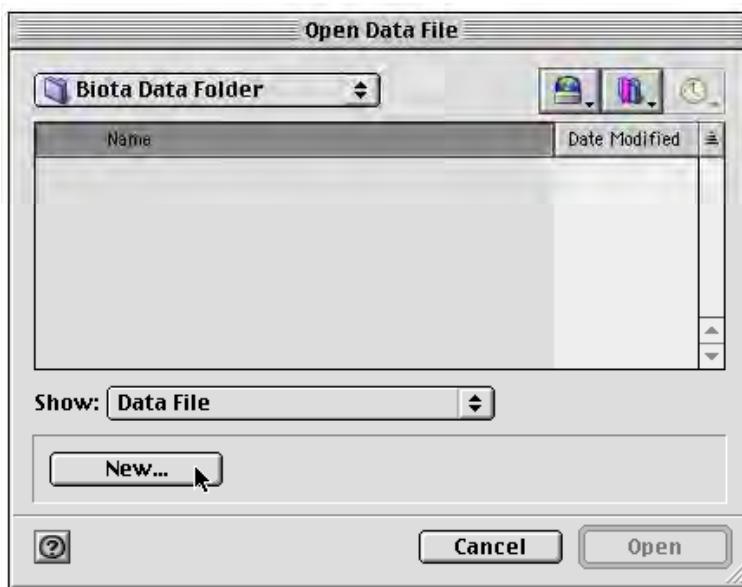
To the user, a segmented Data File behaves just the same as a unitary Data File. Addressing of data in the segments is handled transparently by 4D Engine, 4D Server, or 4th Dimension.

To use a Data File with segments on two or more hard disks, you must have the disk drives accessible simultaneously to the same computer.

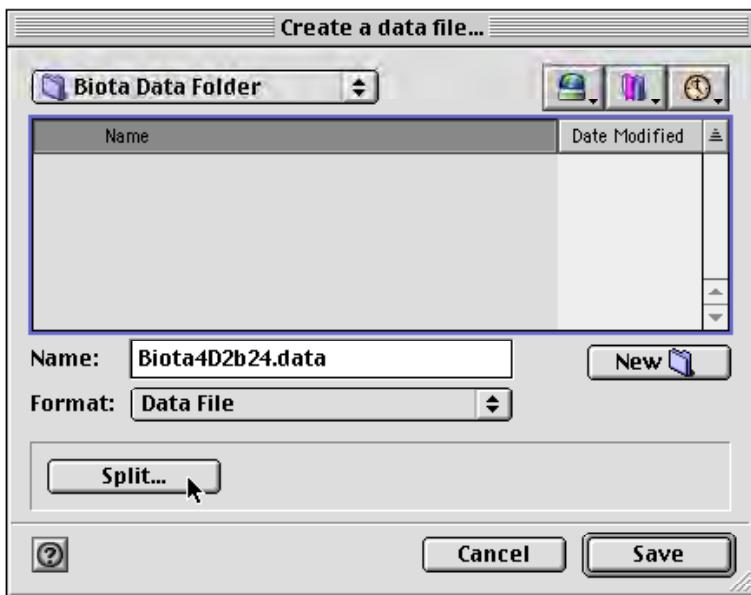
Segmenting a New Data File

If you expect a new Data File to become very large in the course of time, you may want to segment it from the outset.

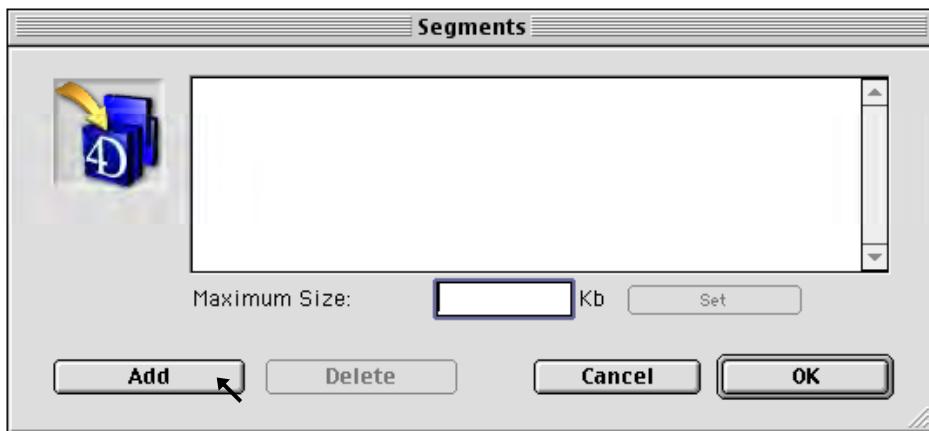
1. **Create a new, empty Biota Data File**, following the instructions in the section “[Creating an Empty Biota Data File While Launching Biota](#)” in Chapter 3.
2. **When the “Open a Data File” window appears (below), click the “New” button.** (Macintosh screens are shown here. The Windows screens differ in appearance but not in function.)



The “Create a data file” window appears.

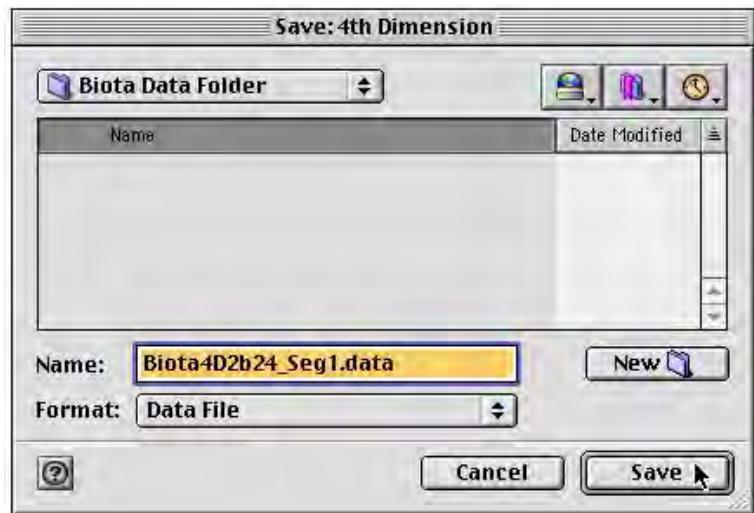


3. Click the “Split” button (above) instead of the Save button. (A default name will appear in the “Save as” box, but you can ignore it for now.) The Data Segment Manager appears.

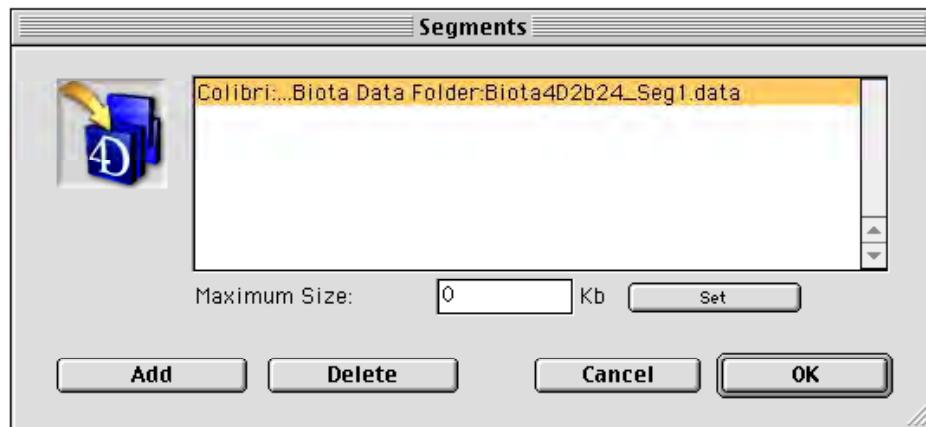


4. Click the Add button (above) to create a data segment.

A “Save” file window appears.

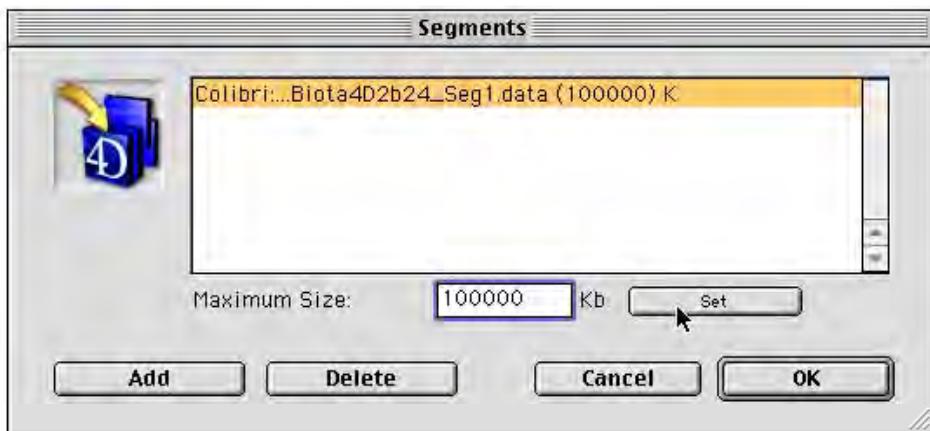


5. Enter the segment name (above).
6. Click the “Save” button. The Data Segment Manager reappears, showing the new data segment.



7. To set a maximum size for the segment (e.g., the space you expect to have available on your hard disk, minus a margin of safety):
 - a. Select the segment name in the Data Segment Manager (shown above).
 - b. Enter a numerical value (in KB) in the Maximum Size entry area. The maximum is 2,000,000 KB (2 gigabytes).
 - c. Click the “Set” button to register the maximum value.

The size limit for the segment now appears in the segment list.



8. **Create as many additional segments as you wish** by following steps 4 through 7, above.
9. **To delete a new segment** you have just created, select it in the Data Segment Manager and click the “Delete” button.

NOTE: You cannot delete an existing segment with the “Delete” button, only a new segment just created. To delete an existing segment, see “Deleting Existing Segments or Splitting an Existing Data File into Segments,” later in this chapter.

Adding a New Segment to an Existing Data File

If a Data File (or the latest Data File segment) becomes as large as you want it to be, you can add a new segment. If you get the error message below, you *must* either add a new segment or increase the size of an existing segment.



1. **From the Special menu in Biota, choose “Add a Data Segment.”** The Data Segment Manager appears. If the User Password system has been activated, only the Administrator can use this command.



2. Follow [Steps 4 through 8](#) in the previous section, “[Segmenting a New Data File](#).”

NOTE: You can use the Data Segment Manager to *reduce* the maximum size limit for an existing segment, but if you enter a value less than the *current* size of the segment, the value is increased automatically to the current size to protect the data in the segment.

Deleting Existing Segments or Splitting an Existing Data File into Segments

WARNING: Never delete data file segments directly by deleting the files themselves in the operating system environment, even if they have not been used. Always use the method below, instead.

If you reduce the size of a Data File and want to delete a segment, decide you no longer need a Data File segmented, or wish to split an existing Data File into segments, you can use 4D Tools to reconfigure the Data File segmentation.

1. Follow the instructions for compacting a Data File in the section “[Compacting or Re-indexing a Data File](#)” (up to Step 5), earlier in this appendix.
2. In the “Save” file window with the instruction “Create a data file,” click the “Split” button (instead of the “Save” button).
The Data Segment Manager appears.
3. Follow [Steps 3 through 9](#) in the section “[Segmenting a New Data File](#)” to reconfigure the segmentation (from scratch) as you wish.

Appendix J

Biota Data File Conversion: Mac OS and Windows

Biota Data Files can easily be converted between Mac OS and Windows formats. The process takes only a few seconds, regardless of file size. Once the appropriate conversion is applied, Biota Data Files are completely cross-compatible. In addition, external image file linkages (see Chapter 19, “[Images](#)”) are also completely transportable, as long a the same folder structure is replicated.

Like all Mac OS files, Biota Data Files on the Mac OS platform have two internal parts—the *Data Fork* and the *Resource Fork*—which together appear to the user as a single disk file in the Mac OS environment.

In the Windows operating system, in contrast, a Biota Data “File” actually becomes two separate files with the same name but different extensions:

- **A large file with the extension “.4DB,”** which appears as a file of type “Data” in Windows. This Windows file corresponds precisely to the Mac OS Data Fork.
- **A small file with the extension “.RSR,”** which appears as a file of type “Resource” in Windows. This Windows file corresponds precisely to the Mac OS Resource Fork.

To open a Biota Data File in Windows, the “.4DB” file and the corresponding “.RSR” file must both be in the same folder (directory).

NOTE: The Biota *application* cannot be converted between Windows and Mac OS. To work with Biota Data Files on both platforms, you need to purchase separate Windows and Mac OS versions of the BiotaApp application, or use Biota4D under 4D Server (see Appendix H, “[Using Biota4D with 4D Server or 4th Dimension](#)”).

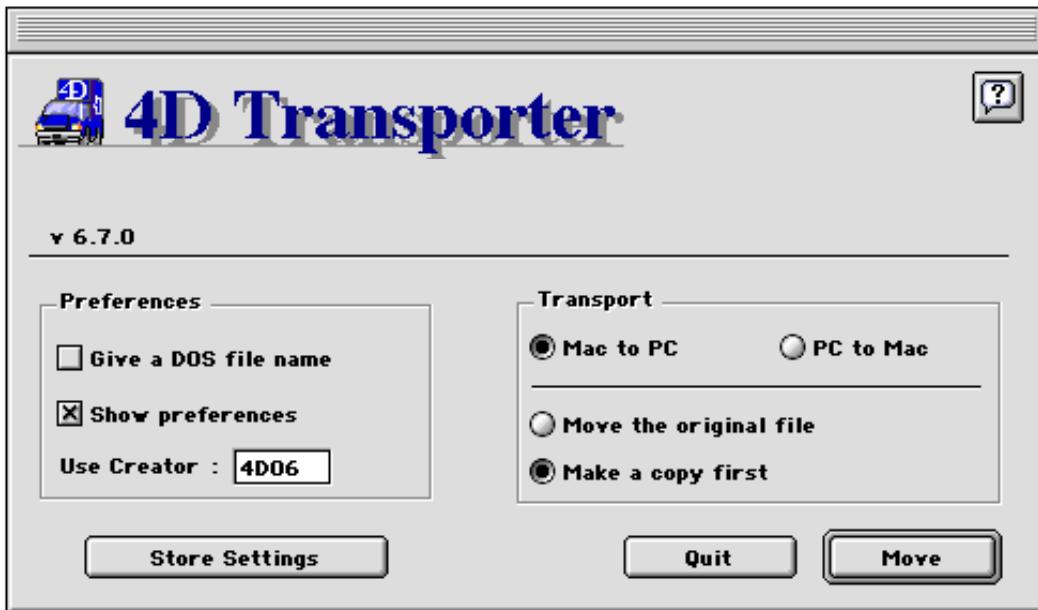
Data File Conversion: Step by Step

Regardless of whether you are converting a Windows Data File to Mac OS format, or a Mac OS Data File to Windows format, the conversion takes place only under Mac OS, using a special utility application called “4D Transporter.” You can find 4D Transporter on the Biota distribution CD, or download it from the [Biota Website](#) (<http://viceroy.eeb.uconn.edu/biota>) or from www.4d.com.

1. Back up the Data File to be converted.

- **Mac OS to Windows:** On the Mac OS machine, make a backup copy of the Data File to be converted and move the copy to a different folder or directory, for safety.
- **Windows to Macintosh:** On the Windows machine, make a backup copy of both the “.4DB” data file to be converted and also its associated “.RSR” resource file and move the copies to a different folder or directory, for safety.

2. ***Windows to Macintosh:*** Move the “.4DB” data file to be converted and its associated “.RSR” resource file to the Mac OS machine (on a CD, a removable drive, or over a network), and place them in a new folder, by themselves.
3. **On the Mac OS machine, launch 4D Transporter.** (Under OS X, Transporter runs in the Classic environment.) An option screen appears.



4. **Set the conversion (“Transport”) direction.**
 - ***Mac OS to Windows:*** Choose “Mac to PC” in the “Transport” panel.
 - ***Windows to Macintosh:*** Choose “PC to Mac” in the “Transport” panel.
5. **Choose a copy option in the lower part of the Transport panel.** If you made a backup in Step 1, you could choose “Move the original file.” Otherwise, or as an extra precaution, choose “Make a copy first.” (In the Transporter window, “move” means “convert.”)
6. **If you chose “Mac to PC,” the “Give a DOS File Name” checkbox is enabled. If you want a file name that conforms to DOS restrictions, check this box and** Transporter will invent something based on the consonants in your Mac OS file name. If you leave this box unchecked (recommended!), your Mac OS filename will be preserved in the Windows version (with extensions added).
7. **Click the “Move” button in the 4D Transporter window.** The file navigation window for your operating system appears.
8. **In the file navigation window, find and select the Biota Data File to be converted.**
 - ***Mac OS to Windows:*** Select the Biota Data File.
 - ***Windows to Macintosh:*** Select the “.4DB” file.

4D Transporter creates the new file (PC to Mac) or files (Mac to PC), and places the file or files in a new folder, named for your Data File, with extension “.PC” for the Mac OS to Windows conversion, or “.MAC” for the Windows to Mac OS conversion. Move the new PC files to your PC, or the new Mac file to its appropriate location. The Transporter window then reappears, to allow further conversions.
9. **Click the Quit button when you are done.**

Appendix K

Barcodes

Barcodes speed data entry (see “[Entering Specimen Data: The ‘General’ Tab](#)” in Chapter 11 and “[Using the ‘Input Specimen Series’ and ‘Input and Identify Specimen Series’ Tools](#)” in Chapter 13), record retrieval (see “[Using the ‘Find Specimen Series’ and ‘Find and Identify Specimen Series’ Tools](#)” in Chapter 13), and specimen loan management (see “[Recording a New Loan](#)” and “[Two Ways to Use the Loan Records Screens to Record Returns](#)” in Chapter 21). Biota can be set up to look for and recognize barcodes (see “[Setting Default Prefixes for Recognizing Specimen and Species Record Codes](#)” in Chapter 8) and to strip and replace barcode alphanumeric prefixes for automated specimen series entry and retrieval (see “[Substituting Different Prefixes for Barcode Prefixes in the Data File](#)” in Chapter 8).

If the barcode labels you want to use do not need to be particularly minute, you can print your own barcodes (for example, in Code 39) on acid free, plain or adhesive-backed stock using a commercially available barcode font and an ordinary text editor and laser printer.

For very small labels (e.g., 0.56 x 0.35 inches), proprietary miniature barcode fonts (using image-based or “stacked” codes) are currently the only option. You can have them printed commercially, or purchase a special barcode printer and make them yourself. Barcodes preprinted on polyester stock have become a de facto standard in entomology for pin labels (no adhesive backing). Project ALAS (see the [Preface](#)) uses the same labels, but with a permanent adhesive backing, for slide-mounted material (see “[Slide Specimen Labels](#)” in Chapter 15).

To use barcodes, you need a barcode “reader”—a *visible laser scanner*. The scanner simply acts as an alternative input device to the keyboard, reading and entering characters from the barcode, just as if you had typed them in manually on the keyboard.

Because of the fast-moving state of the technology, it lies beyond the scope of this manual to provide specific brand recommendations for commercial barcodes or scanners. Whatever you decide to use, be certain that ordinary, human-readable versions of the same information appear on your labeled specimens in some form, just in case barcode readers of the future no longer support the barcode font you choose.

Appendix L

Troubleshooting and Support

If you are having a problem with Biota, first look through the “Troubleshooting” section below for help. If you cannot find the answer there, please consult the [Detailed Table of Contents](#), or do an Acrobat search of the Manual. If you are still unable to solve the problem, see the [Biota Support](#) section of this appendix.

Troubleshooting

This section is organized by the following subheadings (use the links to get to the appropriate section):

- [Problems with Data Files](#)
- [Problems with Passwords](#)
- [Problems with Windows and Records](#)
- [English and Spanish Screens and Dialogues](#)
- [Error Messages](#)

Where a problem might reasonably be placed in two different categories, you will probably find it listed in both.

Problems with Data Files

- **I can't get Biota to create a new, empty Data File. It keeps on opening the same existing file.** To create a new, empty Biota Data File, *press and hold the OPTION key (Macintosh) or ALT key (Windows)* while launching Biota. (If Biota is already launched, quit Biota first, then launch it again.)
If the user password system has been activated, you will need to press and hold the OPTION key (Macintosh) or ALT key (Windows) while clicking the “Connect” button in the Password window.
Be sure to hold the key down firmly until the file navigation window for your operating system appears. Click the “New...” button (not the “Open” button) to create a new Data File. Biota will take a few moments to do this, so be patient. See [“Creating an Empty Biota Data File While Launching Biota”](#) for more details.
Alternatively, you can use the “Create Data File” item in Biota’s File menu to create a new Data File. See [“Opening a Biota Data File or Creating a New Biota File from Within Biota”](#) in Chapter 3 for details.
- **I can't get Biota to open a different, existing Data File. It keeps on opening the same old file.** To choose among existing Biota Data Files, *press and hold the OPTION key (Macintosh) or ALT key (Windows)* while launching Biota. (If Biota is already launched, quit Biota first, then launch it again.)

If the user password system has been activated, you will need to press and hold the OPTION key (Macintosh) or ALT key (Windows) while clicking the “Connect” button in the Password window.

Be sure to hold the key down firmly until the file navigation window for your operating system appears, then find the Biota Data File you wish to open and double-click it (or select it and click the Open button). See “[Opening a Biota Data File When Launching Biota](#)” for more details.

Alternatively, you can use the “Open Data File” item in Biota’s File menu to open a different Data File. See “[Opening a Biota Data File or Creating a New Biota File from Within Biota](#)” in Chapter 3 for details.

- **I deleted hundreds of records from my Data File, but the file is still the same size.** When you delete records, Biota reuses the “holes” for new records. Meanwhile, the Data File stays the same size unless you compact it using 4D Tools. See “[Compacting or Re-indexing a Data File](#)” in Appendix I.
- **I can’t find a “Save” command to save the changes I have made to my Data File.** Biota uses temporary buffers in RAM to keep track of any changes you make in the active Data File. Every three minutes, Biota automatically saves these changes to disk and clears the buffers. (There is one exception: Each group of new records you create or modify using commands from the Series menu is saved immediately.)

If you want to force Biota to save changes immediately, press the keys COMMAND+W (Mac OS) or CTRL+W (Windows) at any time.

When you quit Biota, any changes made since the last automatic save are recorded in the Data File. See “[Saving Changes in a Biota Data File](#)” in Chapter 3 for details.

- **What is the small window (shown on the right) that appears in the lower left corner of my screen periodically while I am running Biota?** This window is displayed while Biota is saving changes to your Data File (see the previous question).
- **When I try to open my Data File, I get an error message that the file is damaged and cannot be opened.** A disk error has occurred, possibly as a result of a power failure or other improper shutdown while data were being saved.

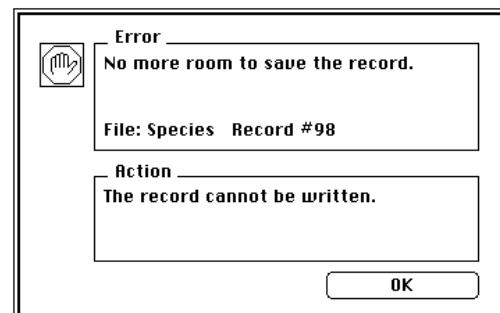


See Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#),” for instructions on using 4D Tools to attempt recovery on a copy of the damaged Data File. With the Data File backed up to another disk, you may also wish to use a generic disk repair utility to diagnose the disk for more general problems.

If all else fails, you will have to use the most current backup of your Data File instead. (Always back up regularly!) But first make a backup of the backup, for safety’s sake—on a different disk, if possible.

- **When I try to create a new record, I get an error screen reading “No more room to save the record.”**

Either your hard disk is full, or (if you have segmented the Data File) the maximum size has been reached in all existing segments of the Data File. See “[Adding a New Segment to an Existing Data File](#)” in Appendix I.



Problems with Passwords

- **I can't get my User Password to work.** Check each of the following:
 - ◊ **Passwords are case sensitive.** If you create a password or are assigned a password that includes uppercase and/or lowercase letters, you must always reproduce the case of each letter precisely.
 - ◊ **Be sure the CAPS LOCK key is not on.**
 - ◊ **Make sure you are entering the correct User Name** in the Password window. (User Names are *not* case sensitive.)
 - ◊ **Make sure you are opening the correct copy of Biota.** User passwords are saved with the Biota application file, not the Data File.

If none of these suggestions solves the problem, ask the database Administrator to assign you a new password. If you *are* the Administrator, install a fresh copy of Biota and reestablish the user Password system (see “[Activating the User Password System](#)” in Chapter 26) or contact Biota Support for help (“[Biota Support](#),” later in this appendix).

For full details, see Chapter 26, “[Security: Passwords and Access Privileges](#).”
- **I have forgotten my user password.** Ask the database Administrator to assign you a new password. If you *are* the Administrator, install a fresh copy of Biota and reestablish the user Password system (see “[Activating the User Password System](#)” in Chapter 26) or contact Biota Support for help (“[Biota Support](#),” later in this appendix).
- **When I try to open a Data File, Biota asks for a “Data File Password.”**
 - ◊ **Make sure you are launching the right copy of Biota and the right Data File.** When the Data File password link is activated for a particular Data File, a copy of the Data File password is stored in the Biota application file. The copy in the Biota application file must precisely match the copy of the password in the Data File. See “[Using the Data File Password Link](#)” in Chapter 26.
 - ◊ **Ask the database Administrator to open the Data File or supply the password.** Once successfully entered, the Data File Password will not be requested again until a new copy or a new version of Biota is installed. See “[Opening a Password-Protected Data File with a New Copy or New Version of Biota](#)” in Chapter 26.
 - ◊ **If you are the Administrator, and you have forgotten or lost the Data File Password,** contact Biota Support for help—and don’t despair, there is a way.... (see “[Biota Support](#),” later in this appendix).

Problems with Biota Windows and Records

- **How can I find out which windows are currently open?** Move the window aside or minimize it. There is no menu list of open windows.
- **I get a cursor that looks like a page behind another page, and I can't get a window to respond.**  Another window requires attention before you can proceed. (You clicked in an inactive window.) To return to the active window, press any key on the keyboard. (The keystroke is not recorded.)

- In Input screens, the “Carry” and “Delete” buttons are inactivated (dimmed), and I can’t enter or change any data. The User Name you signed on with when you launched Biota is not authorized to create, edit, or delete records. Ask your database Administrator to change your access privileges if you need to be able to carry out these actions. See “[Users, User Names, Passwords, Access Levels, and Privileges](#)” in Chapter 26.
- What is the small window (shown on the right) that appears in the lower left corner of my screen periodically while I am running Biota? This window is displayed while Biota is automatically saving changes to your Data File. 
- When I try to open a record in an Input screen, I get a “Locked Object” message that the record already being edited. See the item “[4D: Locked Record message](#)” in the “[Errors](#)” section, later in this appendix.



- When I load a Record Set Pointer file from the File menu, the wrong records (or no records) are displayed.
 - ◊ Either: The Record Set Pointer file was saved for a different Biota table (see “[Loading a Record Set Pointer File](#)” in Chapter 3).
 - ◊ Or: Some of the records referenced by the Record Set Pointer file have been deleted since the time the Record Set Pointer file was created.

English and Spanish Screens and Dialogues

- Some of the screens and dialogues are in Spanish. I want them all in English.
 - ◊ Either: The Language setting in the Preferences screen (Special menu) is set to Spanish. Change the setting to English. See “[The ‘Language’ Tab](#)” in Appendix B.
 - ◊ Or: If the user Password system has been enabled, your User Name may have been assigned a special startup procedure that sets the Language toggle to Spanish. Ask the database Administrator to change the startup procedure to specify English. See “[Editing a User’s Password and Profile](#)” in Chapter 26.
- Only some of the screens and dialogues are in Spanish. I want all screens and menus in Spanish. When the Language toggle has been set to Spanish, most instructions, dialogues, and error messages are displayed in Spanish—with the exception of screens and dialogues accessible only to the Administrator, which are presented only in English. Menus and commonly used input and Record Listing screens are also in English only, since these are viewed repeatedly and are thus much more easily learned than instructions, dialogues, and error messages.

If it would be helpful for future versions of Biota to include Spanish versions of particular screens or messages that are currently only in English, please contact Biota Support (see “[Biota Support](#),” later in this appendix).

Error Messages

Three kinds of error messages may appear: Biota error messages, operating system error messages, and 4th Dimension error messages.

- **Biota error messages** are treated fully in the appropriate chapters of this book. In other words, if you get an error message while you are importing records, look in Chapter 28 (“[Importing Data](#)”) in the section “[Displays and Error Messages During Record Importing or Updating](#).”
- **Error messages displayed by your operating system** are not treated here. Please consult the documentation that came with your computer or operating system upgrade.
- **4th Dimension Error messages** regarding problems that *you* can correct yourself are listed in this section.

Note: If you get a 4th Dimension error message not listed below, you may have discovered a bug in Biota’s code. See examples and instructions in the “[Bug Reports](#)” section, later in this chapter.

- **4D: Locked Record message.** Record locking, a feature of all database applications that allow multitasking, protects records from being edited in two places at once. Each time you choose a command from a Biota menu a new process is launched. Certain buttons also launch separate processes (e.g., Print buttons and Child Records buttons).

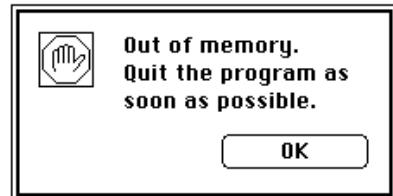
If you see a message like the one above, *it means that you are trying to display, in an Input screen, a record that is also the current record in another Biota process that still has an open window.*



- ◊ **If you are using BiotaApp (or Biota4D under 4th Dimension)** the other open window is on your own screen.
- ◊ **If you are running Biota under 4D Server**, the other open window may be on your screen or on the screen of another concurrent user. In the latter case, the first line of the Locked Record message will read “The Record is already being edited by *User Name*,” where User Name is the Password screen sign-on name of the other user.
- ◊ **The name of the process that appears in the locked record error window** is a shortened version of the menu command or the name of the button that launched the process. (In the example above, the process was launched by the process “pAllFam,” which corresponds to the “All Families” command in the Find menu.)
- ◊ **When you click the “OK” button in the Locked Record error window**, the record you were attempting to display will nonetheless be displayed, *but in read-only mode*. If you need to edit the record, find the offending open window and

close it. Then dismiss the record in the current process, reopen it (to set it in read-write mode), and edit it.

- **4D: “Out of memory” error message.** If you see the message below, quit Biota (you may have to wait for a process to be completed). Close other programs if possible, and re-launch Biota. If the problem persists, please contact Biota Support (see “[Biota Support](#)” later in this appendix). (**Note:** Mac OS 9 users can increase memory allocation to Biota; choose “Get Info” from the File menu in the Mac desktop.)
- **4D: When I try to open my Data File, I get an error message that the file is damaged and cannot be opened.** A disk error has occurred, possibly as a result of a power failure or other improper shutdown while data were being saved.

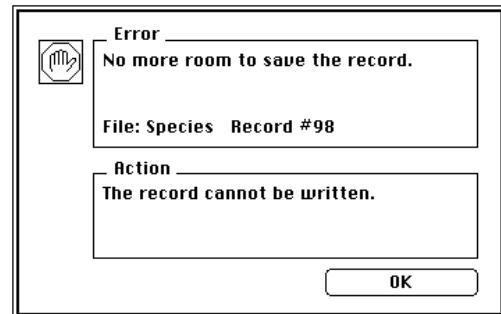


See Appendix I, “[Data File Backup, Recovery, Compacting, and Segmenting](#),” for instructions on using 4D Tools to attempt recovery on a copy of the damaged Data File. With the Data File backed up to another disk, you may also wish to use a generic disk repair utility to diagnose the disk for more general problems.

If all else fails, you will have to use the most current backup of your Data File instead. (Always back up regularly!) But first make a backup of the backup, for safety’s sake—on a different disk, if possible.

- **4D: When I try to create a new record, I get an error screen reading “No more room to save the record.”**

Either your hard disk is full, or (if you have segmented the Data File) the maximum size has been reached in all existing segments of the Data File. See “[Adding a New Segment to an Existing Data File](#)” in Appendix I.



Biota Support

Biota support starts with this book, which has deliberately been written in much more detail than many manuals, to provide you with full, rapid access to the information you need.

“How To” Questions

This book is the first place to go to find out if Biota can do something you want done. Please use the [Detailed Table of Contents](#), or, if necessary, Acrobat’s “Search” tool to see if you can find the answer you need.

Often, there is more than one way to do a task with Biota, but usually there is a fast way and a slow way. If some task seems to take longer than you think it should, try looking up the topic in the [Detailed Table of Contents](#) for alternative approaches.

Visit the Biota Web Site for Help and Information

The Biota Web site, at <http://viceroy.eeb.uconn.edu/biota>, is the first place to turn for post-release updates to Biota documentation, suggestions for efficient use, warnings, workarounds for any bugs that have been discovered since Biota was released, and announcements of Biota upgrades and future plans.

Support by Electronic Mail

- **Problems with Biota licenses or distribution media (CD).** Please contact Biota's publisher, Sinauer Associates: support@sinauer.com
- **Problems with orders for Biota** from Sinauer or Biota resellers. Please contact Biota's publisher, Sinauer Associates: orders@Sinauer.com
- **Technical problems with Biota or problems with the Biota Website.** If you are a Registered Biota owner, you may request email help with problems you can't solve with the help of this Manual. Please contact Biota's author, Robert Colwell: colwell@uconnvm.uconn.edu

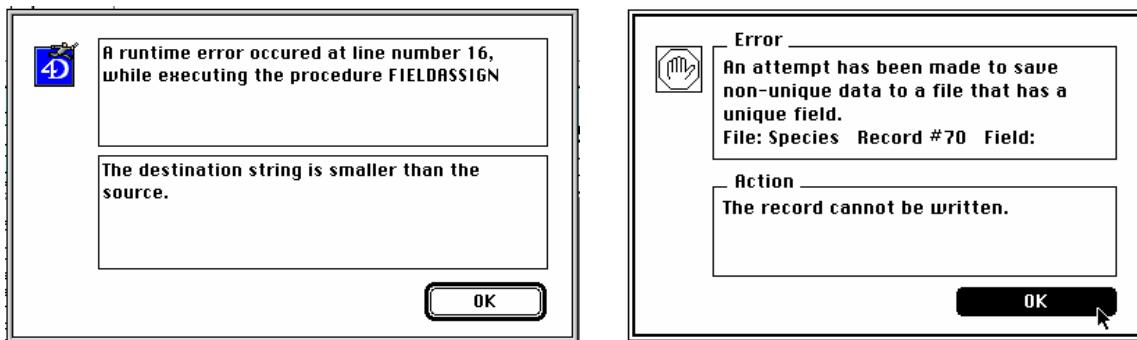
Please do not telephone. Please do not contact the publisher, Sinauer Associates, with technical questions.

Bug Reports

Every effort has been made to beta-test Biota thoroughly, and all known programming bugs have been corrected. In any program this complex (more than 11,000 objects, including nearly 5000 methods and 380 forms), however, users invariably prove that completely bug-free behavior is only a theoretical possibility.

If Biota does something you did not expect, first try consulting this book, including the section on "[Troubleshooting](#)," earlier in this appendix, to see if the behavior is normal.

If something happens that is clearly not intended, you may have found a bug. If a 4th Dimension error window appears that is not discussed in the Errors section, earlier in this appendix (see below for two examples), you have certainly found a bug.



- **If you believe you have discovered a bug,** please record the following:
 1. **A description of the problem.** To be most useful the description of the problem should include a full account of the steps that led up to it. If at all possible, try making it happen again until you are sure what steps reliably produce the problem. *If the problem cannot be reproduced, it cannot be fixed.*

2. **Any data that were involved.** If the problem seems to concern a particular data record, please write down exactly what was in the record.
 3. **Version of Biota.** From the File menu in Biota, select “About Biota.” Record the Version and Date of the copy of Biota that you are using, and indicate whether it is BiotaApp (the stand-alone version) or Biota4D (running under 4D Server or 4th Dimension).
 4. **Your computer model and processor.**
 5. **The operating system and version number you are using.**
- **Send this information by e-mail** to Biota’s author, Robert Colwell:
colwell@uconnvm.uconn.edu:

Suggestions for Improving Biota

Biota’s current tools and features evolved over a period of more than ten years, under the constant guidance of Biota users. Suggestions for improvement are warmly welcomed. Please use the contact information in the previous section.