Guide to Using a Symbiota-based Portal

developed for users of the Consortium of California Herbaria (CCH2) Portal

Version 5.0

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Contents

1: Navigating the CCH2 portal website

The portal can be accessed at http://www.cch2.org.

From the homepage (shown above), you can search collections and view data and images, even if you do not have an account in the portal, by clicking the "**Search Collections**" tab in the toolbar at the top left side of the page. The "**Map Search**" tab can be used to search specimens within a certain geographic area. The "**Image Search**" and "**Browse Images**" tabs can be used to locate images of certain taxa.
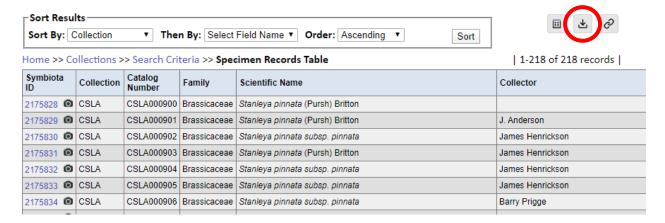
When using the "**Search Collections**" tool, you will be prompted to select the collections within which the search will be conducted. Check or uncheck the desired boxes on this page, click "Search >", and enter the remaining search parameters (e.g., the scientific name of the desired specimen) in the appropriate boxes. You can display the results in a list, which will show most specimen data and image thumbnails, by clicking "List Display" to conduct the search, or you can display the results in a table by clicking "Table Display."

To create or use your user account, edit or add specimen data, or use other Symbiota tools, log in at the right side of the toolbar (see *2: Creating a new user* and *3: Managing your profile and collections(s)*).

For a video tutorial of the basic uses of a Symbiota-based portal, visit the SCAN TCN website below. Note that the SCAN portal is not identical to the CCH2 portal, but the layout will be similar
http://www.lep-net.org/?page_id=403

1:1 Downloading specimen data

To download data about a specific set of specimens, search for the specimens of interest using the "**Search Collections"** tool as described above and click "Table Display." In the search results, click the download button (circled below). A new window will pop up to display download options. Select the desired options and click Download Data.

If the Compressed ZIP file option is checked, the results will download in a ZIP file, which you will need to extract before you can access and edit the files inside. If you checked all the Data Extensions boxes, you will find the following files in your ZIP file:

- **occurences.csv :** core specimen data (i.e., scientific name, collector, locality, etc.)
- **images.csv :** a list of web links and metadata for images associated with the specimen records
- **identifications.csv :** the annotation history (i.e., past identifications) of the specimen records
- **eml.xml :** text file describing the source of the specimen data in a standardized way
- **meta.xml :** text file that lists the data standards applied to the occurrences, images, and identifications fields (i.e., where to find definitions for the fields used in these csv files)

2: Creating a new user

Users must create their own accounts by clicking "New Account" near the top right side of the portal website. They will be prompted to provide a login name, password, and contact information. When creating an account, make sure to record your login name and password in a safe place for future reference. These can be recovered via email if necessary. Once you have finished entering the required information, click the box next to "I am not a robot" and click "Create Login."

A new user will not be able to manage collection data until they are granted appropriate permissions (see *19: Managing user permissions*).

3: Managing your profile and collections(s)

To manage your collection(s), click "My Profile" at the top right corner of the portal homepage. You will see a page like the one below.

The "Species Checklists" tab allows you to create and share personal species checklists for research, education, or other uses (see *29: Research checklists*). Species in the checklist can be linked to voucher specimens, enabling you to download custom checklists of specimens for the species on your list.

The "Occurrence Management" tab is where you will manage your specimen and observational data. Upon clicking this tab, you will see a "Collection Management" box. If you have administrative or data editing permissions for a collection, the name of the collection will be listed in this box. If you do not see your collection listed in this box, contact your portal manager or administrator so they can grant you appropriate permissions.

The "User Profile" tab can be used to change your name, email address, affiliation, password, and other account information.

Depending upon your administrative permissions, when you click on name of your collection in the "Collection Management" box you will see one, both, or neither of the following control panels.

3:1 Data Editor Control Panel

The Data Editor Control Panel is used to add and edit specimen records. Data editing permissions can be granted to a portal user without that user receiving full administrative permissions (see *19: Managing user permissions*). The Data Editor Control Panel can be accessed by logging in to the portal, clicking "My Profile," and clicking the "Occurrence Management" tab. Each of the tools in this panel is briefly described on the following page.

Add New Occurrence Record – This tool is used to create new specimen records from label data. See *4:1 Adding a new record by entering label data.*

Create New Records Using Image – This tool is used to create new specimen records by uploading an image then entering specimen data. See *4:2 Adding a new record using an image*.

Add Skeletal Records – This tool is used to quickly create specimen records with minimal information, usually during the process of imaging. These records provide "skeletal" data that can be filled in during later transcription steps by, e.g., technicians or citizen scientists. See *6: Adding skeletal records*.

Edit Existing Occurrence Records – This tool is used to add or edit data of records that already exist in the portal. See *7: Editing existing specimen records*.

Add Batch Determinations/Nomenclatural Adjustments – This tool can be used to add determination/annotation information and/or change the scientific name of a number of specimens all at once. You can define whether the change is due to a new determination (i.e., identification and annotation by a taxonomic expert) or adjusted nomenclature for the taxon based on taxonomic research. See *8: Adding determination/annotation data*.

Print Specimen Labels – This tool can be used to print specimen labels or barcodes for records with data entered in the portal. Editors can create and save custom label formats or use formats that have been established by the collection. This tool allows collectors to enter their collection data directly into the portal and print pre-formatted labels rather than requiring collectors to type and format labels only to have technicians re-type label data later in the process. The labels can be printed from the browser, downloaded as a CSV file, or downloaded as a Word file.

Print Annotations Labels – This tool allows collection managers or determiners to print pre-formatted annotation labels after entering determination data via the "Add Batch Determinations/Nomenclatural Adjustments" tool. The labels can be printed from the browser, downloaded as a CSV file, or downloaded as a Word file.

Labels/Annotations –The labels can be printed from the browser, downloaded as a CSV file, or downloaded as a Word file. See *12: Printing* .

Occurrence Trait Coding Tools – These tools enable scoring of specimen traits, such as phenological status, from images or label text of specimens. More guidance will be provided on these tools in a future version of this manual.

Batch Georeference Specimens - This tool can be used to update the geographic coordinates of a number of specimens all at once. See

13. Printing annotation/determination labels

To use this tool, you will need to have first added the annotated specimens to the annotation print queue. This can be done either individually, via the Occurrence Editor (see *8:1 Adding individual determinations/annotations*), or in batch using the Add Batch Determinations/Nomenclatural Adjustments tool (see *8:2 Batch adding determinations/annotations*).

To print annotation labels, navigate to the Data Editor Control Panel (see *3:1 Data Editor Control Panel*) and click "Print Annotations Labels." A table will be displayed that lists all the specimens in the Annotation Print Queue. Check the boxes in the leftmost column next to the specimen records for which you wish to print annotations. To view a specimen record, either click the collector name and number (to view public record display) or click the pencil icon next to the collector name and number (to view occurrence editor for that record). Customize your annotation label using the provided options and select either Print in Browser or Export to DOCX (to export as a Microsoft Word document). Check the box next to "Remove selected annotations from queue" to remove these specimens from the print queue after you click one of the print buttons.

☐	#	Collector	Scientific Name	Determination
☑	1	David Keil 35016 ✐	Nemophila menziesii	test, test

Annotation Printing

Header: [_____]

Footer: [OBI - Robert F. Hoover Herbarium, Cal Poly State University (OBI)]

☐ Print species authors for infraspecific taxa   Border Width: [1 ▾]   [Print in Browser]
☐ Print Catalog Numbers   Rows per page: [3 ▾]   [Export to DOCX]
☐ Remove selected annotations from queue   Spacing between labels: [5]

14: Scoring/coding specimen traits

Several tools have been developed to enable users to annotate specimen records for their traits. The traits available to score vary between portals, and new traits can be developed as needed (contact your portal administrator for more information).

14:1 Scoring/coding individual specimen traits in the occurrence editor

A trait can be scored for an individual specimen record in the Occurrence Editor (see *7: Editing existing specimen records*) by clicking the Traits tab. The trait(s) available for scoring will be displayed as boxes containing the available scoring schema(s). Select the trait values corresponding to the specimen and click the Save Edits button. You can also remove trait information by clicking the Delete Coding button.

14:2 Scoring/coding specimen traits from images

To score multiple specimens of the same taxon or from the same region, use the Trait Coding from Images tool. From the Data Editor Control Panel (see *3:1 Data Editor Control Panel*), click Occurrence Trait Coding Tools, then Trait Coding from Images.

In the Filter box, select the trait that you wish to score, followed by the name of the taxon for which you wish to score (if applicable). Phenological Traits from the Trait dropdown menu. You can also refine your search by using the All Source Types and All Counties & All States dropdown lists.

- **All Source Types:** this field allows you to view and re-score specimens that have already been scored using another method (e.g., text mining). Leave this as is unless you are specifically working on re-annotating specimens.

- **All Countries & All States:** this field provides a dropdown menu of all countries and U.S. states that are indexed in CCH2. If you select one of these geographic criteria, the tool will only show you specimens from that country/state.

Filter

[Select Trait (required)   ▾]
[All Source Types   ▾]
[All Counties & All States   ▾]
[All Taxa   ]
[Load Images]

Click the Load Images button. On the next page, you will see an image of a specimen of the selected taxon on the left, and an Action Panel on the right (see screenshot on next page). Note that you can edit

the contents of the Filter box here as well. Depending on the scoring schema available for the trait you are scoring, you may be able to view more scoring options by clicking the black triangle inside the Action Panel. Select the trait values that you wish to apply to the specimen and click Save and Next.

14:3 Scoring/coding specimen traits from label text

It is also possible to score traits of batches of specimens using the text of the specimens' labels. To access and use this tool, navigate to Data Editor Control Panel (see *3:1 Data Editor Control Panel*), click Occurrence Trait Coding Tools, and select "Trait Mining from Verbatim Text". In the Harvesting Filter box, select the Occurrence trait that you would like to score.

For the "Verbatim text source" field, select the database field that you want the tool to display. The options include: Habitat, Substrate, Occurrence Remarks (Notes), Dynamic Properties, Verbatim Attributes (Description), Behavior, Reproductive Condition (Phenology), Life Stage, and Sex. In the "Filter by text (optional)" field, you can enter any text string by which you wish to filter the results. For example, if you enter "fw", the tool will provide all values for that field that contain "fw". This field is optional, but including a search string will significantly narrow your search results. When choosing strings to enter in this field, consider searching for misspelled and abbreviated versions of the values you expect. For example, if you are searching for specimens that you can score as flowering, you could search for "fowering" or "fwrr" as well as "flowering" and "fwr". In the "Filter by taxon (optional)" field, you can enter the name of a taxon by which you wish to filter the results. This field is also optional.

Once you have filled out the desired fields, click the Get Field Values button. The result will look similar to the screenshot on the next page. The Harvesting Filter box is still visible, and the box below

will list all the unique strings (values) found in the specified database field that align with your search criteria. The numbers in brackets to the right of each string value indicates how many specimen records have that exact value in the specified database field.

```
┌─ Harvesting Filter ──────────────────────────────────────────────────┐
│                                                                       │
│  Occurrence trait: [Angiosperm Phenological Traits ▼]                 │
│  Verbatim text source: [Reproductive Condition        ▼]              │
│  Filter by text (optional): [flowering            ]                   │
│  Filter by taxon (optional): [                    ]   [Get Field Values] │
│                                                                       │
└───────────────────────────────────────────────────────────────────────┘

┌─ Reproductive Condition ─────────────────────────────────────────────┐
│                                                                       │
│  Select Source Field Value(s) - hold down control or shift buttons to select more than one value │
│  ┌─────────────────────────────────────────────────────────────────┐ ▲│
│  │ flowering - [121]                                               │  │
│  │ flowering/fruiting - [6]                                        │  │
│  │ flowering|fruiting - [55]                                       │  │
│  │ none flowering - [2]                                            │  │
│  │ none yet flowering - [1]                                       │  │
│  │ past flowering - [1]                                           │  │
│  │                                                                 │  │
│  │                                                                 │  │
│  │                                                                 │  │
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│  └─────────────────────────────────────────────────────────────────┘  │
│  ◯ reproductive   ▶                                                    │
│  ◯ sterile                                                             │
│  ◯ not scorable                                                        │
│  Notes: [                    ]                                         │
│                                                                       │
│  Status: [---------------------- ▼]                                    │
│                                                                       │
│    [Batch Assign State(s)]  [Reset Form]                              │
│                                                                       │
└───────────────────────────────────────────────────────────────────────┘
```
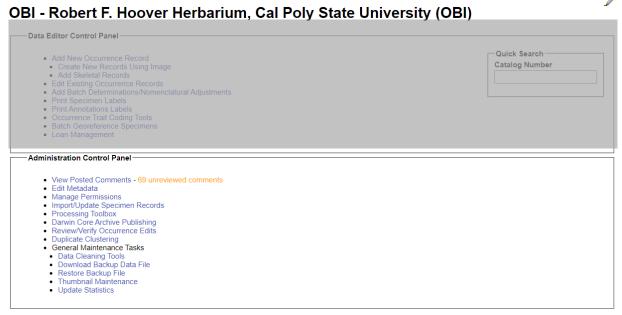
Select the value or values from the list that you wish to score. To select several values from the list that you wish to give the same phenological score, hold Ctrl and click on each value in the list. Select the appropriate score from the trait scoring schema at the bottom of the lower box. Depending on the scoring schema available for the trait you are scoring, you may be able to view more scoring options by clicking the black triangle next to the schema. From this list, select the traits that you wish to apply to this specimen. Traits that you do not wish to score can be left blank. When you are satisfied with your scoring(s), click the Batch Assign State(s) button. If you make a mistake, click Reset Form (Caution: this will un-select all of your selected text fields as well, so be careful when selecting traits!).
15: Batch georeferencing specimens.
Loan Management – This tool can be used to keep track of outgoing and incoming loans, gifts, and exchanges of specimens using the appropriate tab on the Loan Management Main Menu. See *16: Managing loans, gifts, and exchanges*.

3:2 Administration Control Panel

The Administration Control Panel is used to perform higher-level data processing and is thus only available to users with administrative permissions (see *19: Managing user permissions*). It can be accessed by logging in to the portal, clicking "My Profile," and clicking the "Occurrence Management" tab. The tools available in the Administration Control Panel are described below.
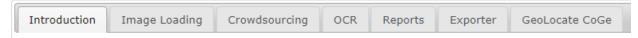
OBI - Robert F. Hoover Herbarium, Cal Poly State University (OBI)

Data Editor Control Panel

- Add New Occurrence Record
  - Create New Records Using Image
  - Add Skeletal Records
- Edit Existing Occurrence Records
- Add Batch Determinations/Nomenclatural Adjustments
- Print Specimen Labels
- Print Annotations Labels
- Occurrence Trait Coding Tools
- Batch Georeference Specimens
- Loan Management

Quick Search
Catalog Number

Administration Control Panel

- View Posted Comments - 69 unreviewed comments
- Edit Metadata
- Manage Permissions
- Import/Update Specimen Records
- Processing Toolbox
- Darwin Core Archive Publishing
- Review/Verify Occurrence Edits
- Duplicate Clustering
- General Maintenance Tasks
  - Data Cleaning Tools
  - Download Backup Data File
  - Restore Backup File
  - Thumbnail Maintenance
  - Update Statistics

View Posted Comments – Portal users can post comments on the records of individual specimens if, for example, they notice a typographic error or mis-associated image, or if they suspect a taxon is misidentified. With this tool, the administrator can view the posted comments, mark them as reviewed, hide them from public viewing, or delete them by clicking the appropriate button. See *17: Viewing and vetting comments*.

Edit Metadata – This navigates to the Metadata Editor page where you can change your institution name, description, contact information (contact person, email address, etc.), homepage, license, GUID source, or other information. See *18: Editing metadata (summary and contact information) for your collection*.

Manage Permissions – This tool can be used to manage which users have which permissions. See *19: Managing user permissions*46.

Import/Update Specimen Records – This tool allows the user to batch add or update specimen records using one of many sources types including a CSV file, Notes from Nature transcriptions, DarwinCore archives, IPT import, and others. See *20: Importing record data*.

Processing Toolbox – This link navigates to a set of tools for processing specimens (see tabs below). See *21: Using the processing toolbox*.

| Introduction | Image Loading | Crowdsourcing | OCR | Reports | Exporter | GeoLocate CoGe |

Darwin Core Archive Publishing – This tool allows the user to publish occurrence data to an aggregator by uploading a Darwin Core Archive. See *22: Darwin Core archive publishing*.

Review/Verify Occurrence Edits – This tool can be used by the administrator to review edits to specimen records that have been made by other users. See *23: Reviewing edits to specimen records*.

Duplicate Clustering – This tool allows the user to view and evaluate potential duplicate specimens housed at other institutions by matching specimens with the same collector, collector number, and collection date. The user can view all duplicate specimens or just duplicate specimens with conflicting identifications. See *24: Duplicate clustering*.

General Maintenance Tasks

Data Cleaning Tools – Available tools include a duplicate record identification tool for discovering accidental duplicate catalog numbers (see *25:1 Duplicate catalog numbers*); a political geography tool to help fix and standardize country, state/province, and county designations (see *25:2 Geographic cleaning tools*); and a taxonomy tool that aids in locating and fixing taxonomic errors and inconsistencies (see *25:3 Taxonomic cleaning tools*).

Download Backup Data File – This tool allows the user to download a copy of all collection data besides images. This file can be used for archiving or as a backup before making batch edits to the collection. See *26: Downloading a copy of your database*.

Restore Backup File – If systematic errors in the collection have been discovered, likely resulting from an erroneous batch editing process, the collection data can be reset to a previous "version" of the data using this tool, provided the user has previously downloaded a backup data file, preferably shortly before the erroneous batch process. See *27: Restoring your database with a previously downloaded copy*.

Thumbnail Maintenance – This tool will build thumbnail images based on the specimen images

Update Statistics – Click this link to update collection statistics such as specimen counts and to update null fields (e.g., scientific name fields for specimens that were only identified to family) within the collection. See *28: Collection statistics*.

4: Adding specimen records

New specimen records are primarily added in one of four ways: (1) using the Add New Occurrence Record tool (see *4:1 Adding a new record by entering label data*), (2) using the Add Skeletal Records tool (see *6: Adding skeletal records*), (3) using the Create New Records Using Image tool (see *4:2 Adding a new record using an image*), or (4) by clicking the new record button ($\geq^*$) while on the Occurrence Editor page (see next screenshot; also *7: Editing existing specimen records*).

Home >> Collection Management >> Public Display >> Editor |<   << | 1 of 86446 | >>   >| >*

| Occurrence Data | Determination History | Images | Linked Resources | Traits | Admin |

—Collector Info—

4:1 Adding a new record by entering label data

Select Add New Occurrence Record from the Data Editor Control Panel (*3:1 Data Editor Control Panel*). Enter the specimen information into the provided fields. See *7:2 Explanation of Occurrence Data fields* for information about the available data fields.

Before you click Add record to create the new record, you can select one of three options for the next action you will perform, shown below. Go to New Record and Carryover Locality Information is useful for entering data from a single collection event that will share locality information. Remain on Editing Page should be used when the user wishes to double-check the record or add supplementary information such as images or annotations.

4:2 Adding a new record using an image

Using this tool, you can upload (or enter a URL to) an image that will establish a new occurrence record. From the Data Editor Control Panel (*3:1 Data Editor Control Panel*), select Create New Records Using Image (nested under Add New Occurrence Record). To upload an image, click the Choose File button and select the image you wish to upload. To use a URL, click the Enter URL link on the right side of the form.

Before upload, you can also define the processing status of the new record and enter any skeletal data for the record, including Catalog Number, Scientific Name, Country, State/Province, and County. Checking the box next to OCR Text using Tesseract OCR engine (if applicable) will run optical character recognition on the image that will attempt to parse text from the image that can potentially be used to fill out the remaining fields in the future.

5: Searching and sorting specimen records

(adapted from Skema & Barber 2018)

The Record Search Form in the portal provides the means to search and sort your entire collection. Access the form by navigating to your collection management page (see *3: Managing your profile and collections(s)*), then click "Edit Existing Occurrence Records" in the Data Editor Control Panel. You will see a Record Search Form like that in the next screenshot.

You can enter a search term in any field shown. Hover over a field to see particular instructions for how to best enter search terms for that field (e.g., must enter space before and after dash when entering a range into catalog number). To search using any data field not shown on the form, select a field from the dropdown menu next to "Custom Field 1," select a modifier from the dropdown menu next to it, and enter the search term in the last bo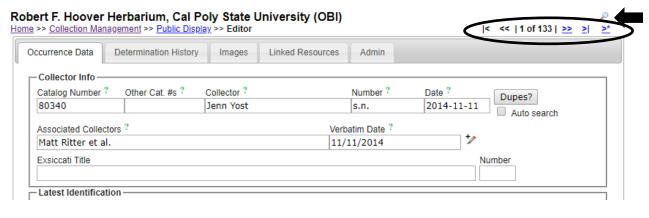x to the right on that line. You may add additional custom fields by clicking on the pencil with the plus sign ( ) at the end of the line for Custom Field 1. You can search for records using as many fields as you wish.

NOTE

A straight search term returns only exact matches. For example, if you enter "Edgar T. Wherry" in the "Collector" field, you will only be returned those records with the exact same spelling, spacing, and punctuation as your entry. Use a percent sign (%) to loosen the search parameters. This acts as a 'contains' statement. For example, entering "%Wherry" will return any collector name with Wherry in it (e.g., Edgar T. Wherry, E.T. Wherry, Edgar T Wherry, Amelia Wherry Spencer). Searching with percent signs can also be a good way to find spelling errors in your collection's data.

To sort the results of your search, use the "Sort by:" field in the lower right corner. For example, if you select "Date Last Modified" from the Sort by drop down, then select "descending" from the dropdown menu next to it, you will be returned a table of all records in order of when they were modified from most recent to least recent.

You can view the results of your search by clicking "Display Editor" or "Display Table." If you click "Display Editor," you will see the editing window (see *7: Editing existing specimen records*) for the first record that matches your search, and the other records that match your search can be viewed by clicking the arrows to the top right of the form (circled in black below). If you click "Display Table," the results of your search will be displayed as a table that includes most data fields available for these records.

NOTE

To change the parameters of your search, sort the results by different criteria, change the results display, or perform a new search, click the magnifying glass icon (🔍) at the top right corner of the page (see arrow on previous screenshot).

6: Adding skeletal records

(adapted from the instructions available on the portal)

The Add Skeletal Records feature allows users to quickly create digital records with a small amount of data for a large number of physical specimens. This tool is helpful for collections that aim to build a basic understanding of their holdings while rapidly digitizing their collection.

This tool can be used to collect basic collection information, for example, during the imaging process. The imaging team can enter the basic collection information shared by the batch of specimens being processed, and each time they scan a barcode into the catalog number field, a record is added to the system with these skeletal data. Complete data can be entered by clicking on the catalog number,

but a recommended workflow would be to process the full label data directly from the image of the specimen label at a later stage.

1. To add a skeletal record, navigate to the Add Skeletal Records tool via the Data Editor Control Panel (see *3:1 Data Editor Control Panel*). You will see a page like that below.

2. To control which fields are shown on the skeletal record entry form, click the Display Option symbol (a small, grey table) located above the Scientific Name field (circled above).
3. In the dropdown menu of options, check or uncheck the boxes next to the desired fields to be shown. The following fields are commonly recommended for skeletal data entry: Scientific Name, Family, State/Province, and County/Parish.
4. Select the preferred action that the data entry module will use when a record already exists for a scanned catalog (barcode) number. It is recommended to use the "Restrict entry if record exists" option for the CAP TCN project.
   Note: Even if you choose the "Append values to existing records" option, skeletal data will not copy over existing field values.
5. If using the fields recommended above, enter the scientific name by beginning to type the name from the specimen label, then selecting the appropriate name from the dropdown list.
6. If desired and/or possible (given the data provided on the specimen sheet), enter the State/Province and the County/Parish of the specimen if the specimen was collected in the U.S. or Canada. The authorship and family of the name of the taxon will automatically populate if the taxon is in the portal's taxon table.
7. Enter the barcode number into the Catalog Number field by clicking inside the Catalog Number field and scanning the barcode of the specimen.
8. Once all fields are filled, click Add Record.

IMPORTANT NOTES

- After Add Record is clicked, the data in the Skeletal Data box fields will NOT be cleared. Only the Catalog Number field will be cleared. This is designed to facilitate rapid skeletal data entry for folders of similar specimens (i.e., specimens of the same species). Close attention should be paid to these fields when transitioning between species or specimen localities. It is easy to forget to change the data in these fields.

- In the event that a user needs to edit a previously entered skeletal record, you can click the catalog number of the record as it is listed in the Records box below the Skeletal Data box (circled below). Note that this list will disappear if the page is refreshed. You can also add an image to the record from this page by clicking the icon to the right of the listed catalog number.

Display Instructions

Robert F. Hoover Herbarium, Cal Poly State University

- The length of the imaging session, total count of specimens, and rate of specimen addition (in units of records per hour) are visible in the top right corner of the Skeletal Data box. This can be helpful when assessing the efficiency of alternative workflows.

7: Editing existing specimen records

(adapted from Skema & Barber, 2018)

1. Log in to the CCH2 Portal and navigate to the Data Editor Control Panel by clicking "My Profile," the "Occurrence Management" tab, then the name of your collection in the "Collection Management" box.
2. Under "Data Editor Control Panel," click "Edit Existing Occurrence Records." Click "Display Table" to get a table of every record in your collection OR search for a specific record using by entering search terms in the appropriate fields (see *4:2 Adding a new record* using an image

Using this tool, you can upload (or enter a URL to) an image that will establish a new occurrence record. From the Data Editor Control Panel (*3:1 Data Editor Control Panel*), select Create New Records Using Image (nested under Add New Occurrence Record). To upload an image, click the Choose File button and select the image you wish to upload. To use a URL, click the Enter URL link on the right side of the form.

Before upload, you can also define the processing status of the new record and enter any skeletal data for the record, including Catalog Number, Scientific Name, Country, State/Province, and County. Checking the box next to OCR Text using Tesseract OCR engine (if applicable) will run optical character recognition on the image that will attempt to parse text from the image that can potentially be used to fill out the remaining fields in the future.

3. 5: Searching and sorting specimen records for help with searching and sorting specimen records).
4. To access a record, click on its Symbiota ID in the far left column, which will take you to the Record Editor page, seen on page 19. See *7:1 Explanation of Record Editor tabs* and *7:2 Explanation of Occurrence Data fields*. You can click on the green question mark next to any field to get further explanation of its use.
5. Edit a record by changing, adding, or removing data from the fields in the "Occurrence Data" tab. Once record editing is complete, change the processing status as appropriate, and save the work by clicking on "Save Edits" button at base of Occurrence Data tab in Record Editor or by hitting 'Enter' once or twice on your keyboard, depending on the browser and/or operating system.

NOTES

- If an image of the specimen is available, you can view it to help edit the record.

- To increase the specimen image size, hover over any outer boundary of the image until you see an arrow and drag to the desired size.

- To zoom in on one area of the image, hold down the Ctrl key (Cmd on Mac) and click on an area of interest. Alternatively, you can hold down the Shift key, left click, and drag the cursor up. To zoom out, do the same but drag down.

7:1 Explanation of Record Editor tabs

Upon opening the Record Editor page, you will see 4-5 tabs, depending on your level of permissions. The image shown below is of the Record Editor page for a user with administrative permissions. A brief explanation of each tab is provided below.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)
Home >> Collection Management >> Public Display >> Editor

| Occurrence Data | Determination History | Images | Linked Resources | Admin |

Occurrence Data – See explanation of fields on page 18.
Determination History – where annotations are shown and can be entered. Annotations can also be batch uploaded from separate files. See *8:1 Adding individual determinations/annotations.*
Images – provides information on image(s) associated with the record. See *9: Adding images to specimen records / editing images mapped to specimen records*.
Linked Resources – allows linkage of checklists, duplicates, and genetic resources to the record
Admin – tracks changes made to Edit History, allows for transfers of specimens between collections, and provides a means for deleting an occurrence record. Only users with administrative permissions (see *19: Managing user permissions*) can delete specimen records.
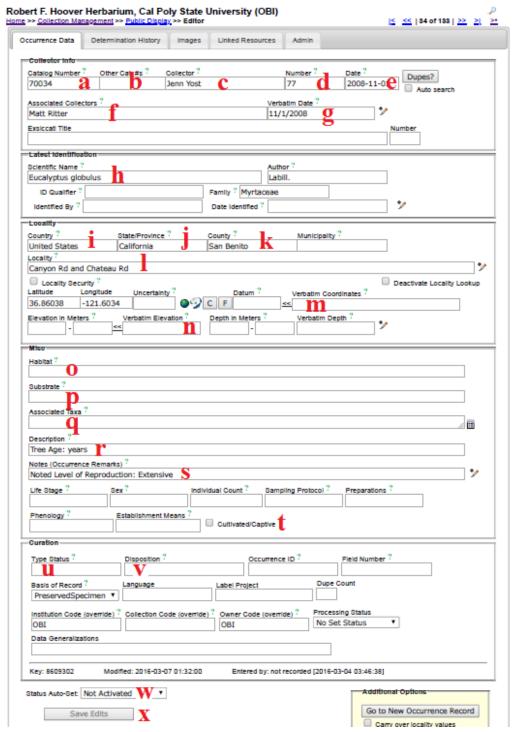
7:2 Explanation of Occurrence Data fields

(adapted from Skema & Barber 2018)
The major fields of interest are described in the following two pages. In the portal, you can click on the green question mark next to any field to get further explanation of the use of that field. Additional fields are viewable by clicking the pencil icon to the right of some fields. For further explanation of all fields, visit http://symbiota.org/docs/data-entry-guides-for-openherbarium/.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)
Home >> Collection Management >> Public Display >> Editor |< << | 34 of 133 | >> >| >‖

| Occurrence Data | Determination History | Images | Linked Resources | Admin |

Collector Info
Catalog Number ?   Other Cat #s ?   Collector ?   Number ?   Date ?   Dupes?
70034 **a**   **b**   Jenn Yost **c**   77 **d**   2008-11-0 **e**
                                                                                    ☐ Auto search

Associated Collectors ?   Verbatim Date ?
Matt Ritter **f**   11/1/2008 **g**   ✎

Exsiccati Title   Number

Latest Identification
Scientific Name ?   Author ?
Eucalyptus globulus **h**   Labill.
ID Qualifier ?   Family ? Myrtaceae
Identified By ?   Date Identified ?   ✎

Locality
Country ?   State/Province ?   County ?   Municipality ?
United States **i** California **j** San Benito **k**
Locality ?
Canyon Rd and Chateau Rd **l**   ✎

☐ Locality Security ?   ☐ Deactivate Locality Lookup
Latitude   Longitude   Uncertainty ?   Datum ?   Verbatim Coordinates ?
36.86038   -121.6034   🌐🔍 C F   << **m**

Elevation in Meters ?   Verbatim Elevation ?   Depth in Meters ?   Verbatim Depth ?
   -              << **n**   -   ✎

Misc
Habitat ?
o

Substrate ?
p

Associated Taxa ?
q   📅

Description ?
Tree Age: years **r**

Notes (Occurrence Remarks) ?
Noted Level of Reproduction: Extensive **s**   ✎

Life Stage ?   Sex ?   Individual Count ?   Sampling Protocol ?   Preparations ?

Phenology ?   Establishment Means ?
                                    ☐ Cultivated/Captive **t**

Curation
Type Status ?   Disposition ?   Occurrence ID ?   Field Number ?
u   **v**

Basis of Record ?   Language   Label Project   Dupe Count
PreservedSpecimen ▼

Institution Code (override) ? Collection Code (override) ? Owner Code (override) ? Processing Status
OBI   OBI   No Set Status ▼

Data Generalizations

Key: 8609302   Modified: 2016-03-07 01:32:00   Entered by: not recorded [2016-03-04 03:46:38]

Status Auto-Set: Not Activated **W** ▼   **Additional Options**

    Save Edits **X**   Go to New Occurrence Record
                                                 ☐ Carry over locality values

a **Catalog Number** – the barcode number (and institution code, if included on the barcode label) on the specimen (e.g., OBI00045897)

b **Other Catalog #s** – the accession number of the specimen, if applicable. If your institution already had data in NANSH or the Consortium of California Herbaria, this may have previously been the number in the Catalog Number field.

c   **Collector** – primary or only collector. The name should be in order of "First name Last name". On a specimen, this is often the name that follows "col.", "leg.", and "legit." If no collector is present, "Unknown" should be entered in lieu of other institutional standards.

d   **Number** – collector number. If no number is present, "s.n." (*sine numero* is Latin for 'without number') should be entered in lieu of other institutional standards. If letters or symbols are included in the collector number on the label (e.g., KP-004), they should be included.

e   **Date** – when the specimen was collected in the format YYYY-MM-DD. Institutional standards should be followed for entering 0s when a day or month is omitted, or if a range of dates are listed. See also "Verbatim Date" (g).

f   **Associated Collectors** – collectors following the primary collector. Each name should be in order of "First name Last name." Multiple names should be separated by a semicolon (;).

g   **Verbatim Date** – date as it appears, verbatim, on the label (e.g., July 21st, 2016). This is particularly useful if part of the date is omitted, the date is in another language, or if a range is listed.

h   **Scientific Name** – the scientific name of the specimen. When populating this field, be sure to select an option from the dropdown list rather than typing out the name. If the specimen is filed under a different name than the name on the specimen, this information should be noted in the Notes field (e.g., "filed under...") in lieu of other institutional standards.

i   **Country** – the country in which the specimen was collected. If the specimen was collected in the U.S., "United States" should be entered in this field.

j   **State/Province** – the state in which the specimen was collected, if in the U.S., or the province if the specimen was collected in Canada. The state/province name should be entered as a full name rather than an abbreviation (e.g., "California" instead of "CA").

k   **County** – the county (Louisiana: parish; Alaska: borough) in which the specimen was collected. County designations (e.g., "Co." or "County") should not be included in this field. This value should be selected from the dropdown list.

l   **Locality** – geographic description of where plant was collected. This should not include country, state, or county information, since these data are found in alternate fields, unless the locality includes a description of an area within the county or state (e.g., "southwest corner of Jefferson county" or "northeast Arizona"). This field should include directions to the collection location, city names, road names, names of parks, etc. Note that you can check the "Locality Security" box if the locality information should be protected (e.g., protected species location).

m   **Verbatim Coordinates** – If latitude and longitude are provided on the sheet, they should be entered in this field and standardized by clicking << . Degree/minutes/seconds lat/longs can be entered by clicking "Tools," entering Lat/Long in degrees, minutes, seconds boxes, and clicking "Insert Lat/Long Values" to convert to decimal. If coordinates were provided on the sheet, "Coordinates recorded at time of collection" should be entered in the Georeference Remarks field.

n   **Elevation in Meters** – if elevation in meters is provided on the sheet, it should be entered in this field. If provided in other unit, e.g., feet, the value can be entered into the "Verbatim Elevation" field with its unit and converted to metric by clicking the << .

o   **Habitat** – environmental conditions in which the plant was found (e.g., marsh, grassy field)

p   **Substrate** – technical definitions given for substrate, e.g., soil type/series or rock formation

q   **Associated Taxa** – other plant taxa listed as growing with the collected specimen. To promote standardization and easy entry into this field, a dropdown list of scientific names in the portal's taxon table can be accessed by clicking the small table icon on the small table icon to the right of the data field.

r **Description** – information specific to the individual plant (e.g., condition, color)

s **Notes (Occurrence Remarks)** – population characteristics (e.g., frequency: rare, common, etc.) and any additional data on the label that does not fit easily into the other data fields. This field can also be used as temporary holder to write notes for specimens that require further review.

t **Cultivated/Captive Checkbox** – this should be checked if the label indicates that the sample was from a cultivated plant

u **Type Status –** the type status (e.g., holotype, isotype) of the specimen. This field should only contain data if the specimen is a type

v **Disposition –** the location of the specimen in the herbarium or on loan. This field is especially useful if the specimen is being used for a display, research project, or education use, or if the specimen has two different species on it (i.e., it can only be filed with one of the species).

w **Processing Status** – this field is used to indicate the record's stage in the quality control workflow (see Appendix 1: Processing Status for instructions)

x **Save Edits** – click to save record. If the button is unclickable, click anywhere on screen outside of a field, then click "Save Edits" button again.

7:3 Adding annotations/determinations

See *8: Adding determination/annotation data.*

7:4 Batch editing specimen records

(adapted from Skema & Barber 2018)

NOTE: Caution!

Exercise caution when using this tool. Technicians are not advised to perform batch edits. We also recommend downloading a copy of your database (see *26: Downloading a copy of your database* of this guide) prior to making batch edits

For batch editing of scientific names, see *8: Adding determination/annotation data*.

1. There are two options for batch editing specimen records: you can change a value for the entire set of records in your collection or change a value for a selected set of records. To change all records, click on "Display Table" in the Record Search Form (see page 14), then click the edit icon ( ) above the resulting table of all records from your collection. Continue to step 3.

2. To change a value for a selected set of records, first search for the records of interest using the search form (see page 14). Once you have the set of records to which you would like to make a batch edit, click on the edit icon ( ) at the top of your selected table of records.

3. From the dropdown menu next to "Field Name" in Batch Update, select the field you want to edit.

4. In "Current Value:" enter the text that is presently in the field you want to edit.

5. In "New Value:" enter the text that you want to be in the edited field.

6. Choose if you want to match the whole field or just match any part.

7. Click "Batch Update Field" to enact your batch edit. A pop-up screen will tell you the number of records to be updated, warn you that the replace operation cannot be undone, and prompt you to OK the update. Proceed with caution and see examples below.

NOTE: Caution!

It is easy to inadvertently change text you did not intend to change. Generally, the more specific your "Current Value:" text, the less likely you are to run into unintended consequences. If possible, get an estimate from your record table of how many records should be affected, and check that against the number of records cited in the warning. If the numbers do not match, rethink your strategy.

It is not possible to check the record count when sorting by "Modified By" first. Doing so returns a count of the number of fields edited by the "Modified By" user for all records to be affected, rather than the number of records to be affected.

Examples

Example of a good use of batch edit: Standardizing plant collector names. If you are standardizing all Wherry's collections to "Edgar T. Wherry," then you could enter "E. T. Wherry" in Current Value and "Edgar T. Wherry" in New Value in batch edit for the collector field name, and update. Repeat for alternate forms of this name (e.g., "E T Wherry," Edgar T Wherry").

Example of a bad use of batch edit: Changing cardinal directions. For example, if you entered "n." in Current Value and "N" in New Value in batch edit for the locality in an attempt to change lower case abbreviated instances of the cardinal direction north, you would accomplish that, but you would also change any other character string with "n." such as a sentence ending in the letter n. This would result in batch misplacements of "N" where "n." should be. For example, "Next to the station. East side" would be transformed into "Next to the statioN East side."

7:5 Batch editing scientific names

(adapted from Skema & Barber 2018)

There are two options for batch editing scientific names, each appropriate for different situations.

- Taxonomic cleaning tools are one way to change scientific names. To use these, click on "Data Cleaning Tools" in your Administration Control Panel (see *3:2 Administration Control Panel*). Scroll down to the Taxonomy section and click "Analyze taxonomic names." Select the desired resource by checking the box next to it (Catalog of Life, Tropicos, or both). Leave "Names Processed per Run" at 20 and leave "Start Index" blank. Select the radio dial next to "Semi-Manual" and then click "Analyze Taxonomic Names." Carefully look through the list. When you find a suggested name that is correct, click "remap to this taxon." These tools may be useful if you have scientific names that are misspelled.
- The nomenclature adjustment tool may be useful if the names are spelled correctly but are otherwise incorrect or outdated. To use it, click "Add Batch Determinations/Nomenclatural Adjustments" in your Administration Control Panel. See *8: Adding determination/annotation data* for instructions on how to use this tool.

8: Adding determination/annotation data

8:1 Adding individual determinations/annotations

To annotate an individual record or add previous determinations, navigate to the specimen in the Occurrence Editor (see *7: Editing existing specimen records*) and click the Determination History tab. If no previous annotations exist, you will see a message that says "There are no historic annotations for this specimen" and a box labeled Add a New Determination. If an annotation already exists on the

specimen, you will see that annotation. In the latter situation, click the green plus sign to add a new annotation.

In the Add a New Determination Box, enter, at minimum, the scientific name, determiner (person who identified the specimen, if known. Enter "unknown" if not known), and the date (or "n.d." if not known), at minimum. You can also add an identification qualifier (e.g., "cf." or "aff."), a reference, and notes, and you can select a confidence of determination, if instructed by your collection. By default, if the date of determination is newer than that previous date of determination, the Make this the current determination box will be checked once you move your cursor out of the Date box. If you want this determination to be the most up-to-date identification for the specimen, keep this box checked (or check it, if it was not auto-checked). If you wish to print this annotation label now or in the future, also check the Add to Annotation Print Cue box. Click Submit Determination.

NOTE

If the specimen previously had an identification and you have checked the box next to "Make this the current determination," a historic annotation will be added to the record automatically as shown in the next screenshot. For this reason, you do not need to manually add a historic determination before you add a new determination.
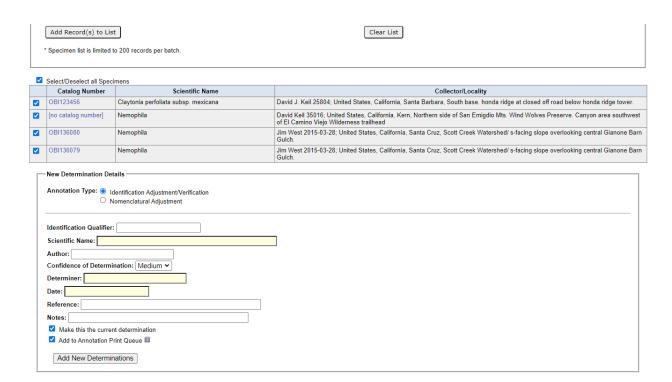

8:2 Batch adding determinations/annotations

You can add many annotations at once using the Add Batch Determinations/Nomenclatural Adjustments tool. Navigate to this tool by accessing the Data Editor Control Panel (see *3:1 Data Editor Control Panel*) and clicking "Add Batch Determinations/Nomenclatural Adjustments." To select the specimens to which determination data will be added ("Define Specimen Recordset"), either enter a list of catalog numbers (separated by commas) in the "Catalog Number:" field or select a taxon to evaluate by entering its name in the "Taxon:" field. Click the Add Record(s) to List button.

A table of specimens of the indicated taxon will appear below the "Define Specimen Recordset" box (see next screenshot). You can then select all the specimens that you wish to annotate by checking or unchecking the boxes in the leftmost column of the table. Use the "Select/Deselect all Specimens" box to uncheck or check all the boxes if you would prefer to select specimens one by one.

	Catalog Number	Scientific Name	Collector/Locality
☑	OBI123456	Claytonia perfoliata subsp. mexicana	David J. Keil 25804; United States, California, Santa Barbara, South base. honda ridge at closed off road below honda ridge tower.
☑	[no catalog number]	Nemophila	David Keil 35016; United States, California, Kern, Northern side of San Emigdio Mts. Wind Wolves Preserve. Canyon area southwest of El Camino Viejo Wilderness trailhead
☑	OBI136080	Nemophila	Jim West 2015-03-28; United States, California, Santa Cruz, Scott Creek Watershed/ s-facing slope overlooking central Gianone Barn Gulch.
☑	OBI136079	Nemophila	Jim West 2015-03-28; United States, California, Santa Cruz, Scott Creek Watershed/ s-facing slope overlooking central Gianone Barn Gulch.

Add information about the name change in the "New Determination Details" box. Here you can indicate whether the change is due to a new identification ("Identification Adjustment/Verification") or a nomenclatural change ("Nomenclatural Adjustment"). An identification qualifier (e.g., "aff." or "cf.") can be added in the "Identification Qualifier:" field. Enter the new scientific name in the "Scientific Name" field, and the "Author:" field will automatically populate if the taxon is already in the taxon table. If the taxon is not in the taxon table, you will have to manually enter the author of the scientific name. You should also enter the name of the determiner in the "Determiner:" field, as well as the full date of determination in the "Date:" field. You can indicate the confidence in the determination (Low, Medium, or High) in the "Confidence of Determination:" field, list your determination references in the "Reference:" field, or include any other notes in the "Notes:" field. Finally, if you check the "Make this the current determination" box, the scientific name will be updated for the selected records. Otherwise, the determination will be added to the specimens' records, but the most current ID name will not be changed.
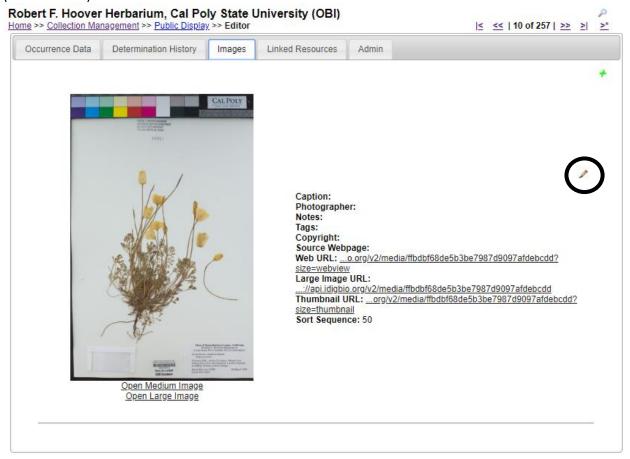
If you wish to print the annotation labels in the future, check the "Add to Annotation Print Queue" box (see *13. Printing annotation/determination labels*).

9: Adding images to specimen records / editing images mapped to specimen records

Images should primarily be added to specimen records by batch uploading via the Processing Toolbox (see *21:1 Image loading*), though it is possible to upload images individually to a specimen record. The reason for this is that image files are not intended to be stored with the CCH2 database itself. Rather, our images are stored on external (CyVerse) servers—which are built to handle large numbers of high-resolution files—and these images are linked to their respective CCH2 records using URLs provided by CyVerse. The servers where the specimen records are held are not equipped to handle thousands of hgh-resolution images.

A user can view and edit images associated with a specimen record by navigating to the occurrence record editor (see page 19) and clicking the Images tab. The web URLs that link to a small version of the image (Web URL), high-resolution image (Large Image URL), and thumbnail version of the image (Thumbnail URL) can be accessed on this page. The image can also be viewed using one of the links below the image, Open Medium Image or Open Large Image.

To edit these links or metadata regarding the image, click the pencil icon on the right side of this tab (circled below).

On the resulting page (see next screenshot), you can add information about the image (Edit Image Data box), delete the image (Delete Image box), remap the image to a different occurrence record (Remap to Another Specimen box), or completely disassociate the image from all specimen records (Disassociate Image from all Specimen Records box).

---Edit Image Data---

Caption:

Photographer:
Select Photographer ▼ ✏️
Notes:

Copyright:

Source Webpage:

Web URL:
https://api.idigbio.org/v2/media/ffbdbf68de5b3be7987d9097afdebcdd?size=webview
Large Image URL:
https://api.idigbio.org/v2/media/ffbdbf68de5b3be7987d9097afdebcdd
Thumbnail URL:
https://api.idigbio.org/v2/media/ffbdbf68de5b3be7987d9097afdebcdd?size=thumbnail
Sort Sequence:
50
Tags:
☐ Image shows an organism.
☐ Image shows label data.
☐ Image shows an annotation/identification label.
☐ Image has typed or printed text.
☐ Image has handwritten label text.
☐ Field image of habitat.
☐ There is a problem with this image.
☐ Image contains a diagnostic character.
☐ Image contains the adult organism.
☐ Image contains the immature organism.

[Submit Image Edits]

---Delete Image---

☐ Remove image from server
(Note: leaving unchecked removes image from database without removing from server)

[Delete Image]

---Remap to Another Specimen---

Occurrence Record #: [   ]   Open Occurrence Linking Aid

[Remap Image]

---Disassociate Image from all Specimen Records---

[Disassociate Image]
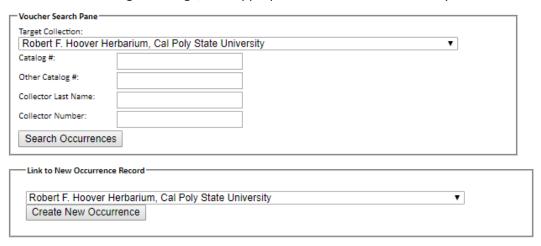
* Image will only be available from Taxon Profile page

9:1 Deleting an image

In the Delete Image box, simply click the Delete Image button. You do not need to check the Remove image from server box, since our images are not stored on the central CCH2 server (see explanation on page 24). **NOTE:** If you wish to move the image to a different specimen record rather than delete it entirely, see *9:2 Remapping an image to another specimen*.

9:2 Remapping an image to another specimen

If an image has been associated with the wrong specimen record, it is possible to simply re-map the image to the correct specimen record rather than delete the image from the wrong record and re-upload it to the correct record.

To do this, navigate to the Remap to Another Specimen box on the Images tab of the Record Editor page (see previous page) and click Open Occurrence Linking Aid. A new window will pop up that will prompt you to search for the correct specimen record by entering a catalog number, other catalog number, collector name, collector number, or combination of these fields. Alternatively, you can choose to create a new record using this image, if an appropriate record does not already exist.

Once you click Search Occurrences, specimen records that match the search criteria will be displayed. Select the appropriate occurrence record, and this window will close and auto-populate the Remap to Another Specimen box. Click "Remap Image." The image will be removed from this specimen record and added to the selected specimen record.

10: Linking external resources to specimen records

Resources related to a given specimen can be recorded in the Linked Resources tab on the Record Editor page (see page 19). The following resources are currently linkable to a specimen record:

1. Associated occurrences (other specimens or observations associated with the given specimen that are not necessarily duplicates of that specimen)
2. Checklists for which the specimen is a voucher (Checklist Voucher Linkages box)
3. Duplicate records, even those housed at collections other than your own (Duplicate Specimens box)
4. Genetic data such as sequences listed on GenBank (Genetic Resources box)

11: Deleting specimen records

Only users with Administrator permissions can delete a specimen record, and only the portal manager(s) can delete more than one specimen record at a time. This is designed to protect data integrity, such as GUIDs and links to other tables in the database.

Deleting a specimen record is only appropriate when that specimen no longer exists or the record was added erroneously (e.g., it was an exact duplicate of an existing record). You should not delete a record for the purpose of updating it or adding a new version of the record.

To delete a record, navigate to the occurrence editor page (see *7: Editing existing specimen records*) and click the Admin tab. Click the "Evaluate record for deletion" button to determine whether the record can be safely deleted. If an image exists for the record, you will need to disassociate the image from the specimen (see *9: Adding images to specimen records / editing images mapped to specimen records*) prior to deleting the record. If there are no warnings at this point, click the Delete Occurrence button.

12: Printing specimen labels

To print specimen labels, navigate to the Data Editor Control Panel (see *3:1 Data Editor Control Panel*) and click "Print Specimen Labels." Search for the desired specimens by entering search terms in one or many of the available fields in the "Define Specimen Recordset" box and clicking "Filter Specimen Records." Select all the specimens for which you want to print labels by checking or unchecking the boxes in the leftmost column of the table. Use the "Select/Deselect all Specimens" box to check or uncheck all the boxes as necessary.

☑	1	David J. Keil 26876 ✏	Nemophila menziesii var. menziesii	United States; California; San Luis Obispo; North of Nacimiento Lake, .3 miles south from Interlake Road on Bee Rock Road.
☑	1	David J. Keil 27420 ✏	Nemophila menziesii var. menziesii	United States; California; San Luis Obispo; Caliente Range. Along Caliente Ridge Rd. between wildlife guzzler (35°03.432' N x 119°46.937' W) and Caliente Peak.
☑	1	David Keil 34384 ✏	Nemophila menziesii	United States; California; San Luis Obispo; Highway 41 between Creston and Shandon at 3220 Highway 41
☐	1	Lewis S. Rose 39077 ✏	Nemophila menziesii var. atomaria	United States; California; Marin; Nicasio

In the Label Printing box, select the name of the "Label Profile" that you wish to apply to your printed labels. The label profile will specify which fields are printed and the aesthetics of the label. Default (simple) profiles can be found in the "Portal defined profiles" list, and you can select your own saved profile from the "User defined profiles" list. Instructions for defining a label profile can be found in *12:1 Defining a label profile for custom label printing*. After selecting a profile, you can then enter a desired heading (e.g., "Robert F. Hoover Herbarium (OBI)", heading mid-section (e.g., state or family), heading suffix (any additional text information), and label footer (e.g., the name of the project for which the specimen was collected) for all labels to be printed. You can also select from a number of other options in the "Label Printing" box including whether you want to print the specimen barcode.

☐ **Print species authors for infraspecific taxa**

☐ **Print Catalog Numbers**

☐ **Include barcode of Catalog Number**

☐ **Print only Barcode**

Label Type:
[2 columns per page ⌄]

[Print in Browser]

[Export to CSV]

[Export to DOCX]

Once you have selected your desired options, you can print the labels directly from your browser, export the specimen data to a CSV file (similar to an Excel file, this format can be used with mail merge to produce labels), or export the labels to a Word document (DOCX file) by clicking the appropriate button. Note that currently, Word (DOCX) output only generates the old static label format (the "label profile" settings will not be applied). If you click "Print in Browser", you can manually edit the label content by clicking the Edit Labels Content button in the top right corner.

An example label for printing from the browser is shown below. Note that the boxes to include the barcode and the catalog number were checked when generating this label.

Robert F. Hoover Herbarium (OBI)
California California Polytechnic
University, San Luis Obispo

Boraginaceae

Nemophila menziesii Hook. & Arn.

United States, California, Mendocino County, Pt.
Arena light house.
Elev: 15m. (50ft.)
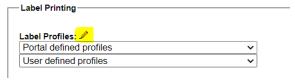Coastal fields.

Lewis S. Rose   68057   1 June 1968
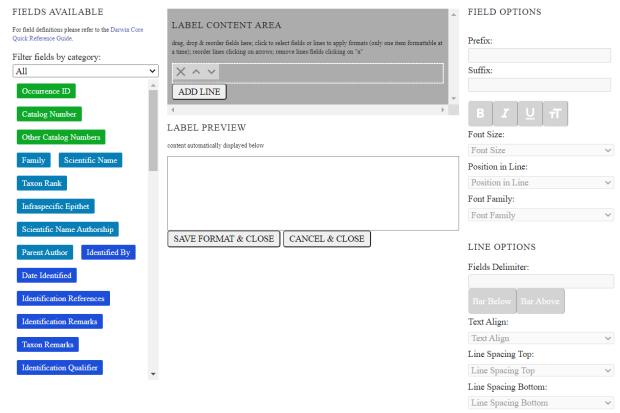
3000

An example label for the Symbiota guide

12:1 Defining a label profile for custom label printing

To create a new label profile that will apply custom formatting to your printed labels, click the pencil icon to the right of Label Profiles (highlighted below).

┌─ **Label Printing** ────────────────────

Label Profiles: ✏️
[Portal defined profiles   ⌄]
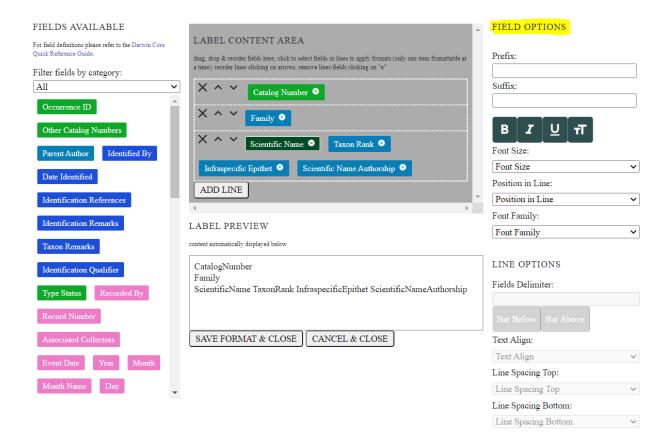[User defined profiles   ⌄]

Then click the green plus sign in the User Profiles box. Enter the title of the user profile and any desired header and footer information. Select the desired options from the Options box.

To further customize the label, click "visual interface" to the right of the "JSON" header. The resulting page will allow you to tailor your label with more detail (see next screenshot).

The format of your label is represented in the grey "Label Content Area" box. This is where you will build the label format. To add fields to your label, drag and drop field names from the left hand list of buttons into the "Label Content Area". As you do this, a preview of the label format will appear in the Label Preview box. Note that you can add as many lines as desired in the Label Content Area by clicking the Add Line button. By clicking on one of the fields that you have added to the Label Content Area, you can also add a prefix or suffix, change the font format, change the size, change the font, and move the position of the field by altering these elements under the Field Options section (highlighted in next screenshot). You can also change the options for an entire line by clicking the line in the Label Content Area (it will turn green) and then editing the options under the Line Options section.

FIELDS AVAILABLE

For field definitions please refer to the Darwin Core Quick Reference Guide.

Filter fields by category:

All

Occurrence ID

Other Catalog Numbers

Parent Author   Identified By

Date Identified

Identification References

Identification Remarks

Taxon Remarks

Identification Qualifier

Type Status   Recorded By

Record Number

Associated Collectors

Event Date   Year   Month

Month Name   Day

LABEL CONTENT AREA

drag, drop & reorder fields here; click to select fields or lines to apply formats (only one item formattable at a time); reorder lines clicking on arrows; remove lines/fields clicking on "x"

X ^ v   Catalog Number ⊗

X ^ v   Family ⊗

X ^ v   Scientific Name ⊗   Taxon Rank ⊗

Infraspecific Epithet ⊗   Scientific Name Authorship ⊗

ADD LINE

LABEL PREVIEW

content automatically displayed below

CatalogNumber
Family
ScientificName TaxonRank InfraspecificEpithet ScientificNameAuthorship

SAVE FORMAT & CLOSE   CANCEL & CLOSE

FIELD OPTIONS

Prefix:

Suffix:

B *I* U ᴛᴛ

Font Size:

Font Size

Position in Line:

Position in Line

Font Family:

Font Family

LINE OPTIONS

Fields Delimiter:

Bar Below   Bar Above

Text Align:

Text Align

Line Spacing Top:

Line Spacing Top

Line Spacing Bottom:

Line Spacing Bottom

NOTES

- The visual interface only works with simplified JSON formats and might not display existing formats correctly. Existing and complex formats can still be edited within the JSON editor.
- The visual interface currently does not support customized page layouts, such as the ones used by packet formats (lichens).
- If you want font families to be consistently printed across systems, you have to pick a font family for each field in the visual editor. Otherwise, the label will default to the browser fonts, and that can differ between operational systems (for instance, users printing labels in Macs will have different fonts than those in Windows systems).
- The current visual/JSON editor does not support labels printed in the Word format. You must print them using the browser, and then print or export to PDF if desired.

13. Printing annotation/determination labels

To use this tool, you will need to have first added the annotated specimens to the annotation print queue. This can be done either individually, via the Occurrence Editor (see *8:1 Adding individual determinations/annotations*), or in batch using the Add Batch Determinations/Nomenclatural Adjustments tool (see *8:2 Batch adding determinations/annotations*).

To print annotation labels, navigate to the Data Editor Control Panel (see *3:1 Data Editor Control Panel*) and click "Print Annotations Labels." A table will be displayed that lists all the specimens in the Annotation Print Queue. Check the boxes in the leftmost column next to the specimen records for which you wish to print annotations. To view a specimen record, either click the collector name and number

(to view public record display) or click the pencil icon next to the collector name and number (to view occurrence editor for that record). Customize your annotation label using the provided options and select either Print in Browser or Export to DOCX (to export as a Microsoft Word document). Check the box next to "Remove selected annotations from queue" to remove these specimens from the print queue after you click one of the print buttons.

☐	#	Collector	Scientific Name	Determination
☑	1	David Keil 35016 🖉	Nemophila menziesii	test, test

Annotation Printing

Header: [   ]

Footer: [OBI - Robert F. Hoover Herbarium, Cal Poly State University (OBI)]

☐ Print species authors for infraspecific taxa   Border Width: [1 ▾]   [Print in Browser]

☐ Print Catalog Numbers   Rows per page: [3 ▾]   [Export to DOCX]

☐ Remove selected annotations from queue   Spacing between labels: [5]

14: Scoring/coding specimen traits

Several tools have been developed to enable users to annotate specimen records for their traits. The traits available to score vary between portals, and new traits can be developed as needed (contact your portal administrator for more information).

14:1 Scoring/coding individual specimen traits in the occurrence editor

A trait can be scored for an individual specimen record in the Occurrence Editor (see *7: Editing existing specimen records*) by clicking the Traits tab. The trait(s) available for scoring will be displayed as boxes containing the available scoring schema(s). Select the trait values corresponding to the specimen and click the Save Edits button. You can also remove trait information by clicking the Delete Coding button.

14:2 Scoring/coding specimen traits from images

To score multiple specimens of the same taxon or from the same region, use the Trait Coding from Images tool. From the Data Editor Control Panel (see *3:1 Data Editor Control Panel*), click Occurrence Trait Coding Tools, then Trait Coding from Images.
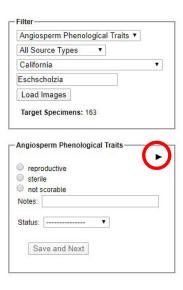
In the Filter box, select the trait that you wish to score, followed by the name of the taxon for which you wish to score (if applicable). Phenological Traits from the Trait dropdown menu. You can also refine your search by using the All Source Types and All Counties & All States dropdown lists.

- **All Source Types:** this field allows you to view and re-score specimens that have already been scored using another method (e.g., text mining). Leave this as is unless you are specifically working on re-annotating specimens.

- **All Countries & All States:** this field provides a dropdown menu of all countries and U.S. states that are indexed in CCH2. If you select one of these geographic criteria, the tool will only show you specimens from that country/state.

Click the Load Images button. On the next page, you will see an image of a specimen of the selected taxon on the left, and an Action Panel on the right (see screenshot on next page). Note that you can edit the contents of the Filter box here as well. Depending on the scoring schema available for the trait you are scoring, you may be able to view more scoring options by clicking the black triangle inside the Action Panel. Select the trait values that you wish to apply to the specimen and click Save and Next.

14:3 Scoring/coding specimen traits from label text

It is also possible to score traits of batches of specimens using the text of the specimens' labels. To access and use this tool, navigate to Data Editor Control Panel (see *3:1 Data Editor Control Panel*), click Occurrence Trait Coding Tools, and select "Trait Mining from Verbatim Text". In the Harvesting Filter box, select the Occurrence trait that you would like to score.

For the "Verbatim text source" field, select the database field that you want the tool to display. The options include: Habitat, Substrate, Occurrence Remarks (Notes), Dynamic Properties, Verbatim

Attributes (Description), Behavior, Reproductive Condition (Phenology), Life Stage, and Sex. In the "Filter by text (optional)" field, you can enter any text string by which you wish to filter the results. For example, if you enter "fw", the tool will provide all values for that field that contain "fw". This field is optional, but including a search string will significantly narrow your search results. When choosing strings to enter in this field, consider searching for misspelled and abbreviated versions of the values you expect. For example, if you are searching for specimens that you can score as flowering, you could search for "fowering" or "fwrr" as well as "flowering" and "fwr". In the "Filter by taxon (optional)" field, you can enter the name of a taxon by which you wish to filter the results. This field is also optional.

Once you have filled out the desired fields, click the Get Field Values button. The result will look similar to the screenshot on the next page. The Harvesting Filter box is still visible, and the box below will list all the unique strings (values) found in the specified database field that align with your search criteria. The numbers in brackets to the right of each string value indicates how many specimen records have that exact value in the specified database field.

```
┌─Harvesting Filter──────────────────────────────────────────────┐
│                                                                  │
│  Occurrence trait: [Angiosperm Phenological Traits ▼]            │
│  Verbatim text source: [Reproductive Condition         ▼]       │
│  Filter by text (optional): [flowering            ]             │
│  Filter by taxon (optional): [                    ]   [Get Field Values] │
│                                                                  │
└──────────────────────────────────────────────────────────────────┘

┌─Reproductive Condition─────────────────────────────────────────┐
│                                                                  │
│  Select Source Field Value(s) - hold down control or shift buttons to select more than one value │
│  ┌──────────────────────────────────────────────────────────┐▲│
│  │ flowering - [121]                                         │ │
│  │ flowering/fruiting - [6]                                  │ │
│  │ flowering|fruiting - [55]                                 │ │
│  │ none flowering - [2]                                      │ │
│  │ none yet flowering - [1]                                  │ │
│  │ past flowering - [1]                                      │ │
│  │                                                           │ │
│  │                                                           │▼│
│  └──────────────────────────────────────────────────────────┘ │
│   ○ reproductive    ►                                           │
│   ○ sterile                                                     │
│   ○ not scorable                                                │
│  Notes: [                    ]                                  │
│                                                                  │
│  Status: [---------------- ▼]                                   │
│                                                                  │
│  [Batch Assign State(s)]  [Reset Form]                          │
│                                                                  │
└──────────────────────────────────────────────────────────────────┘
```

Select the value or values from the list that you wish to score. To select several values from the list that you wish to give the same phenological score, hold Ctrl and click on each value in the list. Select the appropriate score from the trait scoring schema at the bottom of the lower box. Depending on the scoring schema available for the trait you are scoring, you may be able to view more scoring options by clicking the black triangle next to the schema. From this list, select the traits that you wish to apply to this specimen. Traits that you do not wish to score can be left blank. When you are satisfied with your

scoring(s), click the Batch Assign State(s) button. If you make a mistake, click Reset Form (Caution: this will un-select all of your selected text fields as well, so be careful when selecting traits!).
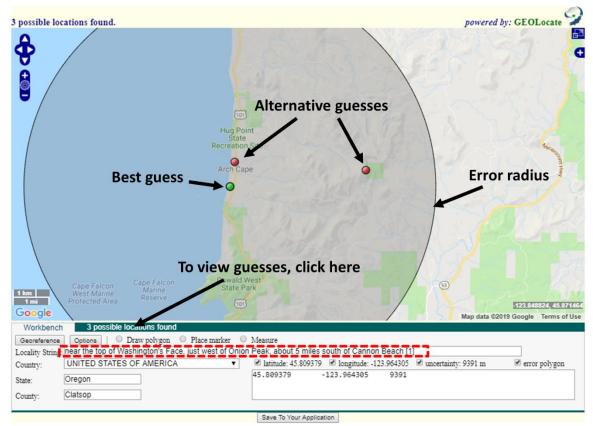
15: Batch georeferencing specimens

The following protocol was developed to describe batch georeferencing specimen records using GeoLocate in CCH2.

1. Log in to your account in the CCH2 portal, click "My Profile," navigate to the "Occurrence Management" tab, and click the name of the institution for which you will be georeferencing.
2. In the Data Editor Control Panel, click "Batch Georeference Specimens."
3. In the Query Form box, select the country, state, and county that you wish to focus on and click the "Generate List" button. You will then see a list of results in the box below the Query Form (see next screenshot).
   - If no results are returned, select a new county or state in the Query Form.

4. Select the entry that you want to work on and click the Geolocate ( ) icon at the top right of the search results. This will open a new GeoLocate window (see next screenshot) displaying a map and, in some cases, possible location(s) for the specimen that GeoLocate inferred from the text.
   - The green dot is GeoLocate's best guess for the locality of the specimen. You may also see red dots, which are alternative guesses.
   - To view the reasons why GeoLocate selected these dots, click the "# possible locations found" tab to the right of the Workbench tab. The words in all caps are those that GeoLocate used to infer a location.
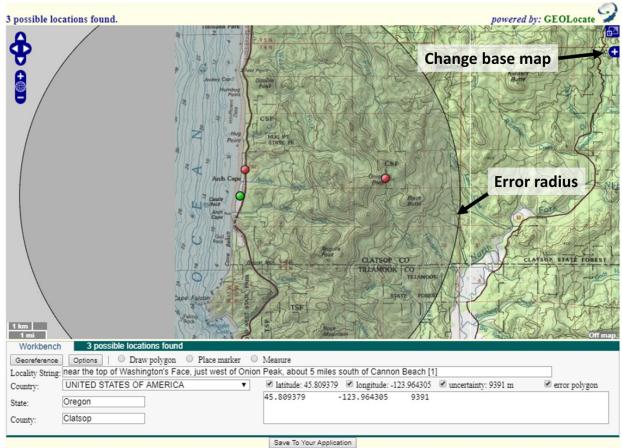
5. Click the "Options" button on the bottom left of the GeoLocate window and ensure the "Do Uncertainty" box is checked. Close the Georeferencing options window.
6. Make sure that all of the boxes (latitude, longitude, uncertainty, and error polygon) near the bottom right of the window are checked.
7. If there are dots on the map, investigate whether any of them could be a good starting point for your georeferencing by comparing the dots' locations on the map to the text in the Locality String (see dashed box in screenshot above). It is possible that none of the dots indicate the correct locality. If this is the case, you can ignore the dots or remove them by clicking the "# possible locations found" tab and clicking the circled 'x' to the left of each rejected entry (see below).
   - When deciding whether to use one of the GeoLocate dots, make sure to check that the state and county where the dot has been placed matches the state and county indicated by the record.
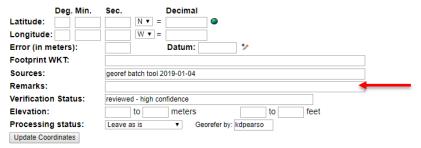
8. Either starting with a GeoLocate dot, if appropriate, or from scratch, use the Locality String to determine an approximate location for the specimen. This will likely require searching other references (e.g., Google maps) for location and feature names.
   - You can change the base layer (i.e., the type of map shown in the GeoLocate window) by clicking the plus symbol in the upper right corner of the window (see next screenshot).

- To measure a distance on the map, click the button next to "Measure" and click on a starting point on the map. You can then move your cursor anywhere on the map and a line will be measured between those two points. The length of the line will be shown in green next to the line. To measure between more than one point, click again to anchor another point. To stop measuring, double click on the ending point of your measurement.

- If there is not enough information in the Locality String to assign an approximate point, view the specimen record by returning to the search results page (see screenshot on page 35) and clicking the pencil icon (✎) on the top right of the search results box. This will bring up the specimen record, where you can see whether there is more locality information in another data field (e.g., habitat) or on the specimen image (if available).

  o If you are still not able to assign an approximate point from this information, scroll down to the bottom of the specimen record until you see the Processing Status field. Select "Expert Required" from the dropdown menu of this field. In the "Notes (Occurrence Remarks)" field above and to the left, enter a brief note in brackets, such as "[Not enough data to georeference]". Click the "Save Edits" button, close the record, and select a new record to georeference.

9. Once you have found an approximate location for the specimen record, click the button next to "Place Marker" and click on the map where you want to place the GeoLocate dot. **Follow the guidelines provided in Table 1 when deciding where to place the dot.**

10. Set the error radius and/or create an error polygon to indicate the uncertainty of the specimen's locality. **Follow the guidelines provided in Table 1 when deciding how large of an error radius to use for a given dot and whether you should use an error polygon.**
    - To edit the size of the error radius, click the green dot on the map and select "Edit Uncertainty" in the pop-up box. Click and drag the grey arrowhead that will appear on the outer rim of the error circle to resize the error radius.
    - To create an error polygon, click the button next to "Create polygon" and click on the map where you want to begin drawing the polygon. A corner of the polygon will be created time you click on the map. To finish the polygon, double click. Once you have completed the polygon, click the green dot again and select "Resize uncertainty to polygon."
        - o To redo a polygon, click the "Clear Polygon" button to the right of the "Options" button.
    - Make sure to note any uncertainty you experienced when setting the error radius. For example, if you were georeferencing a named place that did not have clear boundaries, explain how you determined a suitable error radius by putting a note in the Remarks field on the search results page where you first selected your specimen record (indicated by the arrow below).

11. When you are confident in your GeoLocate point and error radius, click the "Save To Your Application" button at the bottom of the GeoLocate window. You will be taken back to the search results page where you first selected your specimen record (see screenshot on page 35).
    - The coordinates and error will now show up below the search results in the appropriate Latitude, Longitude, and Error fields. If you created an error polygon, its coordinates will be listed in the Footprint WKT field.
12. Click the "Update Coordinates" button at the bottom of the page.
13. Select a new record or set of records to georeference from the search results list and repeat steps 7-13.

Table 1: Guidelines for georeferencing from different types of locality information. Adapted from Wieczorek et al. 2012 "Georeferencing Quick Reference Guide" (http://manisnet.org/GeoreferencingQuickReferenceGuide.pdf)

Locality type	Example	How to place coordinates	How to measure error radius/polygon
Bounded area: locality refers to a geographic feature with discernible spatial boundaries	"Las Vegas" "Puerto Madryn" "San Fernando"	Estimate the geographic center of the boundaries of the named place	Measure the distance from the center of the named place to the border of the named place farthest from the center
Undefined area: locality refers to a geographic feature that does not have a clear spatial boundary	"Hoosier Pass" "Hills south of Los Osos"	Determine the coordinates for the named place as well as possible using visual evidence near the label for the named place on the map	Use half the measured distance from the selected coordinates to the center of the nearest named place. Make note of the named place that you measured to in the "Remarks" field on the search results page.
Street address	"1 Orchard Lane, Berkeley, CA" "319 Stadium Dr., Tallahassee, FL"	Locate the address on, e.g., Google maps, and find this location on the map in GeoLocate.	Use half the measured distance from the selected coordinates to the location of an address on either side of the given address. If the next address is too difficult to determine, use half the distance from the coordinates of the address to the further end of the block on which it sits.
Junction, intersection, crossing	"junction of Coora Rd. and E Siparia Rd.", "bridge over Willamette River", "interscn of CA 166 and 399"	Use the coordinates of the center of the intersection.	Use satellite or aerial images to find the extent of the intersection by measuring the distance from the center to the furthest part of it. If this is not possible, use the number of lanes of the larger of the two roads and multiply by 4 meters.

Locality type	Example	How to place coordinates	How to measure error radius/polygon
River, stream, road, path	"Sacramento River", "Los Osos Valley Road", "Rio Parana"	Make a straight line between the two points on the geographic feature that are most removed from each other, yet still within the administrative boundaries (e.g., county) specified in the locality description. Choose the midpoint of the line.	Use one of the ends of the straight line that you made between the two points on the geographic feature that are most removed from each other, yet still within the specified administrative boundaries.
Mouth or headwaters of a river, confluence of waterways, trailhead	"headwaters of the Missouri River", "Triangle Lake trailhead"	For a river mouth or confluence of waterways, select the midpoint of the line connecting the opposite shores where the waterways meet. For a river source, select the point of highest elevation on the river or create a boundary around the multiple streams contributing to the river and find the geographic center of that bounded area. For a trailhead, select the point where the trail begins.	For a river mouth or confluence of waterways, use the distance from the chosen point to the shore. For a single river source or trailhead, use 10 m.
Near a named place	"vicinity of Mt. Hood", "near the Hoover Dam"	Determine the coordinates as either a **Bounded area** or **Undefined area**, as appropriate.	Determine the distance as either a **Bounded area** or **Undefined area**, as appropriate.
Between two places	"between Atascadero and San Luis Obispo"	Use the midpoint between the centers of the two named places	Use half the distance between the centers of both named places
Direction only, no distance	"N of Berkeley", "SW of Gainesville"	Use the midpoint between the centers of the specified named place and the nearest named place in the specified direction. The nearest named place should be, for the first example, the nearest named place somewhere between NW and NE of Berkeley	Use half the distance between the centers of both named places

Locality type	Example	How to place coordinates	How to measure error radius/polygon
Specified distance in unnamed direction	"5 km outside Calgary", "2 miles from Morro Bay"	Determine the coordinates as either a **Bounded Area** or **Undefined Area**, as appropriate.	The length of the radius should be the same as the distance given in the locality description
Specified distance in a direction, no path given	"50 miles W of Las Vegas", "30 km E of Sacramento"	Find the center of the named place and measure the provided distance in the direction provided in the locality description.	Use half the measured distance from the selected coordinates to the center of the nearest named place. Make note of the named place that you measured to in the "Remarks" field on the search results page.
Specified distance in a direction, path given	"7.9 mi N Beatty, on US 95", "7 mi. W Santa Barbara on 101", "left bank of Mississippi River, 16 mi downstream from Paris"	Find the geographic center of the named place as either a **Bounded area** or **Undefined area**, as appropriate. Use the measuring tool to follow the specified route for the given distance. Use the end point as the coordinates.	Use half the measured distance from the selected coordinates to the center of the nearest named place. Make note of the named place that you measured to in the "Remarks" field on the search results page.

16: Managing loans, gifts, and exchanges

Navigate to the loan management tool by accessing the Data Editor Control Panel (see *Section 3: Managing your profile and collections(s)*) and clicking "Loan Management." You will see the following tabs:

To add a new outgoing loan, click the green plus sign near the right side of the "Outgoing Loans" page. You will be prompted to enter a Loan Identifier (a unique number to mark the identity of the loan) and select an institution to which the loan is being sent from the dropdown list. If the institution is not found in the dropdown list, click the green plus sign to the right of the "Send to Institution:" field and enter the required information. Click "Create Loan" when you have finished entering the required information in the "New Outgoing Loan" box.

Once you click "Create Loan," you will be taken to the Loan Out Details page. Here you can add information about the loan and generate loan paperwork using the appropriate boxes and buttons. Note that you can print an invoice, specimen list, mailing label, and envelope in the Generate Loan Paperwork box at the bottom of the page.

To link specimens to the loan, click the "Specimens" tab, click the green plus sign, enter the catalog number of the desired specimen in the field (preferably by scanning the barcode of the physical specimen), and click "Add Specimen." Repeat as necessary.

To edit an outgoing loan or link specimens to the loan in the future, navigate to the "Outgoing Loans" tab and click on the loan identifier (number or name given to the loan) directly to the right of the appropriate bullet point (see arrow in next screenshot).

To add a new incoming loan, repeat the procedure outlined above using the "Incoming Loans" tab. Note that specimens cannot be linked to incoming loans.

To add a gift or exchange, repeat the procedure outlined above using the Gifts/Exchanges tab. You will be able to enter the number of specimens in either the "gift" boxes or "exchange" box.

17: Viewing and vetting comments

Registered users of the CCH2 portal, regardless of their level of permissions, can post comments on specimen records. This is a useful feature for flagging data quality issues.

To view and vet comments posted on records from your collection, navigate to the Administration Control Panel (see *Section 3: Managing your profile and collections(s)*) and click "View Posted Comments." If there is no orange text to the right of this option, you have no comments that have not yet been reviewed.

On the comments page, you can hide the comment from the public (in cases of sensitive or personal data), mark a comment as reviewed (i.e., you have resolved the issue described by the comment), or delete the comment (in cases of spam or inappropriate content). Spam comments are so far rare in the CCH2 portal, but one should regularly review posted comments to ensure no inappropriate content has been posted to your collection. **If you find any inappropriate comments, please contact the portal manager immediately so they can remove this user from CCH2.** To view the specimen record associated with a record, you can click the blue text (catalog number, collector, collector number, and date) above the comment details.

In the event that you have many comments to work through, you use the Filter Options box to view only comments that were posted by a certain user, have a certain status (public/non-public/reviewed), or were posted within a certain date range.

18: Editing metadata (summary and contact information) for your collection

metadata (noun): a set of data that describes and gives information about other data
[source: Oxford online dictionary]

This section describes how to change or update information about your collection presented on CCH2. Collection metadata (see above) can be edited by navigating to the Administration Control Panel (see *Section 3: Managing your profile and collections(s)*) and clicking "Edit Metadata." By default, you will be taken to the Collection Metadata Editor tab. A number of fields will be available for editing in this tab (see next screenshot). Unless you have special reason to do so, the following fields should not be changed: I*nstitution Code, GUID source, Dataset Type, Management*.

OBI - Robert F. Hoover Herbarium, Cal Poly State University (OBI)

| Collection Metadata Editor | Contacts & Resources |

Edit Collection Information

Institution Code: OBI ❶

Collection Code: ❶

Collection Name: OBI - Robert F. Hoover Herbarium, Cal Poly State University

Description (2000 character max):

The Hoover Herbarium houses 85,000+ specimens of vascular plants, algae, lichens, and bryophytes. The geographic focus is San Luis Obispo County, California. The collection also includes many specimens from other areas of California, other states of the US, particularly Arizona, and some from other regions of the world, especially Mexico. Emphasis areas in the collection include Asteraceae, Lupinus, and cultivated Eucalyptus. Major collections include Robert F. Hoover (1946–1969), David J. Keil (1966–present), Rhonda Riggins (1970s–2000), Tracy Call (mostly Apiaceae—late 1940s–1960s), and Robert J. Rodin (1940s–1977). The collection is used extensively in undergraduate teaching and training.

 Important Collections: Robert F. Hoover

Latitude: 35.302189 🌐

Longitude: -120.659350

Category: Vascular Plants

Allow Public Edits: ☐ ❶

License: CC BY-NC (Attribution-Non-Commercial) ❶

Rights Holder: ❶

Access Rights: ❶

Dataset Type: Preserved Specimens ❶

Management: Live Data ❶

GUID source: Symbiota Generated GUID (UUID) ❶

Publish to Aggregators: GBIF ☑ ❶

Icon URL: https://cch2.org/portal/content/collicon/obi.jpg ❶ Upload Local Image

Sort Sequence: ❶

Collection ID (GUID): ❶

Security Key: 3a095a57-b6a4-11e8-b408-001a64db2964

recordID: 3818d95b-b6a4-11e8-b408-001a64db2964

[Save Edits]

Several fields in this tab require additional explanation:

Allow Public Edits – if this box is checked, any logged-in user of the portal will be able to edit occurrence records for your collection. However, these edits will not be publicly visible unless the user has explicit editing permission for your collection. Instead, the edits will be visible in the Review/Verify Occurrence Edits tool but will be marked as NOT APPLIED (*Section 23: Reviewing edits to specimen records*). An administrator would need to view and change these edits to APPLIED for them to be applied and displayed publicly.

License – an administrator can select the Creative Commons license to be applied to this dataset. For more information about Creative Commons licenses, see https://creativecommons.org/.

Management – "live" managed datasets are edited and managed directly in the portal, while "snapshot" managed data are edited and managed in an institutional database external to the Symbiota portal. "Snapshot" managed collections must be periodically refreshed by uploading a copy of the data into the Symbiota portal or transferring the data via an IPT.

GUID source – this field designates the source field for the globally unique identifiers (GUID) for your specimens. It is best practice that each specimen has a stable GUID assigned to it that does not change. "Live" managed datasets should have a "Symbiota Generated GUID", while "snapshots" must designate which field contains the GUID. We recommend that all databases assign a GUID to each specimen when it is created. Data can only be published to external aggregators (e.g., iDigBio, GBIF) if they have a GUID.

In the Contacts & Resources tab, an administrator can edit the contact information, homepage, and mailing address for the collection. In the Add/Edit External Link Resources box, you can add a URL to a

homepage or other website with more information about your collection. The Contacts box allows you to add the names and information of herbarium personnel. Note that you can define the contact's role. This will be displayed on the public page of your collection, so it is recommended that you use title case when defining this role. You can also include an ORCID ID number for the contact.

At the bottom of this page, you can update the mailing address of your collection. When another collection prepares a loan to send to your institution, they can select this mailing address from a dropdown menu and print a shipping label from CCH2. Therefore, it is important to keep this—as well as all other metadata on this page—up to date.

To add an address if one does not already exist, select the name of your collection from the dropdown list and click the Link Address button or click "Add an institution not on list" below the dropdown list. To edit an existing address, click the pencil icon to the right of the name of your collection. In either case, you will be taken to a page where you can add pertinent address details (see next screenshot). You can also add a shipping contact in this form. If you are adding a new address, make sure to select your collection from the dropdown list under "Link to:".

Add New Institution

Institution Code:

Institution Name:

Institution Name2:

Address:

Address 2:

City:

State/Province:

Postal Code:

Country:

Phone:

Contact:

Email:

URL:

Notes:

Link to: Leave Orphaned

Add Institution

19: Managing user permissions

Non-users may freely access specimen records and images. All users may comment on specimen records. However, only users who have been granted data editing or administrative permissions may edit specimen records and images. There are (generally) three levels of permissions:

- **Data editor:** Users with these permissions will be able to add and edit occurrence records, add batch nomenclatural adjustments, print labels or annotations, batch georeference specimens, score specimen traits, or use the loan management tool. These users will NOT be able to delete records once they are created. Student workers, interns, and other data entry personnel should be granted this level of permission.
- **Administrator:** Users with these permissions have all data editing permissions and can access all the tools in the Administration Control Panel (see *3:2 Administration Control Panel*).
- **Rare Species Reader:** Users with these permissions have no data editing or administrative capabilities. However, they are able to view locality information for rare and protected species, which is normally redacted for non-users and users lacking these or data editor/administrator permissions.

To view and edit user permissions for your collection(s), navigate to your Administration Control Panel (see Section 3) and click "Manage User Permissions."

To add permissions for an existing user, navigate to the "Add a User" box at the bottom of the page (shown below). Select the desired user from the drop-down menu, click the radio button next to the appropriate level of permissions you wish to grant to this user, and click the "Add Permissions for User" button.

To remove permissions from an existing user, find the user's name within the box that corresponds to their current level of permissions and click the red x ( ) to the right of the name. A dialogue box will pop up to ask you whether you are sure of your choice. If you are, click OK.

To change the permissions of an existing user from one level to another, follow the above instructions to first remove their current permissions, then follow the instructions to add the new permissions for the user. It is also possible to add multiple different levels of permissions to the same user, but because this would be redundant, it is recommended to remove the user from one list and add them to the other as described here.

For a video on this topic created by the LepNet TCN, visit their website below. Note that the SCAN portal is not identical to the CCH2 portal, but will be similar in format.

http://www.lep-net.org/?page_id=403

20: Importing record data

There are a number of ways to import data into the portal discussed here:
http://symbiota.org/docs/specimen-search-engine/interoperability-of-specimen-data/
and here:
http://symbiota.org/docs/specimen-upload-procedure-2/

In this section, we will discuss one of the simplest methods of uploading specimen data: importing a comma-separated value (CSV) file. CSV files can be created by using the Save As function in Microsoft Excel or another spreadsheet program and changing the saved file type. A CSV file uploaded to the portal needs only to include a column for catalog number (i.e., barcode number) and can include any number of additional fields, each as its own column in the CSV file.

NOTE

The following steps should NOT be followed if you are simply trying to update a single field or handful of fields in the portal. The Text File Import Tool will entirely replace records that match the catalog numbers in your upload file.

To batch upload specimen data as a CSV file, navigate to the Import/Update Specimen Records tool in the Administration Control Panel (see *3:2 Administration Control Panel*). Click "Full Text File Import."
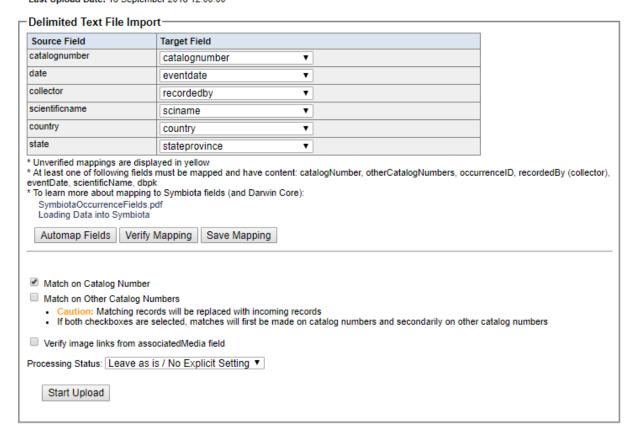
NOTE

If you have batch uploaded data to CCH2 in the past, you may already have a mapping profile saved. To check on this, click "Saved Import Profiles" from the Import/Update Specimen Records options and determine whether any of the saved import profiles meet your current needs. See note on page 34 for instructions on how to save an upload profile.

On the resulting page, click the "Choose File" button and navigate to the desired CSV file. Click "Open." Make sure the "Automap Fields" box is checked, and click the "Analyze File" button. You will then be taken to page that will look similar to the one shown below. The length and contents of the Source Field/Target Field table will depend on what columns were included in the original CSV file.

At this point, you will select which fields in your CSV file (Source Fields) will correspond to which fields in the Symbiota portal (Target Fields). Check that each of the auto-mapped fields was appropriately assigned. Check the Symbiota Data Field Guide (http://symbiota.org/docs/symbiota-occurrence-data-fields-2/) for definitions of each data field, should you have any questions about the appropriate field to which to map your data. Your portal manager can also help you determine the appropriate data field. Once you are satisfied with your field-to-field mapping (see next Notes), click the "Save Mapping" button.

NOTES

- If the scientific names in your CSV file include taxonomic authorship (e.g., *Acer circinatum* Pursh), map this field to the Target Field "scientificname." If the scientific names included in your CSV file do NOT include taxonomic authorship (e.g., *Acer circinatum*), map this field to "sciname."

- Once you have mapped the fields in your CSV file to fields in the database, you can save this mapping for future use. To do so, click the Save Mapping button at the bottom of the mapping table. A message will pop up that says "Enter a profile name and click the Save Map button to create a new Upload Profile". Click OK, then enter a name for the upload profile in the "New profile title:" field that will now appear to the right of the Save Mapping button. Click the Save Mapping button. To access this mapping in the future, you will click "Import/Update Specimen Records" in the Administration Control panel as before, but then select "Saved Import Profiles" from the options. Note that this is helpful only if the file you are uploading has the same columns as the file you uploaded initially.

Change the processing status as appropriate (see *Appendix 1: Processing Status*) for instructions on the use of Processing Status for the CAP TCN) and click "Start Upload." You will be taken to a page that will update periodically while Symbiota ingests your data. Do not navigate away from this page until you see the message "Upload Procedure Complete" (see below).

Data Upload Module

Robert F. Hoover Herbarium, Cal Poly State University
Last Upload Date: 16 February 2018 12:00:00

- Starting Stage 2 cleaning
- Updating existing records...
- Transferring new records...
- Linking records in prep for loading determination history and associatedmedia...
- Specimens linked to exsiccati index
- Records Transferred
- Cleaning house
  - Protecting sensitive species...
    - 0 records protected
  - Updating statistics...
  - Populating global unique identifiers (GUIDs) for all records...
- Upload Procedure Complete (2018-09-18 03:00:12 PM)!

Once the data are uploaded to CCH2 through this process, they are temporarily stored in a "holding table" until you approve their transfer to the central table of the database. Before you approve this transfer, you should view the Pending Data Transfer Report at the bottom of the page. Verify that the correct number of records are being updated and/or added. You can preview these records by clicking the table icon to the immediate right of the desired dataset (circled below), or you can download these records as a CSV by clicking the two boxes icon to the far right of the desired dataset (in a square below). If anything is incorrect, you can fix your CSV file and re-upload it according to the steps you followed above.

Pending Data Transfer Report

Occurrences pending transfer: 132
Records to be updated: 13   Caution: incoming records will replace existing records
New records: 19

Transfer Records to Central Specimen Table

Once you are satisfied that the correct records are being modified, click the Transfer to Central Specimen Table button at the bottom of the screen. **Note that this step is final and is not easy to undo!**

21: Using the processing toolbox

The processing toolbox contains many tools used to facilitate specialized workflows. The tabs available in CCH2 are described below with links to helpful resources.

21:1 Image loading

The image loading tab is used to batch link images that are web-hosted by some server other than the CCH2 server. All or most images should be web-hosted by an external server rather than uploaded directly to the CCH2 server. Currently, most CCH2 images are either web-hosted by the home institution's server or by CyVerse.
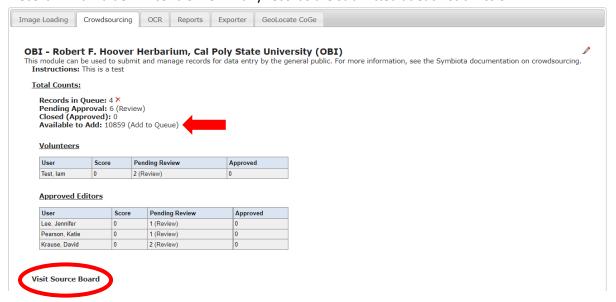
Instructions on how to use this tab to link CyVerse-hosted images to specimen records can be found in the "Protocol for set up and upload of images to CyVerse, then CCH2," which can be found on the project website: https://www.capturingcaliforniasflowers.org/document-library.html.

21:2 Crowdsourcing

(adapted from the Symbiota website)

The crowdsourcing module is used to make unprocessed records accessible for data entry by the general user. To be a crowdsourcer, a user must have a user account, but the user does not need to have editing rights for a particular collection.

Submitting Specimens to the Queue: Only specimens with the processing status of "unprocessed" can be included in a crowdsourcing project. The first step is to add specimens to the crowdsourcing queue by clicking the "Add to Queue" link located to the right of the "available to add" count (see arrow on next screenshot), which is only available when the count is greater than zero. If you have loaded skeletal data collected during the imaging process (e.g. taxon name, country, state, etc), you can further limit which records you submit to the queue by certain values (e.g. only records from a certain state). The "Record Limit" value will control how many records are submitted at each submission.
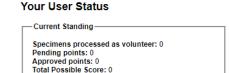
Exposing to Public: The simplest way to open crowdsourcing to the user community is to add a link to the Crowdsourcing Source Board (click Visit Source Board at the bottom of the crowdsourcing tab, circled above) to the main menu or homepage of your institution's website. However, the crowdsourcing project will likely have greater exposure and success if a custom crowdsourcing page is create dedicated to the project with special instructions, educational links, and motivational incentives to participate. For an example, see the LBCC crowdsourcing project: http://lbcc1.acis.ufl.edu/?q=node/21.

Crowdsourced Transcription: Volunteers can add data to records in the queue by logging in to CCH2 and following the link, provided by the collection administrator, to the Source Board (see Exposing to Public). From here, the volunteer can click on the number in the Open Records column to view the records that need to be transcribed. The volunteer can select a specimen from this list, then transcribe the label data from the specimen image according to instructions provided by the institution (see *7: Editing existing specimen records*).

Crowdsourcing Score Board
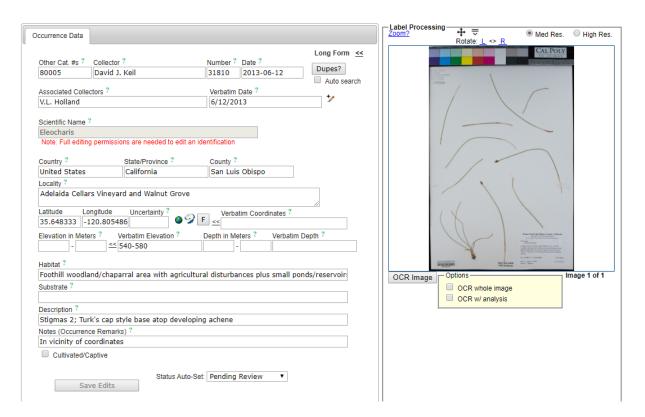
Top Scores

User	Score
Top scores not yet available	------

Your User Status

Current Standing

Specimens processed as volunteer: 0
Pending points: 0
Approved points: 0
Total Possible Score: 0
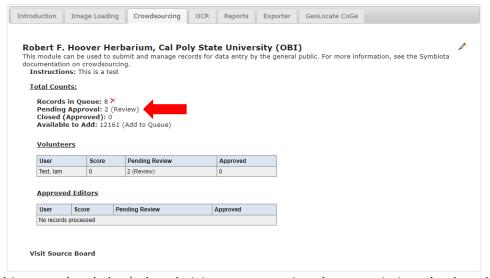
Your Stats by Collections

Collection	Specimen Count	Pending Points	Approved Points	Open Records
Robert F. Hoover Herbarium, Cal Poly State University (OBI)	0	0	0	9

Certain data fields are not available for editing by crowdsourcers. These fields include catalog number, scientific name, and all fields in the determination and image tabs. However, users with explicit editing rights for a particular collection will have access to all fields and editing tabs.
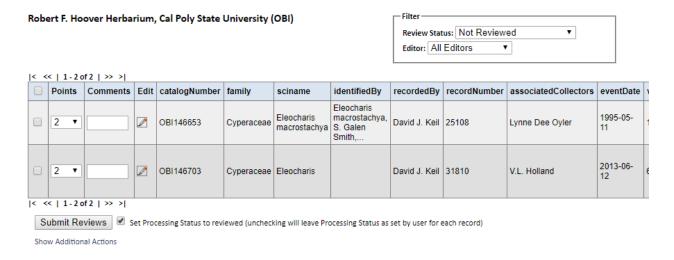
Expert Review of Crowdsourced Transcriptions: Edits made to specimen records through the crowdsourcing module are automatically applied to the records in the database; however, these records are tagged by a given processing status (to be defined by your project, by default, this is currently Pending Review). To review and approve these records, the collection administrator can view all records that are Pending Approval in the crowdsourcing tab (see arrow below).

On the resulting page (see below), the administrator can review the transcriptions that have been made, make comments on the transcriptions (which can be viewed by the volunteer user), and/or assign points for the transcription (if a competitive or quality-assurance scoring system is being used). The administrator can check the box next to any records that the administrator approves, and click Submit Reviews to approve the crowdsourced work. The administrator can alternatively remove points and

change the processing status of records to Not Reviewed, or return records to the crowdsourcing queue to be re-transcribed by clicking the "Show Additional Actions" link at the bottom of the page and selecting from the resulting buttons.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)

Filter
Review Status: Not Reviewed ▼
Editor: All Editors ▼

|< << | 1 - 2 of 2 | >> >|

	Points	Comments	Edit	catalogNumber	family	sciname	identifiedBy	recordedBy	recordNumber	associatedCollectors	eventDate
☐	2 ▼		✏	OBI146653	Cyperaceae	Eleocharis macrostachya	Eleocharis macrostachya, S. Galen Smith,...	David J. Keil	25108	Lynne Dee Oyler	1995-05-11
☐	2 ▼		✏	OBI146703	Cyperaceae	Eleocharis		David J. Keil	31810	V.L. Holland	2013-06-12

|< << | 1 - 2 of 2 | >> >|

Submit Reviews ☑ Set Processing Status to reviewed (unchecking will leave Processing Status as set by user for each record)

Show Additional Actions

21:3 OCR (Optical Character Recognition)

While not currently employed by the CAP project, the Optical Character Recognition tools can be leveraged to create workflows that minimize human keyboarding. OCR recognizes text in specimen images and outputs the interpreted text from the image. It is also possible to upload the results of external OCR analyses using this tab (using the OCR Batch Import Tool).

A user can batch run OCR on a set of specimen images with a certain processing status. You can select the processing status of the image(s) you wish to analyze, then denote how many records the OCR tool will analyze.
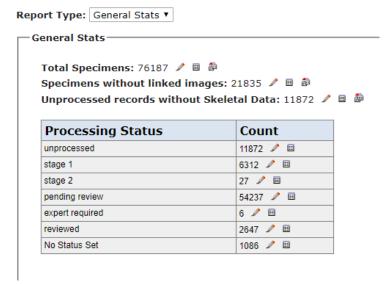
Specimen Image Statistics

Total specimens with images: 54352
"unprocessed" specimens with images: 11871
   with OCR: 3
   without OCR: 11868

Custom Query:
Select Processing Status ▼ | Reset Statistics

Batch OCR Images using the Tesseract OCR Engine

Processing Status: unprocessed ▼
Number of records to process: 100

Run Batch OCR

Note: This feature is dependent on the proper installation of the Tesseract OCR Engine on the hosting server

Note that this tool is rather slow; each image takes about 6 seconds to analyze (~10 images analyzed per minute). The OCR tool does not distinguish label text from other text (e.g., stamps or annotations), and it are not good at parsing hand-written text. The OCR parsing of a specimen can be viewed on the right side of that record's occurrence editor page (see example below). You can save or delete the results of OCR parsing from this page.

21:4 Reports

In this tab, when the Report Type is set to General Stats, you can quickly determine how many specimens are in the database and which processing status each of these specimens is assigned (see next screenshot).
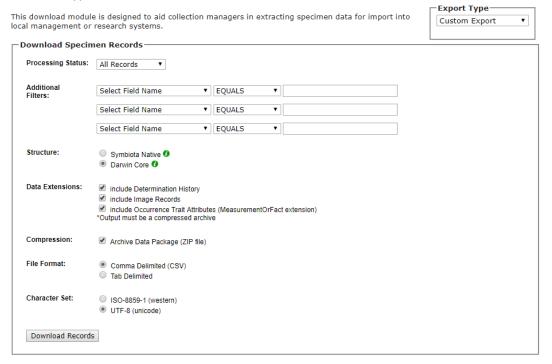

Report Type: General Stats ▼

General Stats

Total Specimens: 76187 ✎ ▤ ▥
Specimens without linked images: 21835 ✎ ▤ ▥
Unprocessed records without Skeletal Data: 11872 ✎ ▤ ▥

Processing Status	Count
unprocessed	11872 ✎ ▤
stage 1	6312 ✎ ▤
stage 2	27 ✎ ▤
pending review	54237 ✎ ▤
expert required	6 ✎ ▤
reviewed	2647 ✎ ▤
No Status Set	1086 ✎ ▤

When the Report Type is set to User Stats, you can view the activity of any given user within a specified duration of time (see next screenshot).

21:5 Exporter

This tool is used to export the specimen records with certain qualities as a DarwinCore Archive or Symbiota native file (for information about each of these file types, click the green "i" on the Exporter page next to the file type name). You can define which records are to be included in the downloaded file by setting the filters. You can decide whether to include the identifications file (include Determination History), the file with links to images (include Image Records), and/or the file that contains trait data coded for the specimens (include Occurrence Trait Attributes). The recommended settings for a download of this type are shown below.

It is also possible to search and download records depending on their georeferenced status by switching the Export Type to Georeference Export. This is primarily used in conjunction with external georeferencing tools such as GeoLocate CoGe (see *21:6 GeoLocate CoGe (Collaborative Georeferencing)*).

21:6 GeoLocate CoGe (Collaborative Georeferencing)

This tool can be used to crowdsource georeferencing of specimens from label data. A manual for using the Collaborative Georeferencing (CoGe) tool can be found here: https://epicc.berkeley.edu/wp-content/uploads/2015/11/UsingGeoLocateforCollaborativeGeoreferencing_2016.pdf and video tutorials can be found here: https://www.geo-locate.org/community/default.html

A user/georeferencer's guide to using GEOLocate CoGe can be found here: https://www.capturingcaliforniasflowers.org/uploads/1/6/3/7/16372936/georeferencingincoge.docx

22: Darwin Core archive publishing

The Darwin Core Archive Publishing tool is used to link specimen records in CCH2 to a global aggregator, such as iDigBio or GBIF. The CCH2 encourages all collections to publish their data to GBIF for maximum research utility.
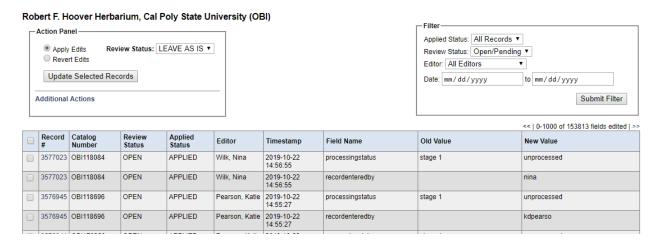
Instructions on how to use this tab to publish to GBIF can be found in the protocol titled "Publishing to GBIF", which can be found on the project website: https://www.capturingcaliforniasflowers.org/document-library.html.

23: Reviewing edits to specimen records

A user with administrator access can review edits that have been made to specimen records by selecting "Review/Verify Occurrence Edits" from the Administration Control Panel (see *3: Managing your profile and collections(s)*). The resulting dashboard will show a table of every edit made to any field of any record, which often means that the list is very long, depending on how much activity the database sees on a daily basis.

You can limit the search using the Filter box in the top right corner. You can search by Applied Status, Review Status, Editor, or Date/Date Range of editing.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)

Action Panel
○ Apply Edits
○ Revert Edits   Review Status: LEAVE AS IS ▼
[Update Selected Records]
Additional Actions

Filter
Applied Status: All Records ▼
Review Status: Open/Pending ▼
Editor: All Editors ▼
Date: mm/dd/yyyy to mm/dd/yyyy
[Submit Filter]

<< | 0-1000 of 153813 fields edited | >>

	Record #	Catalog Number	Review Status	Applied Status	Editor	Timestamp	Field Name	Old Value	New Value
☐	3577023	OBI118084	OPEN	APPLIED	Wilk, Nina	2019-10-22 14:56:55	processingstatus	stage 1	unprocessed
☐	3577023	OBI118084	OPEN	APPLIED	Wilk, Nina	2019-10-22 14:56:55	recordenteredby		nina
☐	3576945	OBI118696	OPEN	APPLIED	Pearson, Katie	2019-10-22 14:55:27	processingstatus	stage 1	unprocessed
☐	3576945	OBI118696	OPEN	APPLIED	Pearson, Katie	2019-10-22 14:55:27	recordenteredby		kdpearso

You can select records by checking the boxes on the left side of the table and decide to approve (Apply Edits) or revert (Revert Edits) the edits made to each field of each record by clicking the appropriate radio button in the Action Panel and then the Update Selected Records button. You can also decide to change the Review Status of these records at this time. The Review Status is independent of and not related to the Processing Status.

If you click "Additional Action" in the Action Panel, you can delete the selected edits, download the selected records, download all records that were returned by the search (i.e., are shown in the resulting table), or print the page using one of the appropriate buttons.

NOTE

All edits in the database, regardless of Review Status, are visible in the database as soon as they are made. This tool is meant to aid in reviewing of edits, but does not serve as a gateway to vetting edits before they are made public.

24: Duplicate clustering

The Duplicate Clustering dashboard can be accessed through the Administration Control Panel (*3:2 Administration Control Panel*). From this dashboard, you can view which records have been linked as duplicates (even across institutions), view just those records with conflicting identifications, and start the Batch Linking process that will automatically search the database as a whole and link records that have the same collector, collector number, and date (even across institutions).

The Duplicate Clusters with Conflicting Identifications tool can be particularly useful for determining whether specimens need annotations. See *25:3:3 Duplicate specimens with potential identification conflicts*.

25: Data Cleaning Tools

Symbiota has a number of useful built-in tools for data cleaning processes. Each of the tools described below can be accessed through the Administration Control Panel (see *3:2 Administration Control Panel*) under Data Cleaning Tools. The Data Cleaning dashboard will look like the next screenshot.

Duplicate Records

These tools will assist in searching this collection of records for duplicate records of the same specimen. If duplicate records exist, this feature offers the ability to merge record values, images, and data relationships into a single record.

⌐List Duplicates based on...─────────────────────

- Catalog Numbers
- Other Catalog Numbers

Political Geography

These tools help standardize country, state/province, and county designations. They are also useful for locating and correcting misspelled geographical political units, and even mismatched units, such as a state designation that does not match the wrong country.

⌐Statistics and Action Panel──────────────────

- Geographic Distributions
- Geography Cleaning Tools

Taxonomy

These tools are meant to aid in locating and fixing taxonomic errors and inconsistencies.

⌐Statistics and Action panel─────────────────────

- Analyze taxonomic names...
- Taxonomic Distributions...
- Duplicate specimens with potential identification conflicts...

25:1 Duplicate catalog numbers

Using the Duplicate Records tool, an administrator can search for records that have duplicate Catalog Numbers or Other Catalog Numbers. When appropriate, the user can then merge duplicate records into a single specimen record.

To use the tool, first select whether you would like to list duplicates based on Catalog Numbers or Other Catalog Numbers from the "List Duplicates based on…" box. If duplicates exist, a table of duplicate records will appear on the resulting page.

NOTICE to SuperAdmin: You can increase upper limit of the number of records that this form can process by increasing the max_input_vars variable within your PHP configuration file. Increasing this variable to 4500 will set the upper limit of this form to 1000 duplicate clusters.
Use the checkboxes to select the records you would like to merge, and the radio buttons to select which target record to merge into.

Merge Duplicate Records   1 to 1 Duplicate Clusters

ID			Catalog Number	Other Catalog Numbers	Scientific Name	Collector	Collection Number	Associated Collectors	Collection Date	Verbatim Date	Country	State	County	Locality
1893839	☐	⦿	OBI100101	47318	Athysanus pusillus	David J. Keil	15784		1982-03-24	24-Mar-82	United States	California	San Luis Obispo	Los Padres NF. La Panza
3679217	☐	○	OBI100101											

Merge Duplicate Records

From here, you can evaluate whether the duplicate records should be edited, merged, or ignored. To view and/or edit a record, click the number in the ID column next to the record you wish to view. This will open that specimen's Record Editor page.

If you decide that the two records should be merged, check the boxes next to both duplicates, then select the radio button that corresponds to the record you wish to make the primary record. If both records have a value in a given field, Symbiota will keep the value that belongs to this primary record and discard the other value. When you are satisfied that the correct information will be retained, click the Merge Duplicate Records button.

NOTE

If there are many duplicate records to evaluate, you can click the checkbox at the top of the checkbox column. This will check all of the boxes in the entire table. You can also select the radio button column header, which will allow Symbiota to auto-select a record to retain for each pair. You will want to vet this list to ensure that the correct record is selected for retention.

25:2 Geographic cleaning tools

The two geographic cleaning tools are the Geographic Distribution viewer and the Geography Cleaning Tool.

25:2:1 Geography Distribution viewer

The Geography Distribution viewer can be used to examine the countries, states, and counties that exist in your database. Any misspellings, non-standardized entries (e.g., "USA" rather than "United States"), or suspected mistakes (e.g., "United Arab Emirates" rather than "United States") can be detected using this tool. To view the state/province values for each country, click the name of the country. Then, to view the county values for each state/province, click the name of the state/province.

A user with administrator permissions can correct errors in country, state/province, and/or county individually by clicking the number next to the place name (circled on next screenshot), or you can search for those records using the record search form and batch edit them (see *7:3 Adding annotations/determinations*
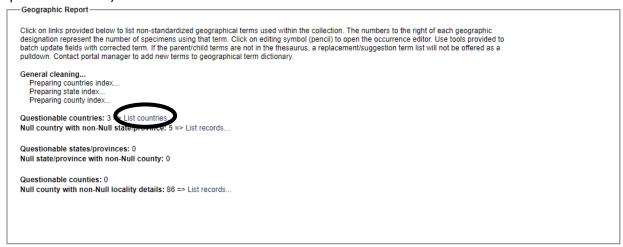
See 8: Adding determination/annotation data.

7:4 Batch editing specimen records).

Geographic Distribution

Click on the specimen record counts within the parenthesis to return the records for that term

- Antigua and Barbuda (2)
- Australia (5)
- Bolivia (5)
- Brazil (6)
- Canada (14)
- China (1)
- Costa Rica (17)
- Ecuador (12)
- El Salvador (3)
- Guam (1)
- Honduras (2)
- Iceland (2)
- India (27)
- Jamaica (2)
- Japan (1)
- Lesotho (25)
- Mexico (165)
- Namibia (20)
- Netherlands (1)
- New Guinea (1)
- New Zealand (1)
- Nigeria (1)
- Peru (15)
- Puerto Rico (2)
- SOUTH AFRICA (88)
- Scotland (2)
- South West Africa (1)
- Sweden (2)
- Switzerland (2)
- Taiwan, Province of China (2)
- USA (162)
- United Arab Emirates (8)
- United Kingdom (8)
- United States (56982)

25:2:2 Geography Cleaning Tool

The Geography Cleaning Tool will search your database for non-standardized geographical terms (countries, states/provinces, and counties) used in your collection. These will be listed as "questionable." To view and potentially edit these records, you can click the "List [terms]…" link (one example circled below).

Geographic Report

Click on links provided below to list non-standardized geographical terms used within the collection. The numbers to the right of each geographic designation represent the number of specimens using that term. Click on editing symbol (pencil) to open the occurrence editor. Use tools provided to batch update fields with corrected term. If the parent/child terms are not in the thesaurus, a replacement/suggestion term list will not be offered as a pulldown. Contact portal manager to add new terms to geographical term dictionary.

General cleaning...
    Preparing countries index...
    Preparing state index...
    Preparing county index...

Questionable countries: 3 => List countries
Null country with non-Null state/province: 5 => List records...

Questionable states/provinces: 0
Null state/province with non-Null county: 0

Questionable counties: 0
Null county with non-Null locality details: 86 => List records...

This tool will also check whether there are records that lack data in the *country*, *state/province*, or *county* fields, yet have geographic data in other fields. For example, the line "Null country with non-Null state/province" lists all records that do not have a *country* value in the specimen record even though there is a state or province listed in the *state/province* field of that record. You can click "List records…" and assign a higher geographic value to those records (see example on next screenshot).

Similar lists are provided for records with empty *state/province* fields but filled *county* fields and for records with empty *county* fields but filled *locality* fields.

NOTES

In a perfect world, the Geography Cleaning Tool would eventually produce 0 records for all lists after the records have been reviewed by the data manager; however, this is usually not possible given the incomplete data provided on many specimens. Data managers should resolve issues as far as they are able, but they should not necessarily expect to clear the lists entirely. Do not fill a field just so that it is removed from one of these lists.

If two countries/states/counties are listed, the field where you would normally put that information should be left blank, and the data should be entered into the next-most detailed field. For example, if the specimen label reads "Kern/Ventura counties", you should leave the *county* field blank and enter "Kern/Ventura counties" in the *locality* field.

25:3 Taxonomic cleaning tools

The taxonomic cleaning tools are great resources for cleaning up misspellings and other taxonomic name entries that do not link to names in the central taxonomic thesaurus. They are "meant to aid in locating and fixing taxonomic errors and inconsistencies," according to the portal description. The available tools are shown in the next screenshot:

25:3:1 Analyze taxonomic names

A video tutorial for using this tool can be found here: https://youtu.be/QAsypzpY-aA.
This function analyzes the values that exist in the Scientific Name field in your database and flags the values that are not linked to the taxonomic thesaurus (i.e., are not linked to a recognized name). Note that this tool does NOT evaluate whether that name is accepted according to current taxonomy. The number of unrecognized scientific names is listed at the top of the Action Menu box.
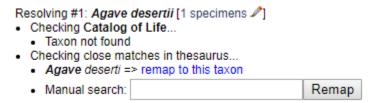
You can evaluate the unrecognized scientific names and link them to the names of the correct taxa by clicking the name of the Taxonomic Resource to which you want to compare the names, selecting the target kingdom (most likely Plantae), and clicking the Analyze Taxonomic Names button. If you wish to begin at a certain name (e.g., you have already checked names up to *Mentzelia*), you can enter this name in the Start Index field. You can also alter the number of names you would like CCH2 to analyze per run in the Names Processed per Run field.

There are multiple types of results from running this tool. In general, the tool will list the name that it is attempting to index (i.e., match to an existing taxonomic name), search Catalog of Life for that name, and, if that name is not found in the Catalog of Life, check the taxonomic thesaurus for similar names to the unrecognized name. You then have several options for resolving the unrecognized name, depending on the type of result. To view the specimen(s) associated with any unrecognized name, click the pencil icon to the right of the name and number of specimens, in brackets. The types of results are explained in more detail below.

Example 1: Misspelling, incomplete name, or orthographic variant

This is the most common type of result. In this case, you discover that the unrecognized name was misspelled or spelled differently than the recognized name. You can click "remap to this taxon" to change the name of the specimen(s) to this recognized name.

Example 2: Unpublished or unrecognized taxon name

- Resolving #2: *Albizia julibrissin var. rosea* [1 specimens ✎]
  - Checking **Catalog of Life**...
    - Taxon not found
  - Checking close matches in thesaurus...
    - *Albizia julibrissin* => remap to this taxon
    - *Albizia julibrissin var. mollis* => remap to this taxon
    - *Albizzia julibrissin* => remap to this taxon
    - Manual search: [_____] [Remap]

In this case, you find that the name listed on the specimen was not published or is not currently listed in the taxonomic thesaurus. You must then use taxonomic expertise to decide whether this specimen should be remapped to a different taxonomic name (if you are confident that they are synonymous) and/or annotated, or if the taxonomic name should be left as is and it should be included in the taxonomic thesaurus. If you believe that a name should be found in the taxonomic thesaurus and you do not find it with a manual search, contact the portal manager.

Example 3: Name exists but is not found in taxonomic thesaurus

- Resolving #47: *Gilia setosissima* (Polemoniaceae) [1 specimens ✎]
  - Checking **Catalog of Life**...
    - Gilia setosissima found within Catalog of Life
    - Gilia skipped due to not matching targeted kingdom: Plantae (!= Animalia)
    - Gilia found within Catalog of Life
  - Taxon **Gilia setosissima** added to thesaurus as synonym of taxon #95743

When CCH2 does not find a name in the taxonomic thesaurus, but it does find the name in the Catalog of Life, it will import the taxonomic name into the taxonomic thesaurus. This will automatically map the specimen's taxonomic name to this newly added entry in the taxonomic thesaurus as well.

If you have not analyzed all the taxonomic names in one pass, you can click the Continue Analyzing Names button to have CCH2 check the next 20 (or whatever number is defined by the user) names.

25:3:2 Taxonomic distributions

Much like the Geographic Distribution viewer (see *25:2:1 Geography Distribution viewer*), the Taxonomic Distribution viewer can be used to examine the families, genera, species, and infraspecific taxa that exist in your database. Misspellings, non-standardized entries, or suspected mistakes can be detected using this tool. To view the genera for each family, click the name of the family. Then, to view the species for each genus, click the name of the genus, and so on.

A user with administrator permissions can correct errors in taxonomic names individually by clicking the number next to the taxonomic name (circled on next screenshot), or the user can search for those records using the record search form and batch edit them (see *7:3 Adding annotations/determinations*

See 8: Adding determination/annotation data.

7:4 Batch editing specimen records).

- Aspleniaceae (19)
- Asteraceae (10120)
- Athyriaceae (8)
- Azollaceae (1)
- Balsaminaceae (2)
- Bataceae (1)
- Berberidaceae (55)
- Betulaceae (59)
- Bignoniaceae (15)
- Blechnaceae (3)
- Boraginaceae (586)
- Brassicaceae (1)
- Brassicaceae (2178)
- Brassicaeae (2)
- Bromeliaceae (1)
- Burseraceae (3)
- Cabombaceae (1)
- Cactaceae (55)
- Calycanthaceae (7)
- Campanulaceae (190)
- Cannabaceae (18)
- Cannaceae (2)

25:3:3 Duplicate specimens with potential identification conflicts

This tool lists the duplicate clusters of specimens (specimens that have the same collector, number, and date, even across different collections; see *24: Duplicate clustering*) for which one or more of the specimens does not have the same taxonomic name. The tool can be used to identify whether there are specimens in your collection that should be annotated to the most recently identified taxonomic name. For example, in the cluster below, OBI and UCR may consider annotating their specimens according to the most recent identification of the SBBG duplicate. The specimen records associated with each specimen can be viewed by clicking on the catalog number of the desired record.

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Robert F. Hoover Herbarium, Cal Poly State University
251 Duplicate Clusters with Identification Differences

Sanders 6538 1986-06-01 ✏️

SBBG:87945 => A. C. Sanders 6538
  Cryptantha intermedia var. intermedia
  Determined by: Michael G. Simpson and Brenda M. Bennett 2019-06-11

OBI131695 => A. C. Sanders 6538
  Cryptantha intermedia

UCR0003112 => A.C. Sanders 6538
  Cryptantha intermedia

26: Downloading a copy of your database

It is recommended that curators or collection managers regularly download and archive a copy of their database in case of emergency. Doing so is quick and easy.

Navigate to the Administration Control Panel (see *3:2 Administration Control Panel*) and select Download Data Backup File.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)

A new window will appear asking you to select the character set (ISO-8859-1 or UTF-8) that will be used in your downloaded dataset. Click the Perform Backup button. The resulting file will be a zipped Darwin Core Archive. In this folder, your specimen data will be found in a comma-separated (CSV) file named "occurrences," the specimen identifications in a CSV file called "identifications," any associated trait data in a file called "measurementOrFact," and links to related media in a file called "images." The archive also contains metadata about your collection and about the fields contained in each of the CSV files. For more information about the format and use of Darwin Core Archives, see the following resources:
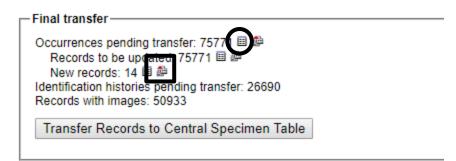
https://github.com/gbif/ipt/wiki/DwCAHowToGuide
https://en.wikipedia.org/wiki/Darwin_Core_Archive

27: Restoring your database with a previously downloaded copy

In the case of catastrophic database error (e.g., erroneous batch edit that cannot be easily reversed), you can replace your entire database by uploading a DarwinCore Archive (DwC-A) to CCH2. Note that you need to have recently downloaded a copy of your database (see *26: Downloading a copy of your database*) with which you can replace your current database.

To replace your database, navigate to the Administration Control Panel (see *3:2 Administration Control Panel*) and click "Restore Backup File" under the General Maintenance Tasks. You can then click Choose File and select a DwC-A with which to replace your dataset. If your DwC-A contains an "identifications" file, make sure that the Restore Determination History box is checked. If your DwC-A contains an "images" file, make sure that the Restore Images box is checked. Click Analyze File.

The file will take some time to load and process. Once this is done, a report called "Final transfer" will be displayed at the bottom of the screen. This report will show you how many records will be updated, how many records are new, how many identifications/determinations will be added, and how many records have images. Ensure that these numbers are as expected. You can preview these records by clicking the table icon to the immediate right of the desired dataset (circled on next screenshot), or you can download these records as a CSV by clicking the two boxes icon to the far right of the desired dataset (in a square on next screenshot). Once you are satisfied that the records will be properly uploaded, click the Transfer Records to Central Specimen Table button. **Note that this change is permanent and cannot be undone!**

28: Collection statistics

Information about the records in your collection is displayed as Collection Statistics at the bottom of your collection profile page. For logged-in users, these data are shown below the Data Editor and Administration Control Panel. Non-users can view this information by clicking "more info..." after the name of the collection on the Search Collections page.

It is important to note that these statistics **are not automatically updated** when new data are added to your collection. Therefore, the curator or data manager should manually update these statistics on a regular basis. To do so, navigate to the Administration Control Panel (see *3:2 Administration Control Panel*) and click "Update Statistics" at the end of the control panel list. Your numbers will be updated as soon as you see the message "Finished updating collection statistics."

The collection statistics can be useful for producing reports or confirming batch changes made to the collection (e.g., batch uploading of specimen records).

29: Research checklists

A research checklist is a list of taxa for a certain region. Checklists are documented by voucher specimens, which may be in several different herbaria. The checklist tool enables linking to voucher specimens, if they are available online, or simply listing their catalog number if not. The voucher tool also enables tracking new potential voucher specimens and re-identification of existing vouchers.

A video introduction to checklists in Symbiota can be viewed here: https://youtu.be/YwBC-52j6Ps. A tutorial for the creation of quick checklists using voucher specimens can be found here: https://youtu.be/L45s7c19kNw

29:1 Creating a checklist

A video tutorial of this process (on a general Symbiota site) is available here:
https://youtu.be/jm2_mn2nClo

1. Login to CCH2 (http://www.cch2.org).
2. Click on "My profile"
3. Under the "Species Checklists" tab, click on the green plus sign:
4. Fill out the "Create New Checklist" box with the desired information.
   a. Most checklists will be a *General Checklist*. Alternatively, you can another list type from the **Checklist Type** dropdown menu. A *Species Exclusion List* is used to curate a subset of taxa that are purposely excluded from another list, and a *Rare, threatened, protected species list* is used to compile a state-level list of rare, threatened, and protected taxa for which locality data will be redacted for specimens in that state.
   b. To indicate that this checklist is a subset within a larger checklist, select the "parent" (larger) checklist from the More **Inclusive Reference Checklist** dropdown menu.
   c. You can define the area included in the checklist by describing it in the **Locality** and **Abstract** fields, including **Latitude** and **Longitude** coordinates, and/or you can define the boundaries of that area geographically by setting a "footprint polygon". To define a "footprint polygon":
      1. Click the globe icon (🌐) inside the **Polygon Footprint** box. A Google map will appear a new window.
      2. Drag the map until it shows the region covered by your checklist, then zoom in until you can see the boundaries of the area.
      3. Click the polygon icon in the top center of the window (🔶), then click around the boundaries of your area.
      4. When you get back to the point where you started, double click the starting point. This will lock the coordinates into the text box at the bottom of the window. Your defined area will shaded in.
      5. If you are dissatisfied with your polygon, you can delete or redraw it by clicking the appropriate button on the bottom right. When you are satisifed with your polygon, click the Save Polygon button.
   • You can decide whether you want to keep this checklist private, or if you want it to be available to the public by selecting Private or Public from the **Access** dropdown menu.

29:2 Adding taxa to a checklist

There are two ways to add taxa to a checklist, either individually (the default process) or via batch upload. You may want to start by adding them individually so you can become familiar with the information that can be uploaded and the care one needs to take in doing so.

29:2:1 Adding individual taxa

A video tutorial of this process (on a general Symbiota site) is available here:
https://youtu.be/jm2_mn2nClo?t=292

1. On the checklist page, click the rightmost pencil icon (labeled spp.) at the top right of the page. This will bring up a panel on the lower right side of the screen.
2. Add the name of a taxon you wish to add. Do NOT include the authorship of the taxon. You can start typing, and a dropdown list will allow you to select the taxon from available options.
   • You cannot add a name that is not present in the taxonomic thesaurus (it will tell you if this is the case). If you find that the taxon you wish to add is not present:

1. Check that your spelling is correct. Use Tropicos (http://tropicos.org) or IPNI (http://www.ipni.org/) to check.
2. If your spelling is correct, contact your portal manager with the name, authorship, and a reference or link to that name in another taxonomic database, and it will be added for you.

3. Fill in the other fields if desired. All of these fields can be left blank:
   - **Family Override**: If you enter the family name here, you will override the family provided by the taxonomic thesaurus. It is advised not to enter anything in this field.
   - **Habitat**: If the taxon is usually found in a particular habitat in the area circumscribed by the checklist, you can include this information here.
   - **Abundance**: Here you can note how frequently/abundantly this taxon is found in the area circumscribed by the checklist. For example, you can use terms like "common," "frequent," or "rare."
   - **Notes**: Any other comments about this taxon pertaining to your checklist area can be put here, for example: "Cultivated ornamental" or "favored by honeybees"
   - **Internal notes:** This field, unlike the others, will be visible only to people authorized to edit the checklist. You might make a note "need to check the species" or "no picture available" for example.
   - **Source:** This field is more likely to be used for research and teaching checklists. For such checklists, it is useful to know whether the information came from a flora, some other publication, or a report by some
4. Click the "Add species to List" button.

29:2:2 Batch uploading taxa

A video tutorial of this process (on a general Symbiota site) is available here:
https://youtu.be/Hnk09MYlMVg

If you have several taxa to add at one time, you can upload them in a CSV (comma separated value) file. The easiest way to create the desired listing is to use Microsoft Excel or OpenOffice Calc and then save the file as a CSV file.

In your CSV file, one column in the file should be labeled sciname. This should contain the scientific name of the taxon WITHOUT the authorship included. In this CSV file, you must be very careful to spell the scientific names correctly. If you have an error in your spelling, you will not be able to load that name into your checklist.

You can also include "family", "habitat", "abundance", and "notes" (see *29:2:1 Adding individual taxa* for description of contents of these fields) columns in this file. An example is shown below.

Sciname	Habitat	Abundance	Notes
Asystasia gangetica	Middle of the field	Rare	Demonstration; correct spelling
Asystasia gangetca	Middle of the field	Unknown	Demonstration; wrong spelling

Below is a screenshot of uploading the previous example "file". Note that only one name, the one that was correctly spelled, was uploaded.

2018 Tiny sample checklist

Authors: Kegen Benson

- Loading checklist...
- Upload status...
  - Taxa successfully loaded: 1
  - Problematic Taxa: 1 (see below)
- General errors: 0

Problematic Taxa Resolution

Cnt	Name	Actions
1	Asystasia gangetca	

To return to the Checklist, click "Return to Checklist" at the top left of the page (circled below).

Home > Return to Checklist >> Checklist Administration

Plants of San Luis Obispo County - OBI SLO County voucher collection

California; San Luis Obispo

You can then view the taxa that were added to the checklist.

2018 Tiny sample checklist *Games*

Authors: Kegen Benson
Citation: Benson, K. 2018. Checklist of the plants on the grounds of Tiny Sample School.
More Details

Families: 1
Genera: 1
Species: 1 (species rank)
Total Taxa: 1 (including subsp. and var.)

ACANTHACEAE

Asystasia gangetica (L.) T. Anders.

Options

Search:

☐ Common Names
☑ Synonyms

Filter:
Original Checklist ▼

☐ Common Names
☐ Display as Images
☐ Notes & Vouchers
☑ Taxon Authors
☐ Show Taxa Alphabetically

Rebuild List

29:3 Adding voucher specimens to a checklist

There are two main ways to add voucher specimens to a research checklist. You can add specific, individual specimens from your own collection to the checklist through the occurrence editor (the page of the specimen record) or add specimens from any collection through the Manage Linked Voucher tool on the checklist page. The second method is described in this video: https://youtu.be/NRW2kh6xln0
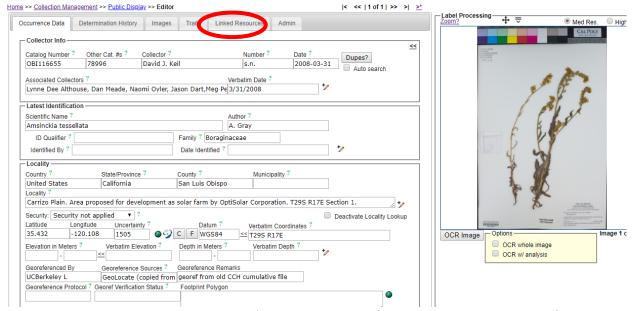
29:3:1 Adding individual specimens from your own collection

1. Look up a specific specimen in your own collection (e.g., by clicking Edit Existing Occurrence Records in your Data Editor Control Panel and searching by a specific catalog number or by using other search terms; see example below).
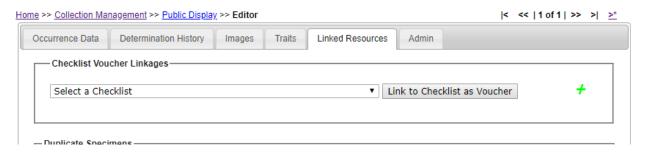
2. On the resulting page, click the Linked Resources tab (circled below).

3. In the Checklist Voucher Linkages box (see next screenshot), select the desired Checklist from the dropdown menu and click Link to Checklist as Voucher. A new window will likely pop up as a result, but you can ignore this window and close the editor. The specimen has been successfully linked as a voucher to the desired checklist.

29:3:2 Adding specimens from any collection (Manage Linked Voucher tool)

A video tutorial of this process (on a general Symbiota site) is available here:
https://youtu.be/NRW2kh6xln0

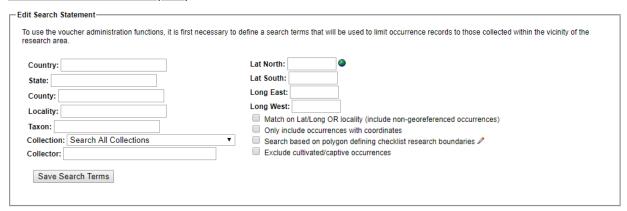1. Navigate to the homepage of your checklist.

2. Click the pencil icon that has a V next to it (the center icon in the top right corner of the page, circled below).

3. If this is the first time you have used this tool, you will be asked to first define the search statement (i.e., search parameters) that will be used to find the specimens that might pertain to your checklist. You can use a variety of fields to define your search, as described below.

NOTE: you will be able to change the search statement in the future, so you are not necessarily defining the bounds in perpetuity.
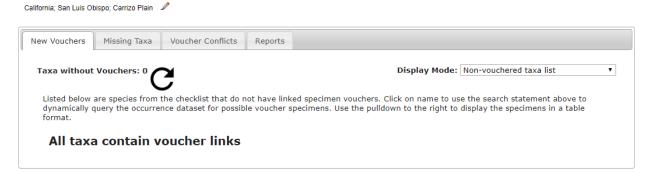

- You can enter **search terms** for a number of fields on the left side of the form.
- You can use the **polygon footprint** that you defined when creating the checklist (see *29:1 Creating a checklist*, step 3c) to search for specimen records by checking the "Search based on polygon defining checklist research boundaries" box. If you did not define a polygon previously, you can also do so from here by clicking the pencil icon to the right of this option and following the steps outlined in *29:1 Creating a checklist*, step 3c.
- You can define a specific **bounding box** by entering the latitude and longitude values that delimit the box, or by defining the lat/long values on a map. To do the latter:

1. Click the globe icon to the right of the Lat North field
2. In the pop-up window, pan and zoom to the location where you want to place the bounding box.
3. Click on the approximate center where you want the bounding box to be located.
4. Adjust the location and size of the bounding box as desired by clicking and dragging inside the box (to move the box) or clicking and dragging one of the circles on the sides or corners of the box (to resize the box).
5. To save the bounding box, click the tiny grey rectangle to the right of the lat/long coordinate fields (circled below)

- There are a number of important **checkboxes** below the Lat/Long fields that you can use to refine your search. For example, you can allow the search to return specimens with the desired search terms OR within certain latitude and longitude coordinates.
- You can use any combination of the above options to search for voucher specimens.
4. Once you have entered the desired search terms, click the Save Search Terms button.
5. There are a number of ways to add voucher specimens from this point.

Flora of the Carrizo Plain (Test)

California; San Luis Obispo; Carrizo Plain ✏

| New Vouchers | Missing Taxa | Voucher Conflicts | Reports |

Taxa without Vouchers: 0 ↻   Display Mode: Non-vouchered taxa list ▼

Listed below are species from the checklist that do not have linked specimen vouchers. Click on name to use the search statement above to dynamically query the occurrence dataset for possible voucher specimens. Use the pulldown to the right to display the specimens in a table format.

All taxa contain voucher links

- If you have already defined a taxon list (see *29:2 Adding taxa to a checklist*) for your checklist, you can add voucher specimens from the **New Vouchers** tab. From this tab, you can:
    1. View taxa that do not currently have voucher specimens in your checklist (select *Non-vouchered taxa list* from the **Display Mode** dropdown list).
    2. View specimen records that match your search criteria and are one of the taxa defined in your taxon list that is NOT currently vouchered (select *Occurrences for non-vouchered taxa* from the **Display Mode** dropdown list).
        - To add voucher specimens from this list, click the box to the left of the specimen record(s) that you wish to add and click the Add Vouchers button.
    3. View specimen records that match your search criteria and are one of the taxa defined in your taxon list, regardless of whether that taxon has been vouchered previously (select *New occurrences for all taxa* from the **Display Mode** dropdown list).
        - To add voucher specimens from this list, click the box to the left of the specimen record(s) that you wish to add and click the Add Vouchers button.
- Regardless of whether you have previously defined a taxon list for your checklist, you can add voucher specimens through the **Missing Taxa** tab. From this tab, you can:
    1. View the taxa that are not found in the checklist currently but are represented by one or more specimens that align with your search criteria (select *Species List* from the **Display Mode** dropdown list).
        - You can then view a list of the specimens associated with each taxon by clicking the page and chain icon (🔗). From there, you can link the desired specimens individually by clicking the add voucher icon (🗒) to the right of the specimen record in the list.
    2. View the specimens that are not yet added as voucher specimens for your checklist but do align with your search criteria (select *Batch Linking* from the **Display Mode** dropdown menu).
        - To add voucher specimens from this list, click the box to the left of the specimen record(s) that you wish to add and click the Add Vouchers button.
    3. View specimen records that align with your search criteria, but have scientific names that are not linked to a particular name in the taxonomic thesaurus (select *Problem Taxa* from the **Display Mode** dropdown menu).
        - To add voucher specimens from this list, enter the name of the taxon to which this specimen belongs into the text box to the right of the specimen's

scientific name. Note that the name you enter in this box must already be found in the list of taxa in your checklist. Click the Link Voucher button.

29:4 Other checklist tools

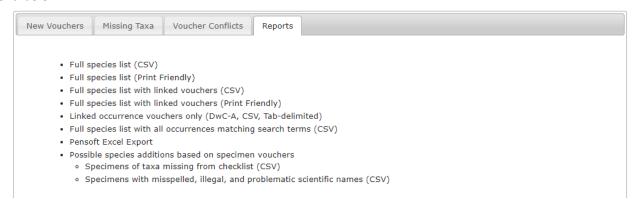### 29:4:1 Voucher conflicts tab

In the Manage Linked Vouchers tool (see *29:3:2 Adding specimens from any collection (Manage Linked Voucher tool)*), you can view a list of specimen vouchers for which their current identifications do not match how they were originally added as part of the checklist. This is generally due to recent annotations.

27:4:2 Reports tab

You can generate a number of useful reports using the Reports tab in the Manage Linked Vouchers tool (see *29:3:2 Adding specimens from any collection (Manage Linked Voucher tool)*), as shown in the menu below.

Appendix 1: Processing Status

(adapted from Skema & Barber 2018)

Processing Status is a field in Symbiota that helps keep track of what stage a record is at in the workflow. There is no one standard for how to use the different levels of Processing Status across all users of Symbiota, although there is some standardization within projects. If each user in a particular collection uses the processing status field consistently, both in remembering to change the status as required, and in assigning the appropriate status, it is of great help to the workflow. The following table shows the recommended definitions for the status levels in Processing Status to use for the California Phenology TCN.

Status	Definition
Unprocessed	skeletal record (typically with just an image and catalog number)
Pending Review	volunteer/technician transcribed record and had no problems/questions **OR** record imported from a dataset that was previously minimally quality controlled
Expert Required	volunteer/technician transcribed or reviewed record and had problem(s)/questions (volunteer/technician should leave concise notes in Occurrence Remarks to explain problem/question)
Reviewed	record transcribed; transcription reviewed and correct **OR** record imported from a dataset that was previously quality controlled
Stage 3	record problematic; to be researched
Closed	record transcribed, georeferenced, and fully reviewed (or as best as possible given available information)

Appendix 2: Data Management Monthly To-Do List

To ensure the highest possible data quality and sustainability of specimen records, we recommend that collections or data managers complete the following tasks at least monthly:

☐ Download and archive a backup copy of your collection data (*26: Downloading a copy of your database*)

☐ Update statistics relating to your collection and record these numbers for your own records (28: Collection statistics)

☐ Review and edit collections metadata, if necessary (18: Editing metadata (summary and contact information) for your collection)

☐ Review and vet comments posted to your records (17: Viewing and vetting comments)

☐ Review and resolve in-house duplicate records (25:1 Duplicate catalog numbers)

☐ Use Geography Cleaning Tool to resolve questionable countries and questionable states/provinces, at minimum, in your records (25:2 Geographic cleaning tools)

☐ Use Taxonomic Cleaning Tool to resolve taxonomic issues in your records *(25:3 Taxonomic cleaning tools*)

References

Skema C, Barber A. 2018. Mid-Atlantic Megalopolis digitization standards and training manual. Morris Arboretum of University of Pennsylvania. Available from https://docs.wixstatic.com/ugd/6f7156_800579c353574e59918cfb541172d749.pdf