

Finding and Reporting Information

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BioLink Reports and Query tools

BioLink provides a range of reports and tools for extracting and reporting information. There are four main types of these tools. *Predefined reports* provide quick access to commonly used information in easy to use predefined formats. *Distribution maps* can be produced using a single menu option. They can range in scale from worldwide to meter-based maps and can include as much or as little detail as required. The *Query Tool* is used to select and report information across an entire BioLink database. All available information can be searched and results can be exported in a range of formats. Finally, *Labels* are used extensively by all biological collections. A dedicated label production facility has been included in BioLink.

Predefined reports

BioLink contains a number of predefined reports that can be quickly and easily generated. These reports provide commonly used information as well as an export facility to transfer data to other programs. Most reports are called directly from the Explorer's. Simply select an item in the Explorer, click the right mouse button and select the **Reports** command followed by the name of the required report. Other reports are called from the **Reports** button on the main BioLink toolbar.

The following reports are supplied.

- *Associates for Taxon Report*: A report listing all associates for the selected taxon (and optionally region).
- *Checklist Report*: A report listing the children of a selected Taxon Explorer item. The details included in the report can be specified as well as the display order of the included taxa.
- *Data Entry Statistics by User Report*: A summary of the number of items created and updated by individual users.
- *Material for Taxon Report*: A list of material records for the selected Taxon Explorer item. Individual material records can be edited directly from this report.
- *Material for Trap Report*: A report of the material associated with a trap or bulk sample.
- *Sites for Taxon Report*: A report of the sites where material for the selected Taxon Explorer item has been collected.
- *Statistics Report*: A list of counts for items associated with the selected Taxon Explorer item. Included are valid and available names (sorted by rank) and number of material records.
- *Storage Location Report*: A list of taxa grouped by their storage location.
- *Taxa for Distribution Region Report*: A list of taxa known to occur in a political region (based on taxon information rather than material records).
- *Taxa for Site Report*: A report of the taxa for which material from the specified region or site is held in the database.

Associates for Taxon Report

A list of Associates for a given taxon can be easily produced by BioLink. To generate this list select a taxon in the Taxon Explorer and press the right mouse button and select the **Associates for Taxon Report** command from the **Report** menu. This will open the Associates for Taxon Report window with the name of the required taxon and (optionally) a region name. To restrict Associates to a given region (when known), find the required region in the Site Explorer and drag and drop its name onto the Report window. Alternatively, the ellipsis button to the right of the region field can be pressed to quickly search for a region. Once the region is properly set press the OK button to create a formatted report for the requested information.

This report can be saved to disk using the **Export** button on toolbar).

Checklist Report

The Checklist report provides a text-based report of items in the Taxon Explorer using the current classification. A number of options are available to select the details included in the report as well as the depth of the classification to display.

To open this report, select an item in the Taxon Explorer, click the right mouse button and select the **Reports** item followed by the **Checklist Report** command. This will open a window displaying a list of display options. These options include the following:

Full Hierarchy: When selected, this option includes the selected Taxon Explorer item and all of its children.

Next Level Down Only: When selected, this option includes the selected Taxon Explorer item and its immediate children only.

Include only Verified Names: When selected, only names that are verified are included in the report. This will eliminate unverified names from the report.

Include Available Names: Selecting this option will include available names in the report.

Include Literature Names: Selecting this option will include literature names in the report.

Include Rank Descriptions to Family Level: This option will include the rank before the taxon name for taxa at and above the family level.

Use User Defined Taxon Order: When this option is selected the taxa will be displayed in the order specified by the user using the Taxon Explorer's **Sort** command.

Once options are set, press the **Preview** button. This will open a window displaying a checklist for the selected taxon with the selected options.

Information in the report can be copied to the clipboard by selecting the text to be copied and pressing Ctrl+C or using the **Copy** command from the toolbar. The entire report can be saved to disk (in RTF - rich text format) by pressing the first toolbar button.. This will open a Save As dialog box where a file name can be specified. To print the report, press the second toolbar button.

Data Entry Statistics by User Report

BioLink can easily produce a summary of the number of items created and updated by individual users. To generate this summary select the **Data Entry Statistics by User Report** command under the **Tools→Reports** menu item on the **Tools** menu. This will open the User Statistics Report window where the name of the user and a date range can be specified. To see a list of current users open the User combo box. Dates can be typed directly in the date fields or clicking the button to the right of the fields can open the calendar control. Once this information has been set press the **OK** button to create a formatted report for the requested information.

This report can be saved to disk (using the **Save As...** command on the **File** menu), printed (using the **Print** command on the **File** menu) or any or all of the text can be selected with the mouse and copied to the Clipboard using the **Copy** command on the toolbar.

Material for Taxon Report

The Material for Taxon Report provides a list of material records for a taxon. This report is especially useful in giving a quick overview of holdings for a taxon and in that the underlying data (Sites, Site Visits, Material and Taxa) can be edited directly from the report. Information in the report can be quickly reorganised by clicking on the column headings to change the sort order and columns can be reordered using drag and drop.

To open this report, select an item in the Taxon Explorer, click the right mouse button and select the **Reports** command followed by the **Material for Taxon List** command. This will open a report results window displaying a list of all material records for the selected taxon and any of its children. To sort the information in the report, click on a column heading. This will sort the information alphabetically by that column.

To edit the underlying information in the report, select a row, open the **Edit** menu or click the right mouse button and select the **Edit Site**, **Edit Site Visit**, **Edit Material** or **Edit Taxon** command. This will open a Details window with information for the request item. To export information in the report to disk, select the **Export** command from the toolbar. This will open the Export Options window. Select the required export type and press the **Export** button. This will open a window where options for the selected export format can be specified. The options available will vary with the format selected. For further details see *Export Options* below.

Material for taxon 'Formicidae' X Welcome X

Filter:

| Taxa | Region | Locality | Lat/Long | Collectors | Dates |
|---------------|-------------|------------------------|-------------------------|------------|-------|
| Rhytidoponera | import Ants | 22°37'47"S 167°31'47"E | 22°37'48"S, 167°31'48"E | Ward,P.S. | |
| Cerapachys | import Ants | 22°37'47"S 167°31'47"E | 22°37'48"S, 167°31'48"E | Ward,P.S. | |
| Paratrechina | import Ants | 22°37'47"S 167°31'47"E | 22°37'48"S, 167°31'48"E | Ward,P.S. | |
| Anochetus | import Ants | 22°37'47"S 167°31'47"E | 22°37'48"S, 167°31'48"E | Ward,P.S. | |
| Pheidole | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Rhytidoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Technomyrmex | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Rhytidoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Rhytidoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Strumigenys | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Pheidole | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Prionogenys | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Cerapachys | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Rhytidoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Formicidae | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Mesoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |
| Rhytidoponera | import Ants | 17°16'48"S 145°37'48"E | 17°16'48"S, 145°37'48"E | Ward,P.S. | |

11730 records retrieved.

Material for Trap Report

This report provides a detailed list of material for the selected trap. It is especially useful in giving a quick overview of material for a trap and in that the underlying data (Sites, Site Visits, Material and Taxa) can be edited directly from the report. Information in the report is formatted in columns can be quickly reorganised by clicking on the column headings to change the sort order and columns can be reordered using drag and drop.

Material for Trap X Welcome X

Filter:

| Taxa | Region | Locality |
|------------------------------------|--|--------------|
| Camponotus nigriceps (Smith, 1858) | Australasian Region: Australia: Australian Capital Territory | Abattoirs, C |

1 records retrieved.

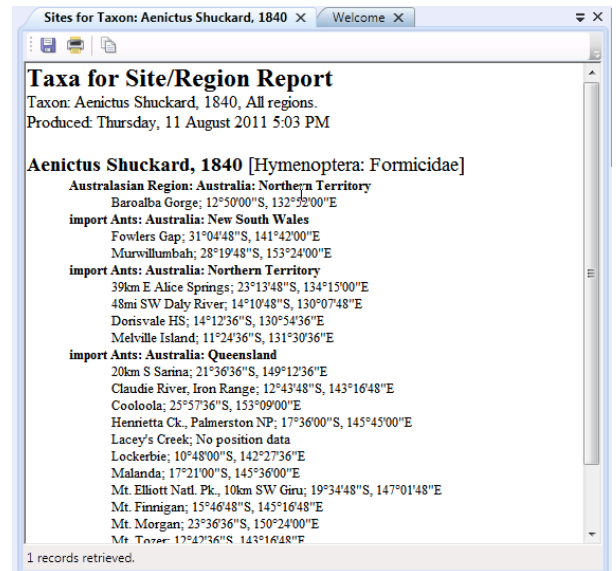
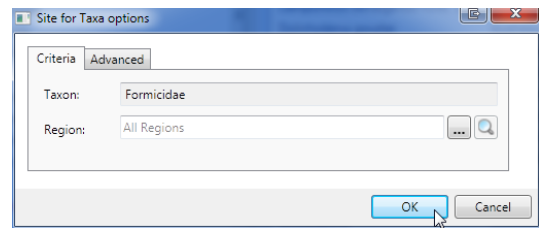
To edit the underlying information in the report, select a row, click the right mouse button and select the **Edit Site**, **Edit Site Visit**, **Edit Material** or **Edit Taxon** command. This will open a Details window with information for the selected item. To export information in the report to disk, select the **Export Data** command from the toolbar. This will open the Export Options window. Select the required export type and press the **Export** button. A window will open where options for the selected export format can be specified. The options available will vary with the format selected. For further details see *Export Options* below.

Sites for Taxon Report

The Sites for Taxon Report provides a text-based report of the collection sites for the currently selected taxon and all of its children. The report is organised by taxon and lists details for each site.

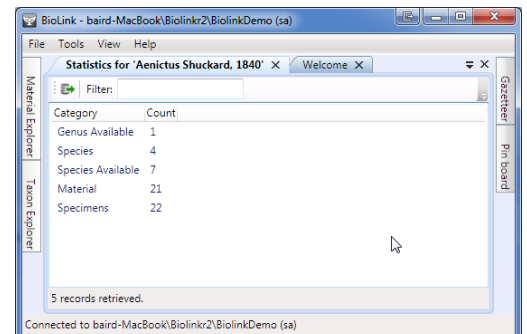
When run, this report opens a dialog box listing the currently selected taxon and (optionally) a geographic region. To specify a region, press the **Ellipsis** button (with the three dots) to the right of the Region/Site box. This will open the a mini Site Explorer where the region can be located and transferred to the dialog box using the **Select** button. Regions can also be dragged from the Site Explorer. Once these items are properly set, press the **OK** button. This will open a window displaying the sites for each taxon in the region.

Information in the report can be copied to the clipboard by selecting the text to be copied and pressing Ctrl+C or using the **Copy** command from the toolbar. The entire report can be saved to disk (in RTF: rich text format) by pressing the first toolbar button. This will open a Save As dialog box where a file name can be specified. To print the report, press the second toolbar button.



Statistics

The Statistics report provides a count of items in the Taxon Explorer grouped by types. Items include all of the children of the selected Taxon Explorer item and include material records. To sort the information in the report, click on a column heading. This will sort the information alphabetically by that column. To export information in the report to disk, select the **Export** command from the toolbar. Select the required export type and press the **Export** button. This will open the Export Options window. Select the required report type and press the **Export** button. This will open a window where options for the selected export format can be specified. The options available will vary with the format selected.



Taxa for Distribution Region Report

This report produces a list of taxa known to occur in a distribution (political) region. This information is entered using the Taxon Detail window called from the Taxon Explorer. For taxa recorded from a region based on specimens, see the *Taxa for Site Report* below.

To open this report, select an area in the Distribution Region Explorer (opened from the **View** menu on the main BioLink menu), click the right mouse button and select the **Taxa for Distribution Region** command. This will open a window containing a list of all specified taxa known to occur in the selected region.

Information in the report can be copied to the clipboard by selecting the text to be copied and pressing Ctrl+C or using the **Copy** command from the toolbar. The entire report can be saved to disk (in RTF: rich text format) by pressing the first toolbar button. This will open a Save As dialog box where a file name can be specified. To print the report press the second toolbar button.

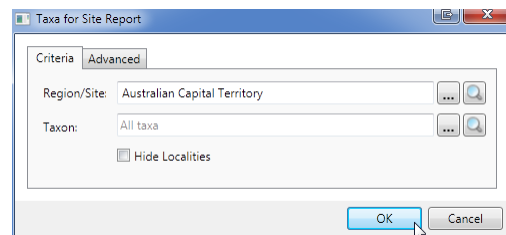


Taxa for Sites Report

The Taxa for Sites Report provides a text-based report of the taxa for which specimens are held from the specified region or site. The report lists the taxa found in the region or at the site, with or without specific collection localities.

To generate this list select either a Region or a Site from the Site Explorer and press the right mouse button and select the **Taxa for Sites Report** command from the **Report** menu. This will open the Taxa For Sites Report window where the required region, (optionally) a taxon name and whether to hide the locality details can be entered. To enter a region or to restrict sites to a given taxon, find the required item in the appropriate Explorer and drag and drop its name onto the Report window. The ellipsis button (with the three dots) to the right of each field can be pressed to open mini explores to quickly find items. If Hide Localities is checked then only taxon names are included in the report. Once these items are complete, press the **Preview** button to create a formatted report for the requested information.

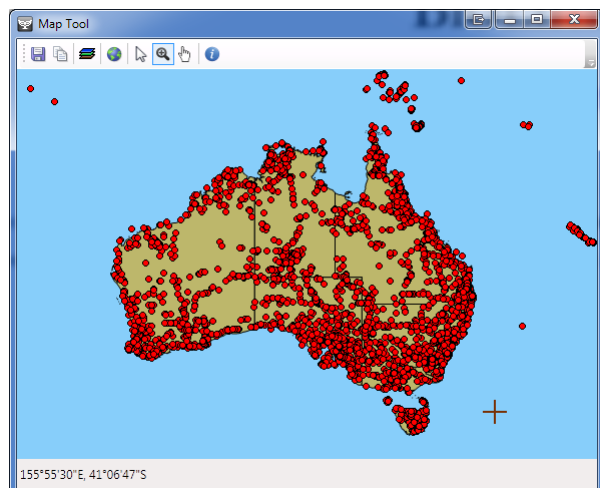
Information in the report can be copied to the clipboard by selecting the text to be copied and pressing Ctrl+C or using the **Copy** command from the toolbar. The entire report can be saved to disk (in RTF: rich text format) by pressing the first toolbar button. This will open a Save As dialog box where a file name can be specified. To print the report press the second toolbar button.



Distribution maps

High quality distribution maps can be produced for any region and any taxon using the Taxon Explorer and the Map tool. These maps are based on ESRI shape files, providing a large range of maps at a number of scales, and available from a number of sources.

To produce a distribution map, open the Taxon Explorer and locate the taxon of interest. The chosen taxon can be of any rank, with maps for higher taxa showing records for the taxon and all of its children (for example, a family will include records for all genera and species within the family). Select the taxon



name in the Explorer, click the right mouse button and select the **Distribution Map...** item.

The Distribution Map Options window will open titled with the name of the taxa to be mapped. The colour, size and style of the point to be used on the map for each taxon can be set in this window. Once the point style for the taxon has been specified, press the **OK** button. The Map tool will then display all geocoded sites for the selected taxon/taxa.

Details concerning any of the displayed points can be retrieved by placing the mouse pointer over the point on the map, clicking the right mouse button and selecting the **Edit Site**, **Edit Site Visit** or **Edit Material** command from the menu. This will open the appropriate Details window for the selected item.

Changing the way the map looks

The map can be zoomed and panned using the mouse pointer and toolbar buttons. To zoom, select the **Magnifying Glass** with the plus sign (+) button on the toolbar. Use the left mouse button to draw a rectangle on the map. The area inside the rectangle will fill the window when the mouse left mouse button is released. Also you can use the mouse wheel to zoom in and out. If the map has been zoomed, the **Hand** button can be used to pan the map. Click the **Hand** button, place the mouse pointer over the map, hold down the left mouse button and move the mouse. The map will move (pan) as the mouse moves. To view the entire map, press the globe button on the toolbar. This will fill the map window with the entire map (Zoom to extents).

For details on changing the map being displayed or its colour, see *The Layers Window* below.

Printing and saving maps

Maps can be saved as a PNG, JPG, BMP, TIFF or GIF image file using the **Save** button on the toolbar. Maps can also be printed using the **Print** button. To transfer a copy of the map to the Windows clipboard, select the **Copy** button.

The layers window

The ‘maps’ displayed by the Map tool are composed of layers. A layer can represent a line or polygon (such as a coast line or state boundary), a series of lines or polygons (such as contour lines) or points (such as a taxon distribution). Any number of layers can be displayed at any given time. In most cases at least two layers will be used, a user-defined boundary layer and a BioLink-created point layer.

The layers displayed by the Map tool can be changed using the Layers window. To open the Layers window press the **Layers** button on the toolbar. Use the **Add** button to add layers and the **Remove** button to remove them. The style used for objects in the layer is set in the Feature group. The styles available will vary with the types of objects. For example, polygons have fill colours, styles and outlines, while lines have only colours and styles. Pressing the **Set Background Colour** button and selecting a colour sets the background colour for the Map tool.

The order of the layers in the Layers window is same order used to display the layers on the map. Layers at the top of the list will appear above lower layers in the list. This means that if layers containing regions (such as countries) are placed above layers with points (such as sites), the points may be hidden by the regions. This problem can be solved by using the **Up** and **Down Arrow** buttons to change the order of layers in the Layers window.

The layer files must be formatted as ESRI Shape files. This is the format used by ESRI’s ArcView and ArcInfo GIS packages. Files in this format are available for a large range of areas and at a number of scales. They can be found on a number of Web sites and translators are available to convert files in other formats into the Shape file format. BioLink provides an assortment of layers but specific projects may require additional layers not provided. See *The Map Tool* chapter for additional information.

Query Tool

The Query Tool is used to select and retrieve information from a BioLink database. Essentially any item or set of items can be searched for using a broad range of conditions, and essentially any subset of related information can be returned. The results of a search can be saved in a number of formats.

To open the Query Tool select the **Query Tool** command under the **Tools** menu.

Using the Query Tool

The Query Tool is composed of two items.

Field List: A list of all fields or data items in the database.

Criteria Window: A window where the search criteria and output options are specified.

Unlike in previous versions of BioLink, results are not displayed attached the Query Tool window, but rather are docked in the centre of the main window in the same manner as report results.

To perform a search first locate the data item(s) of interest in the Field List. Items are organised hierarchically by major group (Nomenclature, Sites, Site Visits, Material and so on) and a short description of the selected item is displayed immediately below the list. Select the required item and either double-click it or press the > button to the right of the list. Continue selecting and transferring fields until all fields required in the report have been copied to the Criteria Window. To remove a field from the Criteria Window select it and press the < button. To remove all fields press the << button.

The order of items in the Criteria Window will be the order they appear in the results. To reorder fields, select the field to be moved and use the **Up** and **Down Arrow** buttons to the left of the Window to reorder the list. By default, all fields are included in reports. To remove a field from reports but leave it in the Criteria Window uncheck the Output box for the field. This will be necessary when a field will be used to select records but that field is not otherwise required. To change the name of a field in reports, enter a new name in the Alias column for that field. To change or specify a sort order for the report click in the Sort column for a field and select Not Sorted, Ascending or Descending for that field. The report will be sorted hierarchically as specified, starting from the top of the list in the Criteria Window.

A “Distinct” clause can be added to the query. This clause will remove identical rows from the results. To add this clause, select the **Distinct** command under **Options** on the **Query** menu. When this menu item is checked, the Distinct clause will be added, when unchecked all rows, including duplicates, will be returned.

Entering search criteria

The final step in conducting a search is to enter the criteria used to select data. In its simplest form this can consist of a single criterion such as ‘= ‘Canberra’’. At its most complex the criteria will involve a number of fields and include pattern matching, value lists and data ranges. Most searches will lay somewhere between these two extremes. For details on constructing search criteria, see *Search Conditions* below.

After search criteria have been entered, the report is run by pressing the green **Arrow** button (fourth from the left) on the Query Tool’s toolbar. The information entered will be evaluated and if errors are found a message box will be displayed listing the error(s) found. If errors are found they will need to be repaired before the report will run. Once the criteria are entered properly and the report run, the results will be displayed in the Report Window along the bottom of the Query Tool

Query Results

Columns based on the fields in the Criteria Window display search results. The column and sort orders can be changed directly in the results window. To change the column orders use drag and drop to move column headings relative to each other. To sort by a column click in it’s heading. Note that these changes will not be used when exporting information and the original sort and display order specified in the Criteria Window will be used.

Exporting results

To export the results of a search click the **Export Details** button on the query results window toolbar. This will open the Export Options window. Select the required report type and press the **Export** button. This will open a

window where options for the selected export format can be specified. The options available will vary with the format selected.

Saving and reusing searches

To save a search criteria, press the **Save Current Query** toolbar button (third from the left). This will open a Save As dialog box where a file name can be entered to save the current query. To open a previously saved query press the **Open Query** toolbar button (second from the left). A File Open dialog box will open where a saved query file can be selected. To start a new query, press the **New Query** toolbar button (first on the left). This will reset the Query Tool, removing any previously entered criteria.

Search conditions

The information returned from a query is based on a set of search conditions or parameters. These parameters can involve a single value for a single field or a number of values scattered across a number of fields and include partial string matches and ranges of values.

The BioLink query tools support four broad types of search conditions that can be applied to individual fields, as follows:

- Comparison operators (such as =, < >, <, and >). For example, this query returns all taxa with the name 'Iridomyrmex'.
Field: Nomenclature.Full Name
Criteria: = 'Iridomyrmex'
- Ranges (BETWEEN and NOT BETWEEN). For example, this query returns all material records containing between two and nine specimens.
Field: MaterialPart.Number of Specimens
Criteria: between 2 and 9
- Lists (IN and NOT IN). For example, this query returns all taxa with the name of either 'Iridomyrmex' or 'Camponotus'.
Field: Nomenclature.Full Name
Criteria: in ('Iridomyrmex', 'Camponotus')
- Pattern matches (LIKE and NOT LIKE). For example, this query returns all taxa with names which start with 'Irido'.
Field: Nomenclature.Full Name
Criteria: like 'Irido*'

These search criteria are explained more fully below. Note that all searches are case-insensitive. For example, searching for 'Portland' and 'portland' will give the same results.

Comparison operators

Comparison operators are used when comparing two values. They are placed between a field and the value it is being compared with. The following operators are available:

| | |
|----|----------------------------------|
| = | equal to |
| > | greater than |
| < | less than |
| >= | greater than or equal to |
| <= | less than or equal to |
| <> | not equal to (SQL-92 compatible) |
| !> | not greater than |
| !< | not less than |
| != | not equal to |

Examples

Field: Site.Locality

Criteria: = 'Canberra'

This will return all records where the locality name is Canberra.

Field: Site.Latitude

Criteria: > 45

This will return all records where the latitude of the locality is recorded as being greater than 45 degrees (north in this case, as southern latitudes are stored as negative).

Range search conditions

A range search is one that returns all records between two specified values. The BETWEEN keyword specifies the range to search. The range is defined as being inclusive, which means that records that have the specified values will also be included. NOT BETWEEN can be used to find records outside the specified range.

Example

Field: Site.Latitude

Criteria: between -23 and 23

This will return all records where the latitude is between 23 degrees south and 23 degrees north (including those recorded as 23°00'00"S and 23°00'00"N).

List search conditions

The IN keyword finds records that match any one of a list of values. The items following the IN keyword must be separated by commas and be enclosed in parentheses (wildcards are not supported).

Example

Field: Nomenclature.Full Name

Criteria: in ('Camponotus', 'Notoncus', 'Opisthopsis')

This will return all records with the taxonomic names *Camponotus*, *Notoncus* or *Opisthopsis* (but see the note under Searching for Taxon Names below).

Pattern matching in search conditions

The LIKE keyword searches for records that match a specified pattern (and NOT LIKE searches for records which do not match this pattern). The pattern contains the character string to search for combined with any combination of the following four wildcards.

| | |
|-----|---|
| % | any string of zero or more characters |
| _ | any single character |
| [] | any single character within the specified range (for example, [a-f]) or set (for example, [abcdef]) |
| [^] | any single character not within the specified range (for example, [^a - f]) or set (for example, [^abcdef]) |

Enclose the wildcard(s) and the character string in single quotation marks, for example:

- LIKE 'Mc%' searches for all strings that begin with the letters Mc (McBadden).
- LIKE '%inger' searches for all strings that end with the letters inger (Ringer, Stringer).
- LIKE '%en%' searches for all strings that contain the letters en anywhere in the string (Bennet, Green, McBadden).
- LIKE '_heryl' searches for all six-letter names ending with the letters heryl (Cheryl, Sheryl).
- LIKE '[CK]ars[eo]n' searches for Carsen, Karsen, Carson and Karson.

- LIKE '[R-Z]inger' searches for all names ending with the letters inger that begin with any single letter from R to Z (Ringer, Singer, Tinger).
- LIKE 'M[^c]%' searches for all names beginning with the letter 'M' that don't have the letter 'c' as the second letter (MacFeather).

Searching for wildcard characters

You can search for wildcard characters. There are two methods for specifying a character that would ordinarily be a wildcard:

- Use the ESCAPE keyword to define an escape character. When the escape character is placed in front of the wildcard in the pattern, the wildcard is interpreted as a character. For example, to search for the string 5% anywhere in a string, use LIKE '%5/%%' ESCAPE '/'

In this LIKE clause, the leading and ending percent signs (%) are interpreted as wildcards, and the percent sign preceded by a slash (/) is interpreted as the % character.

- Use square brackets ([]) to enclose the wildcard by itself. To search for a dash (-), rather than using it to specify a search range, use the dash as the first character inside a set of brackets: LIKE '9[-]5'

The following shows the use of wildcards enclosed in square brackets.

| | |
|----------------|--|
| LIKE '5[%]' | 5% |
| LIKE '5%' | 5 followed by any string of 0 or more characters |
| LIKE '[_]n' | _n |
| LIKE '[_]n' | an, in, on (and so on) |
| LIKE '[a-cdf]' | a, b, c, d, or f |
| LIKE '[-acdf]' | -, a, c, d, or f |
| LIKE '[[]' | [|
| LIKE '[]' |] |

When string comparisons are performed with LIKE, all characters in the pattern string are significant, including every leading and/or trailing blank (space). If a comparison to return all rows with a string LIKE 'abc ' (abc followed by a single space) is requested, a row in which the value of that column is abc (abc without a space) is not returned. The reverse, however, is not true. Trailing blanks in the expression to which the pattern is matched are ignored. If a comparison to return all rows with a string LIKE 'abc' (abc without a space) is requested, all rows that start with abc and have zero or more trailing blanks are returned.

Searching across multiple fields

The above examples use a single field and search criterion to retrieve information. This is the simplest situation. In many cases it is desirable to combine several search criteria. For example, a list of taxa in a particular family and from a particular region may be needed. To perform this query, set the following information in the criterion section of the query tool.

Field: Nomenclature.Full Name

Criteria: = 'Iridomyrmex'

Field: PoliticalRegion.Region Name

Criteria: = 'New South Wales'

BioLink will combine these criteria using the AND operator.

Searching for taxon names, region names and storage locations

Information for taxon names, region names and storage locations are stored hierarchically. That is, they have parent-child relationships. BioLink allows two types of searches when using these items. The first search returns the requested item(s) and all of its(their) children while the second search returns only the required item(s). For example, requesting a genus using the first search will return the genus and all of its species and subspecies. This search with the second method will return only the genus (without its species and subspecies). The first type of search is the default. To specify the second type of search, add the word ONLY after the criterion.

For example, to return the genus *Iridomyrmex* and all of its species enter the following.

Field: Nomenclature.Full Name

Criteria: = 'Iridomyrmex'

To return the genus *Iridomyrmex* alone without its species enter the following.

Field: Nomenclature.Full Name

Criteria: = 'Iridomyrmex' only

Searching for dates

BioLink uses two styles of dates. Collecting dates are stored as eight digit numbers with the first four digits representing the year, the next two the month and the final two the day. This method of storage allows partial dates to be entered and searched. Dates for data entry and modification are stored as full dates. These are appropriate in these cases as complete dates (including time of day) are always available.

To search for Collecting dates enter the required date as a string with eight characters, the first four representing the year, the next two the month and the final two the day. For partial dates enter zeros for the unknown values. Formatted dates and their BioLink equivalents are as follows:

| | |
|-----------------|----------|
| 29 January 1987 | 19870129 |
| January, 1987 | 19870100 |
| 1987 | 19870000 |

Date of entry and modification dates can take a variety of formats but must be in standard US month-day-year order (as supported by Microsoft's SQLServer). Examples are:

Jan. 29, 1987
Jan 29 1987
1-29-1987
1/29/1987

The following are suggestions for searching for collecting dates:

To find material collected on 6 May 1997, enter the following:

Field: SiteVisit.Start Date

Criteria: = 19970506

To find material collected between 6 May and 8 May, 1997, enter the following:

Field: SiteVisit.Start Date

Criteria: between 19970506 and 19970508

To find material collected in May 1997, enter the following:

Field: SiteVisit.Start Date

Criteria: between 19970500 and 19970531

(In fact, setting the last date to 19970599 also works.)

To find material collected on 6 May or 8 May, 1997, enter the following:

Field: SiteVisit.Start Date

Criteria: in (19970506, 19970508)

'More than one way to skin a cat'

Constructing search criteria can be a complicated business and there are often a number of ways to achieve the same result. For example, BioLink will allow you to use the OR operator within a single field. Alternately, you can use the IN keyword. For example, this:

Field: Material.Macrohabitat

Criteria: = 'rainforest' or 'woodland'

is the same as:

Field: Material.Macrohabitat

Criteria: in ('rainforest', 'woodland')

In the example given above it was suggested that to find material collected in May 1997, enter the following:

Field: SiteVisit.Start Date

Criteria: between 19970500 and 19970531

Alternately, this information can be retrieved using the following two criteria.

Field: SiteVisit.Start Date

Criteria: >= 19970500

Field: SiteVisit.Start Date

Criteria: <= 19970531

If one approach to a query doesn't seem to be working it may be possible to try another approach which will.

Labels

Labels are used extensively in most biological collections as part of daily curation practices. Because of their importance, BioLink provides a Label Manager to assemble and manage labels. Combining the Label Manager with a word processor supporting mail merge facilities or other reporting packages provides a flexible and powerful method for generating a wide variety of label formats.

The production of specimen labels is a two step process. First a list of the desired labels is compiled, and second this list is exported for final formatting and printing using a word processor or other report generator. The Label Manager and Export Options window assists in both of these tasks.

Creating label sets

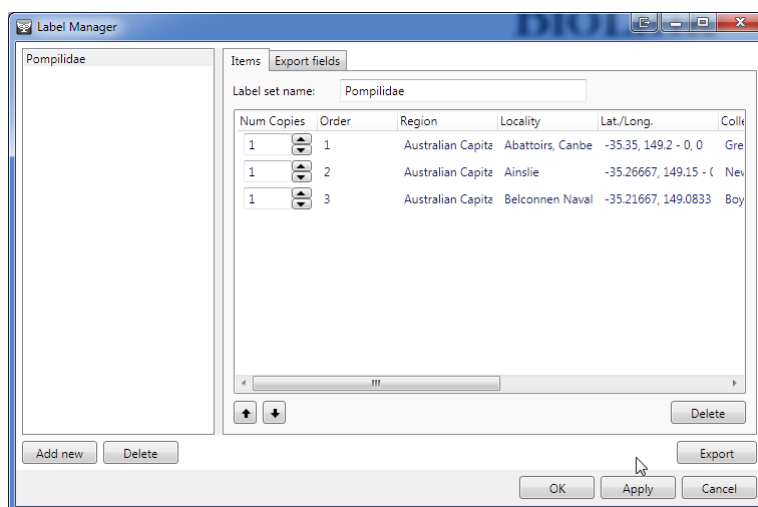
Labels can be created based on information derived from Regions, Sites, Site Visits and Material. To compile a list of labels, open the Label Manager by selecting the **Label Manager** command from the **Tools** menu. Labels are compiled in sets. A list of the current label sets is shown on the left of the window. On the right is a list of the items present in the selected set. To create a new label set press the **Add New** button and enter a name for the set, or to use an existing label set select its name in the list.

Once a label set has been selected, information can be added to it from the Site Explorer and the Site, Site Visit and Material Details windows, and the Rapid Data Entry window. To use the Site Explorer locate the required item (Site, Site Visit or Material) and add it to the list on the right of the Label Manager using drag and drop. Using the Detail windows and Rapid Data Entry, open the record of interest and then select the window's **Add to Label Set** command from the **Edit** menu. This will open a window where a label set can be selected, or a new label set created.

Number of copies and sort order

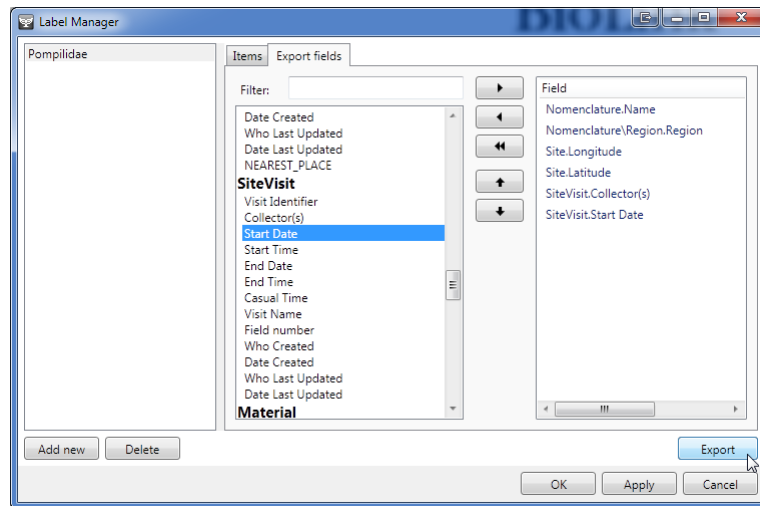
The number of copies of each label to include can be specified in the first column of the Item details panel. To change this number, select the label item or row in the right side of the Label Manager, click the right mouse button and select the **Change Number of Copies** command. Enter the number required and press the **Enter** key. The second column in the list, Order, indicates the sequence items were added to the label set. Each newly added item is given the next number in the sequence.

Labels are exported in the same order that they are displayed. To change the order either click on the headings at the top of each column to sort by that column or select an individual label and use the **Arrow** buttons to move it up or down the list. To resort items back to the order that they were entered, click the Order column heading.



Exporting label information

To specify the BioLink fields to export open the Export Fields tab. The required fields are moved from the list on the left to the Selected Fields list (on the right) using the top **Arrow** (>) button. The lower two **Arrow** buttons remove fields from the Selected Fields list. To export information in the label set select the **Export Label Set** command from the either the **Set** or **Label Items** submenu of the **Items** menu. This will open the Export Options window. Select the required report type and press the **Export** button. This will open a window where options for the selected export format can be specified. The options available will vary with the format selected. For further details see *Export Options* below. If the Delimited File option is selected then the separator used between individual fields should normally be a pipe '|' or comma, quotes around fields should generally not be used and a header line should be included.



Formatting labels

The actual process of formatting labels will need to be done using a word processor or other reporting tool (such as MS Access). To do this with Microsoft Word use the following steps:

1. Open a blank document in Word.
2. On the Tools menu, click **Mail Merge**.
3. Click **Create**, click **Catalog**, and then click **Active Window**.
4. Click **Get Data**.
5. Click **Open Data Source** and locate the file containing the exported labels.
6. After you designate the data source and Word displays a message, click **Edit Main Document**.
7. In the main document, type any text you want to be repeated with each label.
8. Click where you want to insert a label item. Then click **Insert Merge Field** on the Mail Merge toolbar, and click the label item that you want. Items should be separated by spaces and can start on new lines if required.
9. After you complete the main document and insert all of the merge fields, click **Mail Merge Helper** on the Mail Merge toolbar.
10. Click **Merge**.
11. In the Merge to box, click **New document**.
12. Press **Merge**. A new document will be created with the label items specified in Step 8 replaced with the label information from the label export file.
13. To modify the merge format, return the original document by selecting it from the **Window** menu.
14. Repeat Step 8.
15. Repeat Steps 11 and 12.

Once properly formatted, the labels can be printed using the **Print** command on the **File** menu. The merge document (containing the label item names and layout) can be saved and reused with additional label sets.

Export options

BioLink supports a number of formats when saving or exporting data from reports and searches. The following formats are currently supported:

- Delimited Text*: a delimited text file
- Excel 2003 Worksheet*: a Microsoft Excel worksheet
- SQLite database*: SQLite database file

Keyhole Markup File: Google Earth/Google maps kml file

A number of options are available for each of these formats. Details of the available formats are as follows:

Delimited Text

This format exports data as delimited text with one record per row. Options include the name of the file to write data to, the type of delimiter used, whether field names should be included as a header row, and whether values should be surrounded with double quotes.

Excel 2003 Worksheet

The Excel Worksheet export creates a new spreadsheet with each column in the report in a spreadsheet column and with one row per report row. Options include the name of the file to create, whether column names should be placed in the first row of the worksheet, and whether Excel should be launched with the file created during the export.