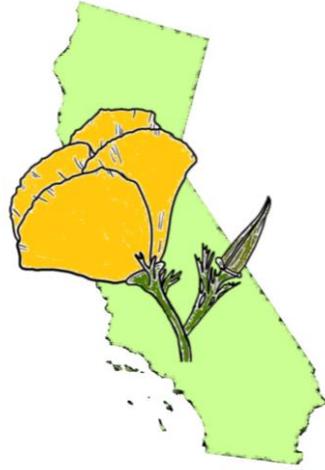# Digitization Manual

for the California Phenology Thematic Collections Network (CAP TCN)

last updated by Katie Pearson

8/10/2020

Contents

1. Project Goals

In 2018, the CAP Network initiated as a collaboration of 22 California herbaria to digitize 904,200 specimens. In 2020, a Partner-to-Existing-Network (PEN) grant was awarded to fund the digitization of 148,180 additional specimens from six additional herbaria and one previously funded CAP herbarium. The combined digitization goals of this new and improve CAP Network are to

- Image 1,052,380 specimens of over 3000 angiosperm taxa (Table 1.1) at 28 collaborating institutions (Table 2.1)
- Transcribe 322,200 specimens and georeference over 336,000 specimens
- Capture phenological data for 1,052,380 specimens

Additional goals include:

- Develop and maintain the Symbiota-based "CCH2" portal
- In collaboration with community experts, develop standards for recording and storing specimen-based phenological data
- Build Symbiota functionality to accommodate newly developed phenological standards
- Engage citizen scientists in transcription and phenological scoring of specimen images

Table 1.1: Taxa targeted for imaging, digitization, and phenological scoring. Families for which all species will be digitized are indicated by "ALL" in the species column. **Note that all specimens of these taxa, regardless of collection location, are to be digitized.**

Family	Species	Family	Species
Acanthaceae	*Avicennia germinans*	Apocynaceae	*Asclepias curassavica*
Adoxaceae	ALL	Apocynaceae	*Asclepias eriocarpa*
Agavaceae	ALL	Apocynaceae	*Asclepias fascicularis*
Altingiaceae	*Liquidambar styraciflua*	Apocynaceae	*Asclepias latifolia*
Amaranthaceae	*Atriplex canescens*	Apocynaceae	*Asclepias linaria*
Amaranthaceae	*Atriplex hymenelytra*	Apocynaceae	*Asclepias speciosa*
Amaranthaceae	*Krascheninnikovia lanata*	Apocynaceae	*Asclepias subulata*
Amaranthaceae	*Salicornia virginica*	Apocynaceae	*Asclepias tuberosa*
Anacardiaceae	*Anacardium excelsum*	Apocynaceae	*Asclepias verticillata*
Anacardiaceae	*Malosma laurina*	Apocynaceae	*Asclepias viridis*
Anacardiaceae	*Rhus glabra*	Apocynaceae	*Funastrum cynanchoides*
Anacardiaceae	*Rhus integrifolia*	Aquifoliaceae	*Ilex aquifolium*
Anacardiaceae	*Rhus ovata*	Araceae	*Lysichiton americanus*
Anacardiaceae	*Toxicodendron diversilobum*	Araliaceae	*Hedera helix*
Apiaceae	*Daucus carota*	Asparagaceae	*Asparagus officinalis*
Apiaceae	*Heracleum maximum*	Asparagaceae	*Camassia quamash*
Apiaceae	*Ligusticum grayi*	Asparagaceae	*Dichelostemma capitatum*
Apiaceae	*Lomatium macrocarpum*	Asparagaceae	*Hesperocallis undulata*
Apocynaceae	*Apocynum androsaemifolium*	Asparagaceae	*Maianthemum dilatatum*
Apocynaceae	*Apocynum cannabinum*	Asparagaceae	*Maianthemum racemosum*
Apocynaceae	*Asclepias asperula*	Asteraceae	*Achillea millefolium*
Apocynaceae	*Asclepias cordifolia*	Asteraceae	*Ambrosia artemisiifolia*

Family	Species
Asteraceae	*Ambrosia dumosa*
Asteraceae	*Ambrosia psilostachya*
Asteraceae	*Anaphalis margaritacea*
Asteraceae	*Antennaria corymbosa*
Asteraceae	*Artemisia californica*
Asteraceae	*Artemisia douglasiana*
Asteraceae	*Artemisia tridentata*
Asteraceae	*Baccharis pilularis*
Asteraceae	*Baccharis salicifolia*
Asteraceae	*Baileya multiradiata*
Asteraceae	*Balsamorhiza sagittata*
Asteraceae	*Centaurea solstitialis*
Asteraceae	*Centaurea stoebe*
Asteraceae	*Cirsium arvense*
Asteraceae	*Cirsium occidentale*
Asteraceae	*Cirsium vulgare*
Asteraceae	*Coreopsis lanceolata*
Asteraceae	*Encelia californica*
Asteraceae	*Encelia farinosa*
Asteraceae	*Ericameria* (all species)
Asteraceae	*Erigeron* (all species)
Asteraceae	*Eriophyllum* (all species)
Asteraceae	*Gaillardia pulchella*
Asteraceae	*Gutierrezia sarothrae*
Asteraceae	*Helianthus annuus*
Asteraceae	*Hieracium aurantiacum*
Asteraceae	*Lessingia germanorum*
Asteraceae	*Leucanthemum vulgare*
Asteraceae	*Malacothrix glabrata*
Asteraceae	*Nothocalais alpestris*
Asteraceae	*Petasites frigidus*
Asteraceae	*Psilostrophe cooperi*
Asteraceae	*Ratibida columnifera*
Asteraceae	*Rudbeckia hirta*
Asteraceae	*Silphium laciniatum*
Asteraceae	*Solidago altissima*
Asteraceae	*Solidago canadensis*
Asteraceae	*Symphyotrichum novae-angliae*

Family	Species
Asteraceae	*Taraxacum officinale*
Asteraceae	*Verbesina encelioides*
Asteraceae	*Wyethia mollis*
Berberidaceae	*Achlys triphylla*
Berberidaceae	*Mahonia aquifolium*
Berberidaceae	*Mahonia nervosa*
Berberidaceae	*Mahonia repens*
Betulaceae	*Alnus incana*
Betulaceae	*Alnus rubra*
Betulaceae	*Alnus viridis*
Betulaceae	*Betula glandulosa*
Betulaceae	*Betula nana*
Betulaceae	*Corylus cornuta*
Bignoniaceae	*Campsis radicans*
Bignoniaceae	*Chilopsis linearis*
Boraginaceae	ALL
Brassicaceae	ALL
Cactaceae	*Carnegiea gigantea*
Cactaceae	*Echinocereus engelmannii*
Cactaceae	*Escobaria vivipara*
Cactaceae	*Opuntia acanthocarpa*
Cactaceae	*Opuntia basilaris*
Campanulaceae	*Campanula griffinii*
Campanulaceae	*Lobelia cardinalis*
Cannabaceae	*Celtis laevigata*
Cannabaceae	*Celtis reticulata*
Caprifoliaceae	*Linnaea borealis*
Caprifoliaceae	*Lonicera involucrata*
Caprifoliaceae	*Lonicera japonica*
Caprifoliaceae	*Lonicera tatarica-arnoldred*
Caprifoliaceae	*Symphoricarpos albus*
Caprifoliaceae	*Symphoricarpos oreophilus*
Caprifoliaceae	*Valeriana sitchensis*
Caryophyllaceae	*Minuartia obtusiloba*
Convolvulaceae	*Calystegia sepium*
Cornaceae	*Cornus nuttallii*
Cornaceae	*Cornus officinalis*
Cornaceae	*Cornus sericea*

Family	Species
Cupressaceae	*Juniperus osteosperma*
Cupressaceae	*Thuja plicata*
Ebenaceae	*Diospyros virginiana*
Elaeagnaceae	*Elaeagnus angustifolia*
Elaeagnaceae	*Shepherdia argentea*
Elaeagnaceae	*Shepherdia canadensis*
Ericaceae	ALL
Euphorbiaceae	*Euphorbia esula*
Euphorbiaceae	*Triadica sebifera*
Fabaceae	*Acacia greggii*
Fabaceae	*Amorpha canescens*
Fabaceae	*Cytisus scoparius*
Fabaceae	*Darlingtonia californica*
Fabaceae	*Gleditsia triacanthos*
Fabaceae	*Lathyrus japonicus*
Fabaceae	*Lathyrus littoralis*
Fabaceae	*Leucaena leucocephala*
Fabaceae	*Lupinus* (all species)
Fabaceae	*Medicago sativa*
Fabaceae	*Melilotus officinalis*
Fabaceae	*Olneya tesota*
Fabaceae	*Parkinsonia florida*
Fabaceae	*Parkinsonia microphylla*
Fabaceae	*Prosopis glandulosa*
Fabaceae	*Prosopis pubescens*
Fabaceae	*Prosopis velutina*
Fabaceae	*Robinia neomexicana*
Fabaceae	*Robinia pseudoacacia*
Fabaceae	*Senna covesii*
Fabaceae	*Trifolium* (all species)
Fagaceae	ALL
Fouquieriaceae	*Fouquieria splendens*
Garryaceae	*Garrya elliptica*
Gentianaceae	*Gentiana calycosa*
Geraniaceae	*Erodium botrys*
Geraniaceae	*Geranium robertianum*
Grossulariaceae	*Ribes aureum*
Grossulariaceae	*Ribes cereum*

Family	Species
Grossulariaceae	*Ribes montigenum*
Grossulariaceae	*Ribes roezlii*
Grossulariaceae	*Ribes sanguineum*
Haloragaceae	*Myriophyllum spicatum*
Hydrangeaceae	*Philadelphus lewisii*
Iridaceae	*Iris douglasiana*
Iridaceae	*Iris giganticaerulea*
Iridaceae	*Iris tenax*
Iridaceae	*Olsynium douglasii*
Iridaceae	*Sisyrinchium bellum*
Lamiaceae	ALL
Lauraceae	*Persea americana*
Lauraceae	*Umbellularia californica*
Liliaceae	*Erythronium grandiflorum*
Liliaceae	*Erythronium oregonum*
Liliaceae	*Fritillaria pudica*
Liliaceae	*Lilium pardalinum*
Liliaceae	*Prosartes hookeri*
Liliaceae	*Tulipa clusiana*
Lythraceae	*Lythrum salicaria*
Malvaceae	*Gossypium hirsutum*
Melanthiaceae	ALL
Menyanthaceae	*Menyanthes trifoliata*
Montiaceae	*Cistanthe umbellata*
Montiaceae	*Claytonia lanceolata*
Montiaceae	*Claytonia perfoliata*
Montiaceae	*Lewisia rediviva*
Nyctaginaceae	*Abronia umbellata*
Nymphaeaceae	*Nuphar lutea*
Nymphaeaceae	*Nymphaea odorata*
Oleaceae	*Forestiera pubescens*
Oleaceae	*Fraxinus latifolia*
Oleaceae	*Fraxinus velutina*
Oleaceae	*Ligustrum* (all species)
Oleaceae	*Olea europaea*
Onagraceae	ALL
Orchidaceae	*Epipactis helleborine*
Orchidaceae	*Goodyera oblongifolia*

Family	Species
Orobanchaceae	ALL
Oxalidaceae	*Oxalis oregana*
Papaveraceae	ALL
Phrymaceae	ALL
Phytolaccaceae	*Phytolacca americana*
Plantaginaceae	ALL
Platanaceae	*Platanus racemosa*
Polemoniaceae	ALL
Polygonaceae	ALL
Pontederiaceae	*Eichhornia crassipes*
Primulaceae	*Dodecatheon pulchellum*
Primulaceae	*Trientalis borealis*
Ranunculaceae	ALL
Rhamnaceae	ALL
Rosaceae	ALL
Rubiaceae	*Cephalanthus occidentalis*
Salicaceae	*Populus angustifolia*
Salicaceae	*Populus balsamifera*
Salicaceae	*Populus fremontii*
Salicaceae	*Populus tremuloides*
Salicaceae	*Populus trichocarpa*
Salicaceae	*Salix gooddingii*
Salicaceae	*Salix hookeriana*
Salicaceae	*Salix laevigata*
Salicaceae	*Salix lasiolepis*
Salicaceae	*Salix planifolia*
Salicaceae	*Salix scouleriana*
Sapindaceae	ALL
Sarraceniaceae	*Sarracenia purpurea*
Saururaceae	*Anemopsis californica*
Saxifragaceae	*Lithophragma bolanderi*
Saxifragaceae	*Tellima grandiflora*
Saxifragaceae	*Tolmiea menziesii*
Scrophulariaceae	*Leucophyllum frutescens*
Scrophulariaceae	*Scrophularia californica*
Simmondsiaceae	*Simmondsia chinensis*
Solanaceae	*Datura wrightii*
Solanaceae	*Lycium torreyi*

Family	Species
Solanaceae	*Solanum dulcamara*
Solanaceae	*Solanum elaeagnifolium*
Solanaceae	*Solanum* (all species)
Typhaceae	*Typha domingensis*
Typhaceae	*Typha latifolia*
Ulmaceae	*Ulmus pumila*
Urticaceae	*Urtica dioica*
Violaceae	*Viola glabella*
Violaceae	*Viola sempervirens*
Vitaceae	*Vitis vinifera*
Zosteraceae	*Zostera marina*
Zygophyllaceae	ALL

Table 2.1: Imaging, databasing, and georeferencing goals of each collaborating institution. Index Herbariorum (Thiers, 2011) codes are given in parentheses. Shaded cells indicate participants added with the 2020 PEN grant. UC = University of California, CSU = California State University

Digitizing institutions and herbarium codes	Organizational structure	Total records in this project	Target specimens to image only	Target specimens to fully database	Target specimens to georeference
(BSCA) Colorado Desert District, California Dept. of Parks and Rec.	Sending to RSA	5,000		5,000	
(CHSC) CSU, Chico	Collaborator	30,000	22,000	8,000	
(CDA) California Department of Food and Agriculture	Collaborator	24,000	10,320	6,000	7,680
(CSLA) CSU, Los Angeles	Collaborator	35,000		35,000	
(CSUSB) CSU, San Bernardino	Sending to RSA	4,200	4,000	200	
(DAV) UC, Davis	Collaborator	50,000	50,000		
(FSC) CSU, Fresno	Collaborator	40,000		40,000	
(HSC) CSU, Humboldt	Collaborator	30,000	30,000	0	100,000
(IRVC) UC, Irvine	Collaborator	35,000		35,000	
(LA) UC, Los Angeles	Collaborator	45,000		45,000	
(LOB) CSU, Long Beach	Collaborator	11,000		11,000	
(MACF) CSU, Fullerton	Collaborator	25,000		25,000	
(OBI) California Polytechnic State University, San Luis Obispo	Collaborator - Lead	40,000		40,000	100,000
(OSC) Oregon State University	Collaborator – Lead for PEN	66,000	66,000		
(PUA) Pacific Union College	Collaborator	19,000	9,500		9,500
(RSA) Rancho Santa Ana Botanic Garden	Collaborator	100,000	80,000	20,000	
(SBBG) Santa Barbara Botanic Garden	Collaborator	80,000	70,000	10,000	
(SD) San Diego Natural History Museum	Collaborator	71,000 +15,000	67,000 +15,000	4,000	100,000
(SDSU) San Diego State University	Collaborator	20,000	20,000		
(SFSU) San Francisco State University	Collaborator	16,200		16,200	16,200
(SFV) CSU, Northridge	Collaborator	25,000	15,000	10,000	
(SHTC) CSU, Stanislaus	Collaborator	3980	1230		2750

Digitizing institutions and herbarium codes (cont'd)	Organizational structure (cont'd)	Records in this project (cont'd)	Specimens to image only (cont'd)	Specimens to fully database (cont'd)	Specimens to georeference (cont'd)
(SJSU) CSU, San Jose	Collaborator	10,200	10,200	0	
(UC/JEPS) UC, Berkeley	Collaborator	100,000	100,000		
(UCSB) UC, Santa Barbara	Collaborator	34,000	30,000	4,000	
(UCSC) UC, Santa Cruz	Collaborator (unfunded)	7,000	4,000	3,000	
(UCR) UC, Riverside	Collaborator	105,000	100,000	5,000	
(UNLV) University of Nevada, Las Vegas	Collaborator	4,000	4,000		
	Totals + PEN	**904,200 +148,180**	**602,200 +89,980**	**302,400 + 22,200**	**300,000 + 36,000**

2. Workflow

The general recommended workflow for this project is shown in the diagram on the next page. The steps are:
   A. Barcode specimens (Section 7)
            *Note: can be combined with imaging (see Section 9)
   B. Image specimens in raw format (Section 8)
   C. Process images, including: add metadata (i.e., copyright information), rotate, crop, sharpen, edit highlights, and export as digital negative (DNG) and jpeg formats (Section 10)
   D. Archive images (both DNGs and copy of JPEGs) to institutional storage
   E. Upload JPEGs to CyVerse, which will create a URL for each image (Section 11)
   F. Load image URLs into CCH2 (Section 11)
   G. *If data already exist in CCH2:* associate new images (and barcode Number) to existing records (and accession numbers) (Section 12)
   H. Transcribe data (Section 13), georeference (Section 14), and score phenology (Section 15) as time and workforce capacity allows.
   I. *After completion of project, not funded:* quality check data
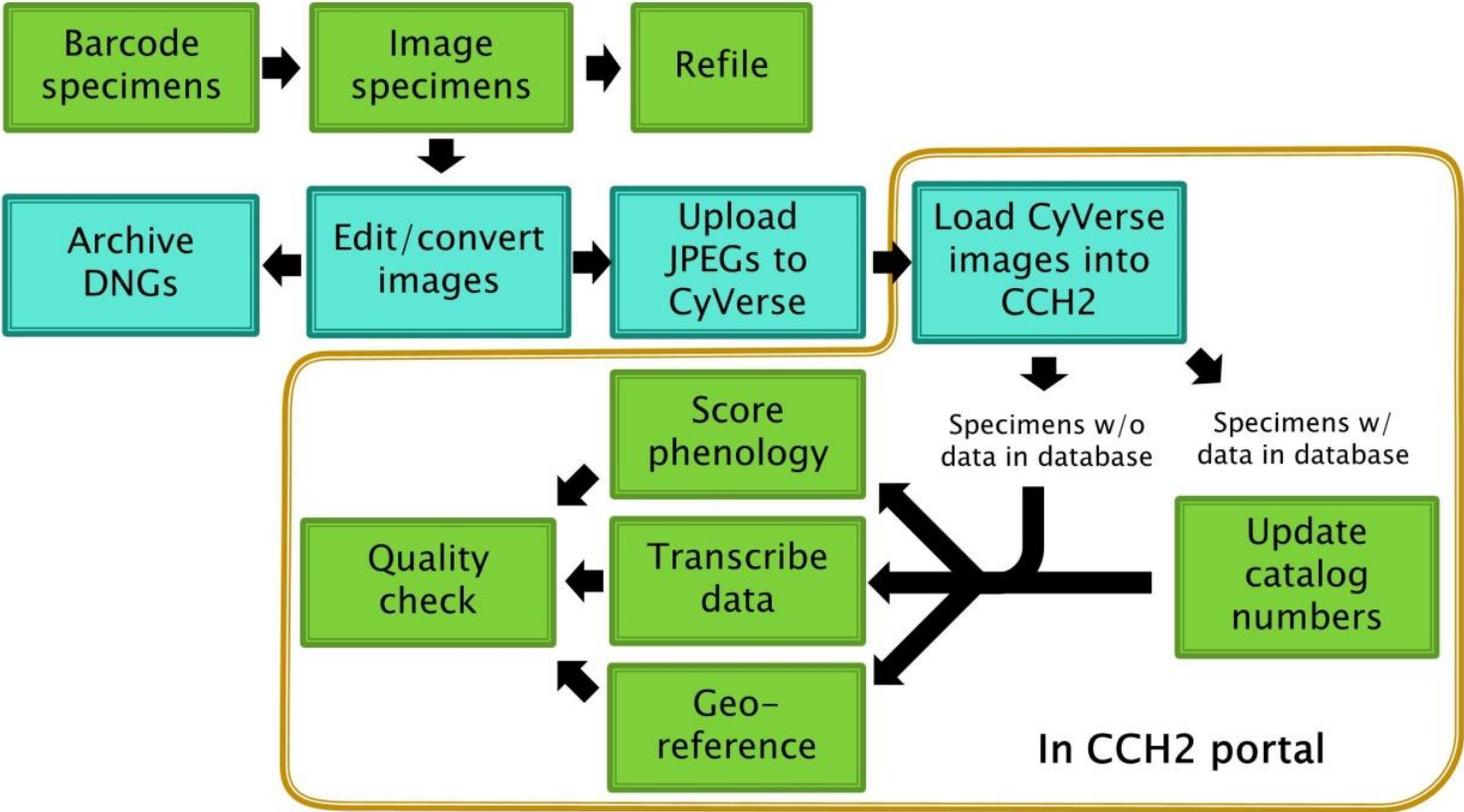
3. Tracking Workflow Progress

One of the most significant challenges of a digitization workflow is tracking the status of specimens and specimen images through the many steps of the digitization process. Here we offer some simple tools to aid in tracking workflow progress.

3.1 Cabinet Logs

Cabinet logs are diagrams that can be placed on the front of each cabinet to track which cubbies of that cabinet have been processed, by whom, and when they were processed. Each rectangle in the cabinet log diagram corresponds to a cubby in the actual cabinet. Once a worker has barcoded or imaged (if these steps are separated) a cubby of specimens, she or he should initial and date under the appropriate process in the corresponding cubby on the diagram.

Cubbies that are out-of-scope for this project (i.e., do not belong to one of the taxa listed in Table 1.1) should be crossed out by a supervisor when the cabinet logs are being placed unless the entire collection is being imaged.

Three example cabinet logs are provided in sections 3.1.1-3.1.3. Cabinet logs in sections 3.1.1 and 3.1.2 are appropriate for institutions that barcode and image in separate steps. A cabinet log such as that provided in section 3.1.3 can be used for institutions that barcode specimens at time of imaging.

3.1.1 Cabinet Log (barcoding and imaging as separate steps)

Cabinet Number: _____

1. Barcoded	Imaged	14. Barcoded	Imaged
2. Barcoded	Imaged	15. Barcoded	Imaged
3. Barcoded	Imaged	16. Barcoded	Imaged
4. Barcoded	Imaged	17. Barcoded	Imaged
5. Barcoded	Imaged	18. Barcoded	Imaged
6. Barcoded	Imaged	19. Barcoded	Imaged
7. Barcoded	Imaged	20. Barcoded	Imaged
8. Barcoded	Imaged	21. Barcoded	Imaged
9. Barcoded	Imaged	22. Barcoded	Imaged
10. Barcoded	Imaged	23. Barcoded	Imaged
11. Barcoded	Imaged	24. Barcoded	Imaged
12. Barcoded	Imaged	25. Barcoded	Imaged
13. Barcoded	Imaged	26. Barcoded	Imaged

Imaging complete: _____Date:_____

3.1.2 Cabinet Log (barcoding and imaging as separate steps, half-cabinet version)

Cabinet Number: _____

1. Barcoded	Imaged	8. Barcoded	Imaged
2. Barcoded	Imaged	9. Barcoded	Imaged
3. Barcoded	Imaged	10. Barcoded	Imaged
4. Barcoded	Imaged	11. Barcoded	Imaged
5. Barcoded	Imaged	12. Barcoded	Imaged
6. Barcoded	Imaged	13. Barcoded	Imaged
7. Barcoded	Imaged	14. Barcoded	Imaged

Imaging complete: _____Date:_____

3.1.3 Cabinet Log (barcoding and imaging in same step, half-cabinet version)

Cabinet Number: _____

1. Imaged	8. Imaged
2. Imaged	9. Imaged
3. Imaged	10. Imaged
4. Imaged	11. Imaged
5. Imaged	12. Imaged
6. Imaged	13. Imaged
7. Imaged	14. Imaged

Imaging complete: _____Date:_____

3.2 Imaging Log

To prevent duplication of work and potential loss of data, it is essential to track the status of each batch of images as it is created, processed, uploaded to CyVerse, loaded into the CCH2 portal, and moved to permanent institutional storage. An imaging log like that shown below can be used to document which processing steps have been completed for each batch of images. The imaging log should be printed and stationed next to the imaging station or **a digital version (e.g., Google Sheets document) can be curated**.

At the beginning of each imaging session, the imaging technician creates a new file on the computer and names it according to the date and the imager's name (e.g., 20190103_Pearson). Similarly, the imaging technician begins each imaging log entry with the date and his or her name. In this way, the processing technician/supervisor will know which batch of digital images corresponds to each imaging log entry. As she or he completes each processing step, the processing technician/supervisor will date and initial the corresponding column in the imaging log. Columns can be added or removed from the example imaging log as necessary. For example, Cal Poly added "Time In" and "Time Out" columns.

| Date	Imager(s)	Starting Cabinet + Cubby	Ending Cabinet + Cubby	Number of images	Processed (date/initials)	Uploaded to CyVerse	Linked to CCH2	Images archived

4. Imaging Station Setup

4.1 General Imaging Station Setup

A simplified diagram of the general imaging station setup is shown below. Camera setting recommendations for the Nikon D800E with AF-S 50 mm f/1.8D lens (see Section 4.2) are also provided.
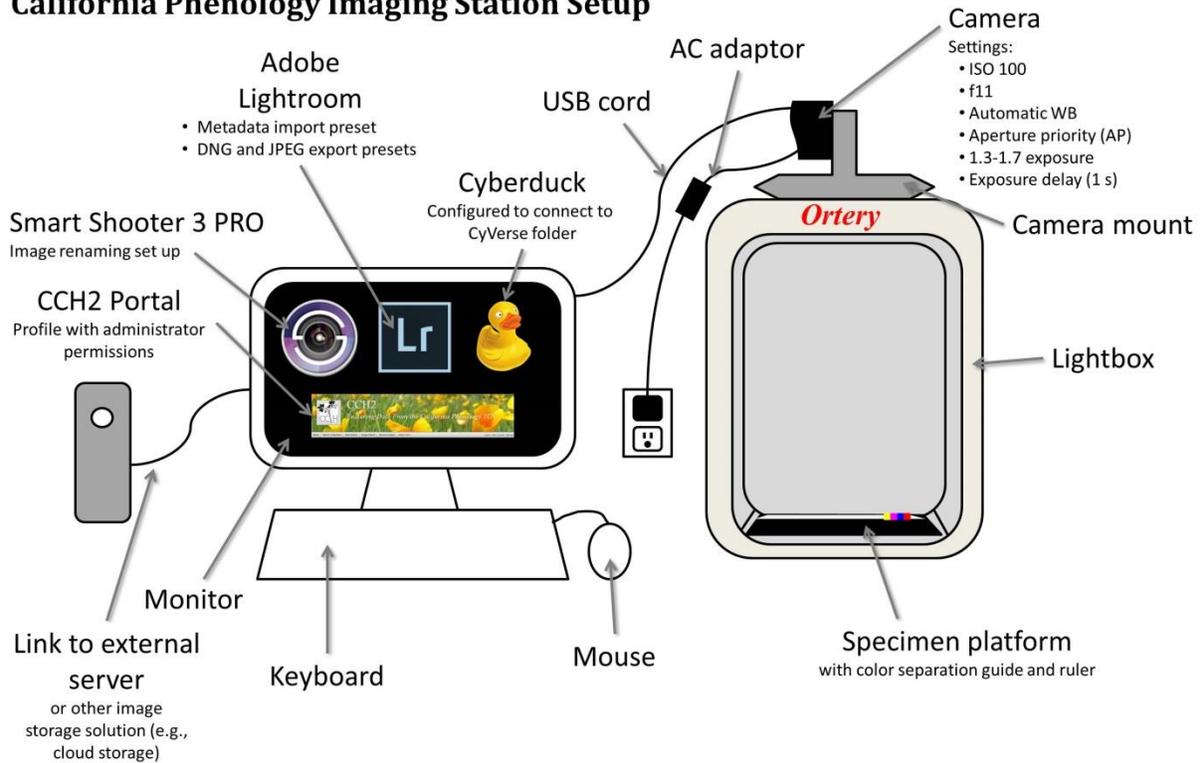
4.2 Equipment Recommendations

The following equipment was recommended for institutions that did not already have imaging stations at the start of the project. Many institutions were able to use preexisting equipment.

Item	Expected price	Source(s)
Nikon D800E 36.3 MP CMOS FX-Format Digital SLR Camera (if you cannot find this model, a D800 or D810 would also work)	$1000-1500	Amazon, etc. (note that this model is no longer supplied by Nikon, you will need to purchase from a third party)
Nikon AF-S FX NIKKOR 50mm f/1.8D Lens	$200	Best Buy, Amazon, etc.
Nikon EP-5B Power Supply Connector	$48	Amazon, etc.
Nikon EH-5b AC Adapter Note: it is possible to purchase off brand Nikon power supplies for much cheaper; however, there are some reports that these have caused the camera to malfunction; purchase at your own risk	$100	Amazon, etc.

Ortery Photosimile 50 lightbox	$2,100 + 300 shipping	Email Grant Grzecka <Ggrzecka@ortery.com>. Say you are with Cal Poly and copy Katie so he knows you're with us. Grant will need your billing and shipping address as well as how you would like to pay. They accept credit card, bank wire transfer, or check.
Symbol LS2208 General Purpose Barcode Scanner	$40-60	Amazon, etc.
Goose neck stand for Symbol Scanner LS2208	$10-30	Amazon, etc.
Tiffen Q-13 Color Separation Guide (Small)	$32	B&H Photo, Amazon, etc.
Imaging computer with 4+ GB of RAM and 500+ GB of internal storage, preferably with a solid state drive (SSD), reasonable graphics card, more than three USB ports (USB 3.0 preferred); Mac or PC OK	up to $1200	Best Buy, Costco, Amazon, etc. Examples: Lenovo IdeaCentre 510A, other Lenovo, Apple iMac
(If desktop computer) Good quality computer monitor		
(If desktop computer) Mouse and keyboard		
Ethernet cable	$5 (likely available for free through IT department)	
Smart Shooter 4 PRO	$195	Tether tools
Adobe Lightroom 6 or Adobe Lightroom Classic CC	$150	Adobe website or institutional license (check with your institution to see whether this is already available to you)
Camera Mount System (see Section 5)	~$60*	*Manufactured at Cal Poly and provided to partners free of charge
Specimen Backdrop (see Section 5)	~$7	Craft store or other source
Barcodes	see Section 6	

4.3 Imaging Software

We recommend the following software:

- **Smart Shooter 4 PRO:** This camera tethering software enables the user to (1) change camera settings on the computer screen (except for exposure delay mode), (2) set the focal point on a specimen and autofocus, (3) take images by clicking a button, and, most importantly, (4) automatically rename images according to their barcode number by clicking a button. Once the name policy is set (see imaging protocol), Smart Shooter 3 PRO will scan the images for barcodes and rename them each according to their barcode number.
- **Adobe Lightroom 6 or Classic CC (Adobe Lightroom CC alone will NOT work):** This software is used to process images and create derivative files. The processing steps include adding metadata (i.e., copyright information, including funding source and institution name), rotating images, cropping, enhancing sharpening, and exporting digital negative (DNG, archival format) and jpeg files for each image.

- **Cyberduck:** This free software is used to facilitate transfer of jpeg images into the CAP TCN community data folder in CyVerse. CyVerse will then make the images web-accessible and assign a URL to each image. The user will then run a process in the CCH2 portal that will link these image URLs to their appropriate specimen records in CCH2.

5. Custom Imaging Equipment

Institutions using the Ortery Photosimile 50 will need a camera mount system and specimen backdrop. The Cal Poly machine shop designed and manufactured camera mount systems for institutions that needed them at the beginning of the grant. The specifications for this camera mount system are provided in Section 5.1. Each institution should manufacture a specimen platform (Section 5.2).

5.1 Camera Mount System

The camera mount shown below was constructed for each institution that purchased an Ortery lightbox.
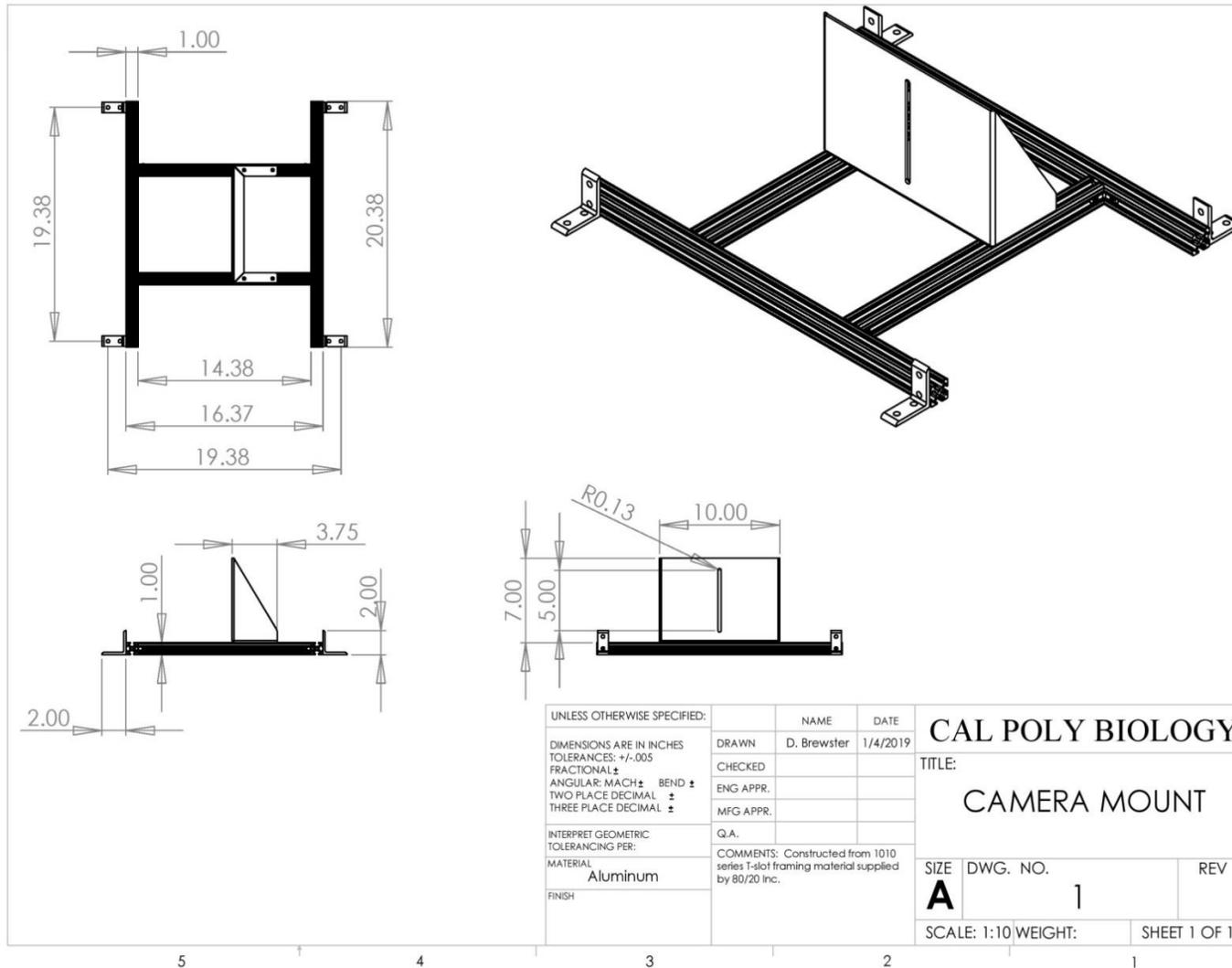
Installing the Camera Mount System

1. Unscrew the four white knobs from the top four corners of the lightbox.
2. Place the camera mount on the lightbox with the black rubber pad of the flat, upright piece facing left (see image below).
3. Use the black knobs to fasten the four corners of the mount to the lightbox (circled in Figure 5.1).
4. Mount the camera on the flat, upright piece by placing the bottom of the camera along the black rubber strip, fitting a black screw through the slot, and tightening it into place
5. Adjust the positioning of the camera to be able to fit an entire specimen and the color bar into the camera's field of view. You can accomplish this by:
    a. moving the camera up or down in the camera mount slot,
    b. using a 4 mm Allen wrench to loosen and tighten the black screws (see arrows on Figure 5.1) that hold the flat, upright piece to the aluminum bars
    c. and using a 2.5 mm Allen wrench to loosen and tighten small hex-head screws in the gussets (L-shaped connectors) that connect the aluminum bars to one another (see arrows on Figure 5.2).
6. Once you have tightened all the screws, double-check the field of view. Even slight adjustments can change the angle of the camera lens and greatly affect the resulting field of view.
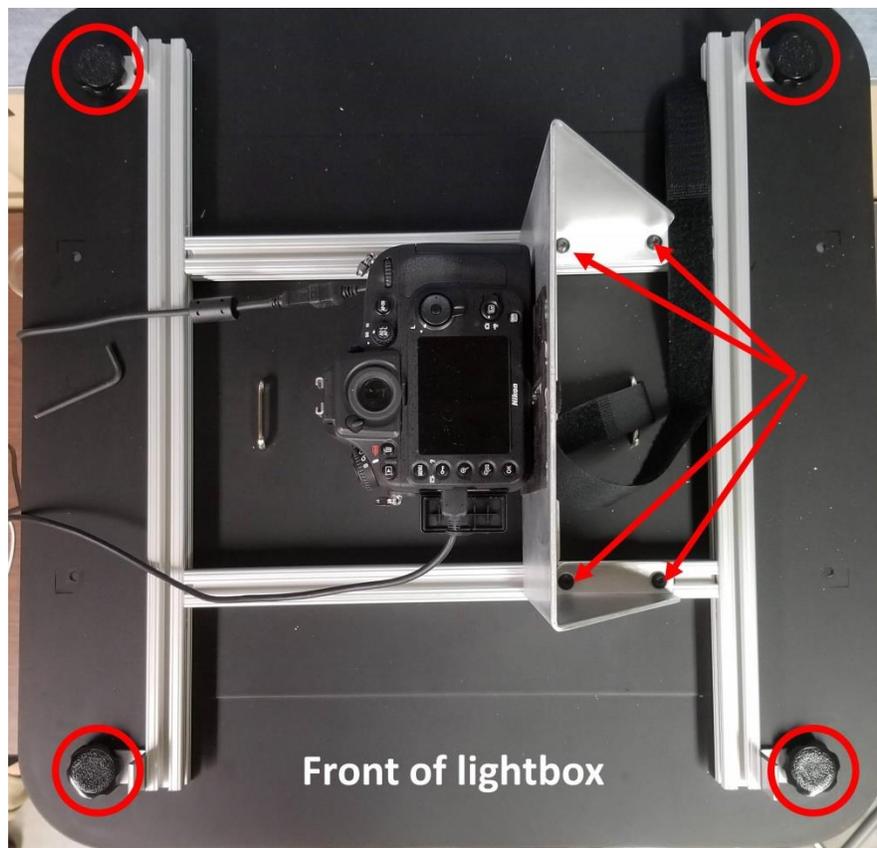
Figure 5.1 Top view of lightbox with installed camera mount. The knobs that secure the mount to the lightbox are circled in red, and the arrows indicate screws that can be tightened or loosened with a 4 mm Allen wrench to move the camera left or right.
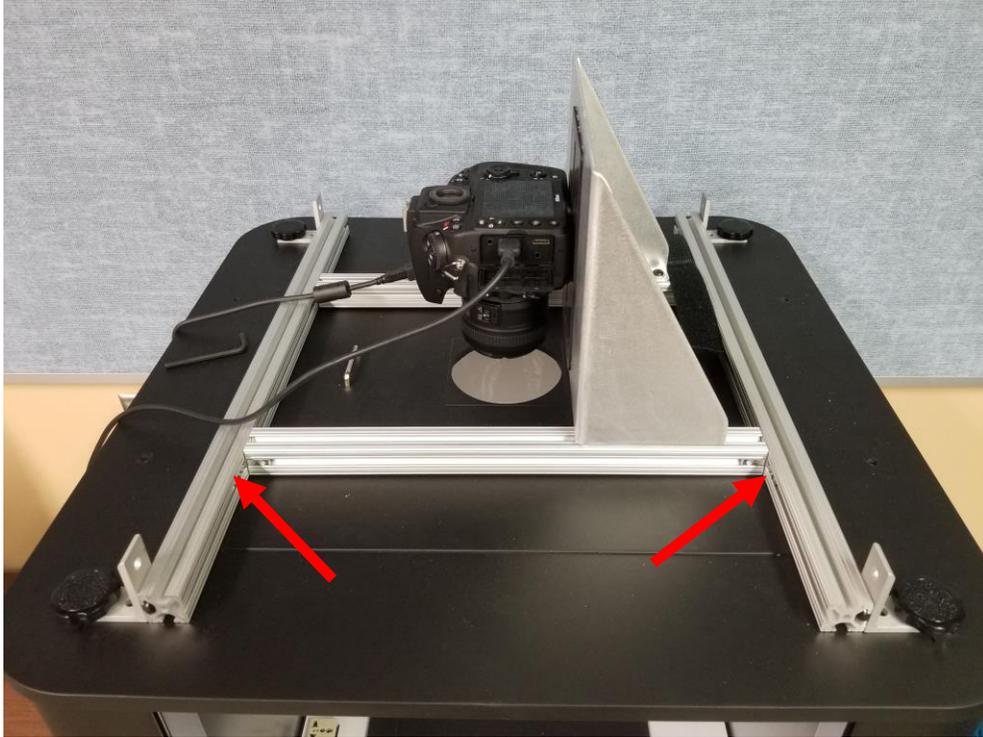
Figure 5.2 Angled view of top of lightbox with installed camera mount. The arrows indicate screws that can be tightened or loosened with a 2.5 mm Allen wrench to move the camera away from or toward the door of the lightbox.

5.2 Specimen Backdrop

(Adapted from Legler 2010, Assembling the Custom Components for Specimen Imaging, Consortium of Pacific Northwest Herbaria)

Supplies

- Black foamboard or fiberboard (approximately 1/8" thick) CLEANLY cut into the following pieces
    - 15" x 20"
    - 15" x 1.5"
    - 18.5" x 1.75"
- Double-sided tape or glue
- Razor blade or X-acto knife
- Metal ruler or other straight-edge for cutting
- Tiffen Q-13 color separation guide (see Section 4.1) or other color guide
- Color printout of your institution's logo, no taller than 2.5 centimeters

Assembly and Installation

1. Cut the foamboard into the necessary sizes, making sure that cuts are clean and straight. Use outside edges whenever possible, which are already straight.
2. Use double-sided tape to attach the 15" x 1.5" strip to one of the 15" ends of the large (15" x 20") sheet. Carefully align the outside edges of the strip with the outside edges of the large sheet. The edge will form the top of the holder.

3. Use double-sided tape to attach the 18.5" by 1.75" strip to the left side of the sheet and under the 15" strip at the top. The strip should tightly abut the previously attached strip, and its outside edge should align with the outside edge of the uncut sheet.
4. Cut the Tiffen color separation guide such that it will completely fit on the 1.5" strip at the top of the specimen backdrop. This will mean cutting off the text of the color control patch (see dashed line below). Do not discard either piece of the color control patch.

5. Cut the ruler at the top of the Tiffen color separation guide down to about 13 centimeters.
6. Use double-sided tape to affix the colored strip, the printout of your institution's logo, and the shortened ruler to the top 1.5" strip, as seen in the photo below.
7. Lay the specimen platform in the lightbox such that the raised strips are to the top and left. The color bar and ruler should be furthest away from the lightbox opening.
8. Before affixing the specimen platform to the lightbox floor with double-sided tape, install the camera mount system. You may need to adjust the position of the specimen platform as you adjust the camera mount so that your images are properly aligned.

6. Barcode Recommendations

All specimens digitized during this project will be labeled with barcodes to facilitate computer-readability of the resulting images and assign a quasi-unique identifier to each specimen. Barcodes are also beneficial for accelerating curation tasks such as preparing and receiving loans.

6.1 Barcode Formatting
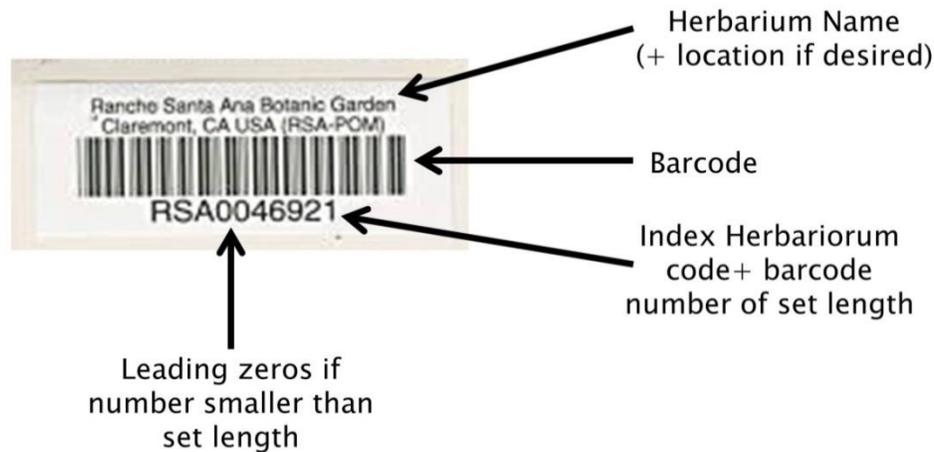
- **Above barcode:** name of institution (optional: location of institution)
- **Barcode:** "code 39" format, which includes letters and numbers
- **Below barcode:** barcode number, consisting of your Index Herbariorum (http://sweetgum.nybg.org/science/ih/) herbarium abbreviation followed by a unique number of a set number of digits.
  - Decide ahead of time how many digits will be in your barcode. Any numbers shorter than the set length of your barcode should be left-padded by zeros. For example, if your barcodes will include 9 digits (which means your institution can have a maximum of 999,999,999 specimens), and you have barcode number 38, your barcode should read: INST000000038. We recommend following this format so that the records can be sorted appropriately in Symbiota, Excel , or other management softwares.
  - We recommend including the IH abbreviation of your institution prior to the barcode number to maximize the "uniqueness" of this barcode number relative to other institutions'.

6.2 Barcode Sourcing

To order barcodes, email Sandra Schmidt <sschmidt@reliancebarcode.com>
In the email, make sure to provide:
- Label Quantity
- Text to be printed above Barcode (2 lines max)
- Number range and the way the number should appear. Specify the number of total digits you want (including leading zeros). For example, OBI100001 – OBI182000 (see below)

Cal Poly investigated purchasing barcodes from Reliance Barcode Solutions, Computype Inc, and Watson Label Solutions. Reliance Barcode Solutions was the most cost-effective at 2-4¢ per barcode. These labels are fully archival and have been used by other institutions including the Utah State University and Florida State University. They can be purchased by the roll or in printed sheets. Below is the estimate from Reliance for barcodes in rolls, which are expected to facilitate quicker barcode application than sheets.

Job Details	
Job Description:	LIB 2 x .611 Paper Rolls 2 x .611 Single labels on 60# Semi Gloss with Matte Lamination Finished in Rolls on Plastic Cores 1000 Labels Per Roll
Comments:	There will be an additional $35.00 Programming Fee UPS Ground shipping is not included in quote.

Component Details			
Component:	LIB 2 x .611 Paper Rolls		
Size:	2 X 0.611	Stock Description:	60 Semi Gloss with 757 Heavy Coat Weight 78# Line
Front Colors:	1	Color:	White
Back Colors:	0	BWT:	0
Bleed:	No	Thickness:	.0000

Quantity	Price	Per M
5,000	$215.75	$43.15
10,000	$335.00	$33.50
20,000	$525.00	$26.25
50,000	$1,122.50	$22.45
80,000	$1,740.00	$21.75
100,000	$2,100.00	$21.00

The quotes from Computype, Inc. and Watson Label Solutions are shown below, for reference:

Computype, Inc.

United States Currency (Base)

Line	Part Number	Description	Rev	Drawing
1	17131101	Digital Ink Jet B274/P236/L107 1.9x.65625 72/Sheet		

72 labels per sheet supplied 6-across x 12-down

Quantity	Unit Price	UM	Net Price	
5,000.00	0.05250	EA	262.50	USD
10,000.00	0.03281	EA	328.10	USD
25,000.00	0.02625	EA	656.25	USD
50,000.00	0.02263	EA	1,131.50	USD
100,000.00	0.02122	EA	2,122.00	USD
200,000.00	0.01791	EA	3,582.00	USD
350,000.00	0.01632	EA	5,712.00	USD
500,000.00	0.01516	EA	7,580.00	USD

FOB:Shipping Point	Terms: Net 30 Days	Ship Via:

Watson Label Solutions

General Description:

2" x 5/8" Single Code 39 Herbarium labels supplied on rolls of 1,000.

WLP Prod N° 02/S55N/AD	Lamination 1 mil matte Polypropylene		Facestock 3 mil matte white polypropylene		Adhesive 2 mil Permanent Acrylic	
Lbl Size W by Ht 2.000" X 0.625"	Tooling 122M	Sheets / Rolls Rolls		Sht Sz / Roll Width approx. 2.0"	Yield 130	Labels / Roll 1,000
Printing Process Digital Imaging	Symbology Code 39	Bar Code Density 9.4 cpi		Number of Characters 11	Check Digit None	
Environment Indoor	End Use 29 Herbarium			Form of Data Sequential		
Colors no		Unwind Direction #2		Missing Label % ZERO	Auto Applied No	

Cost Schedule:

Quantity	Cost/M	Extended Cost
5,000	$114.39	$571.95
10,000	$73.69	$736.90
15,000	$63.14	$947.10
25,000	$54.35	$1,358.75
50,000	$48.61	$2,430.50
75,000	$45.56	$3,417.00
100,000	$43.22	$4,322.00
105,000	$42.83	$4,497.15

One Time Charges:

Programming	Tooling
$150.00	$0.00

Additional Charges:

Proof Charge	Copy/Sequence Change
$0.00	$25.00 (Each if applicable)
Setup Charge	Special Packaging Cost
$0.00	$0.00

Unless otherwise requested, proofs will be sent by U.S. Mail and product shipment will be sent by FEDEX or UPS Ground and billed accordingly.

Special Instructions:

Customer to supply starting number and imprint information.
Customer to supply bill to and ship to information.

Note: Quantities ordered to be divisible by 5,000 in order to maximize material yield in providing rolls of 1,000.

7. Barcoding Protocol

Goals: *This protocol describes how to barcode specimens independently of any other digitization steps.*

(Some content adapted from the Florida State University barcoding protocol by Austin Mast)

1. Determine where you most recently left off barcoding by looking at the cabinet logs taped to the front of the herbarium cabinets (see Section 3.1). The last barcoded cubby will be indicated by initials and a date under the word "Barcoded" on that cubby, while the following cubbies in the diagram will not have initials or a date under "Barcoded".
   - Note that these steps are based off the Cal Poly (OBI) workflow for tracking the imaging status of the cabinets.
2. Remove all the specimens from the next cubby to be barcoded. Bring this cubby of specimens to your barcoding workstation.
3. Place the first/next specimen on a level surface by itself.
4. Apply a barcode 1/8 inch (NO CLOSER) from the bottom left corner of the first specimen (see image below).
   - DO NOT apply a barcode sticker on top of anything else (e.g., herbarium stamp, piece of the specimen, or a label).
   - If there is not space in the bottom left corner, place the barcode somewhere else along the bottom of the specimen. If there is not space at the bottom of the specimen, you may use the top edge of the specimen.
   - If a sheet has an indication that there are two different species on a single sheet, set this sheet aside and notify a supervisor, making sure to record the folder in which the specimen had been filed (Supervisor: see note at end)
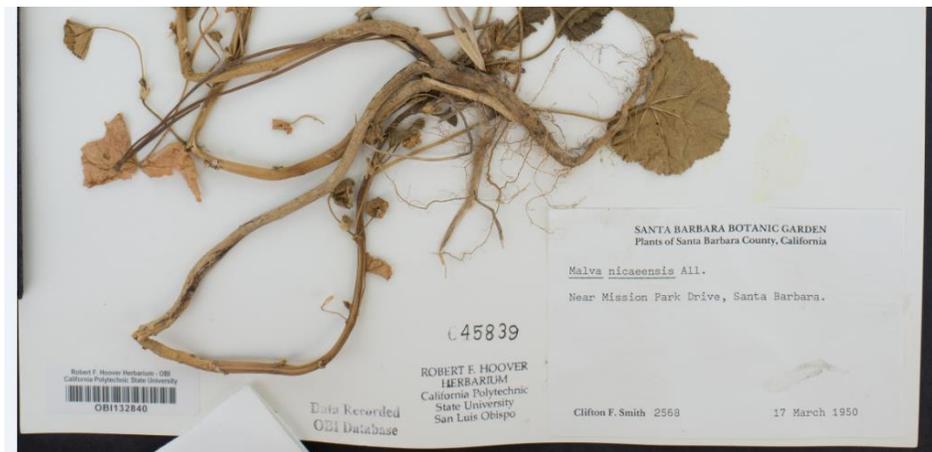
5. Repeat steps 3 and 4 for every specimen in the stack
6. Put away the cubby of specimens. Write your name and the date under the word "Barcoded" on the corresponding cubby on the cabinet diagram.
7. Obtain a new cubby of specimens, keeping track of your progress on the cabinet diagram taped to the outside of the cabinet.

Supervisor Notes

Specimens with multiple specimens on a single sheet should be barcoded once for every specimen on that sheet. Then, when imaging, one image will be taken for each barcode on that sheet (i.e., 3 barcodes = 3 identical images, each with a different image name corresponding to one of the barcodes on the sheet).

Note that the program we are using to rename images at the time of imaging, Smart Shooter 3 will not be able to automatically name specimens with multiple barcodes on the sheet! Therefore, during imaging, the technicians should make a note of which barcodes belong to this anomalous specimen, they will have to manually rename the images accordingly.

Specimens that consist of multiple sheets or items should be treated as a set of botanical duplicates, with each sheet or item receiving its own barcode. Each sheet or item should then have a corresponding record in the database.

8. Imaging Protocol

Goals: This protocol describes how to image previously barcoded specimens using the Ortery lightbox setup, a Nikon D800E, and Smart Shooter 4.

1. Turn on the lightbox using the switch labeled "Front & Rear." Do not turn on the "Back" switch.
2. Ensure that the camera is correctly plugged in to a power source and the computer. The cord that connects to the computer is plugged in to the left side of the camera, and the cord that connects to the power source is plugged in to the right side of the camera, where the battery pack usually is (see image below).

3. Turn on the computer (if necessary) and camera, in that order. The camera's "on" switch is located to the right of the lens on the top of the camera (circled in photo above).
4. Remove the camera lens cap.
5. Ensure that the dial on the left side of the camera body, below the lens, to AF and the switch on the lens, if present, is set to M/A (see photo below).

6. Start an Imaging Log entry by writing the date, your name, and the starting cabinet/cubby numbers in the appropriate fields on the Imaging Log (see Section 3.2).

7. Create a folder on the desktop with the date (YYYYMMDD) and your last name separated by an underscore. Include a zero before single-digit days or months (e.g., if Katie Pearson made a file on October 1st, 2020, the filename should be 20201001_Pearson).

8. Open the application Smart Shooter 4. If you have already turned on the camera, it should automatically be connected (the "Connect" button will be greyed out, as shown below). If not, click the "Detect" button, then the "Connect" button.

If the Camera Controls toolbar is not visible, click "Display" in the menu bar at the top of your screen and click "Camera Controls" in the dropdown menu.

If the camera does not connect, close Smart Shooter 4, turn off the camera, and unplug the camera from the computer. Then plug the camera in to the computer, turn on the camera, and re-open Smart Shooter 4.

9. Press the Cmd and comma keys simultaneously (PC: Ctrl and comma) or, in the menu bar at the top of your screen, click "Smart Shooter 4" followed by "Preferences" (PC: "File" followed by "Options").

10. In the Preferences (PC: Options) window, open the General tab, if it isn't already open.

11. In the box labeled Photo Download Directory, click "Browse" and navigate to the folder that you created in step 7. Click "Open."

12. Open the "Name Policy" tab. Ensure that the text in the "Filename Expression field" is "[Z]" with no quotation marks and no spaces before or after.

13. Open the "Barcode" tab. Ensure that the "Autoscan for Barcodes" box is checked.

14. Click "OK" to close the Preferences (PC: Options) window.
15. Ensure that all the camera settings match those shown in the example below (but see first time set up note). Select the correct values from the dropdown menus as necessary. Don't worry about changing the greyed-out fields. You will not be able to change these values.

Aperture:	11
Shutter Speed:	30
ISO:	100
Exposure ±:	1.7
Quality:	RAW
Program Mode:	Aperture Priority
Metering Mode:	Matrix
White Balance:	AUTO
Focus Mode:	AF Single
Drive Mode:	Single Frame
Mirror Lockup:	

First time set up note:
- Appropriate values of ISO and Exposure may differ depending on your ambient lighting conditions. You will want to experiment with what settings make clear and relatively bright (but not overexposed) images.
  i. Lower values of ISO means that the camera will be less sensitive to light. If you find that your images are **overexposed** (i.e., too bright), decrease this value. If you find that your images are **underexposed** (i.e., too dark), increase this value.
  ii. Lower values of exposure means that the shutter is open for a shorter amount of time, letting in less light. If you find that your images are **overexposed** (i.e., too bright), decrease this value. If you find that your images are **underexposed** (i.e., too dark), increase this value.
- You can also experiment with Shutter Speed. The longer the shutter speed, the brighter the image will be. We have found that it can be helpful to try changing the Program Mode to Manual and selecting 1/13 for Shutter Speed, especially when imaging small or thin specimens, like grasses.
16. Click the checkbox next to "Enable" in the Live View portion of the Camera Control toolbar (indicated in the photo below). You should now be able to see camera's view in the viewscreen. Increase the size of the Preview window by dragging the left edge of the Preview box left. The image will look grainy on the screen, but don't worry, the pictures will not!

| Detect | Disconnect | Connect |
| Video | Auto Focus | Shoot |

Power
Live View
☑ Enable
☐ Zoom
☐ DOF
Storage
Disk
Settings
A/C

17. Determine where imaging was most recently left off by looking at the Cabinet Logs attached to the herbarium cabinet doors (examples in Section 3.1).
    - The last imaged cubby will be indicated by initials and a date under the word "Imaged," while the cubbies that follow on the diagram will not have initials or a date.
18. Remove all the specimens from the next cubby to be imaged and bring them to your workstation, <u>taking care to initial and date on the corresponding cubby of the cabinet log.</u>
19. Place the specimen inside the lightbox, aligning the top left corner of the specimen to the inside corner of the raised pieces of foamboard (see picture below).
    - The ruler and color guide should be at the top of the specimen. If the label is on the bottom right corner of the specimen, like most are, the label should be closest to you and on your right side.

Image credit: Ben Legler, Consortium of Pacific Northwest Herbaria

20. Make sure the entire specimen, ruler, and color guide are visible in the viewscreen and that the specimen does not appear crooked. If the specimen does not appear aligned, the specimen platform or camera may have been jostled or shifted. Adjust the camera and/or specimen platform if necessary.
    - Do NOT untape the specimen platform or unscrew the camera from its mount. Contact a supervisor if you cannot fix the problem without doing so.

21. Adjust the focal point by clicking and dragging the blue square in the Preview window (indicated by the arrow below). The best focus can be achieved by selecting a focal point that is relatively flat and contains mostly vegetation and/or text with little white space. Some examples of good focal points are shown below the screenshot.
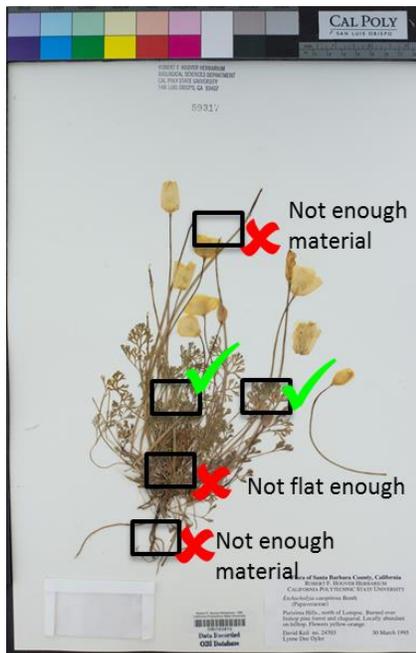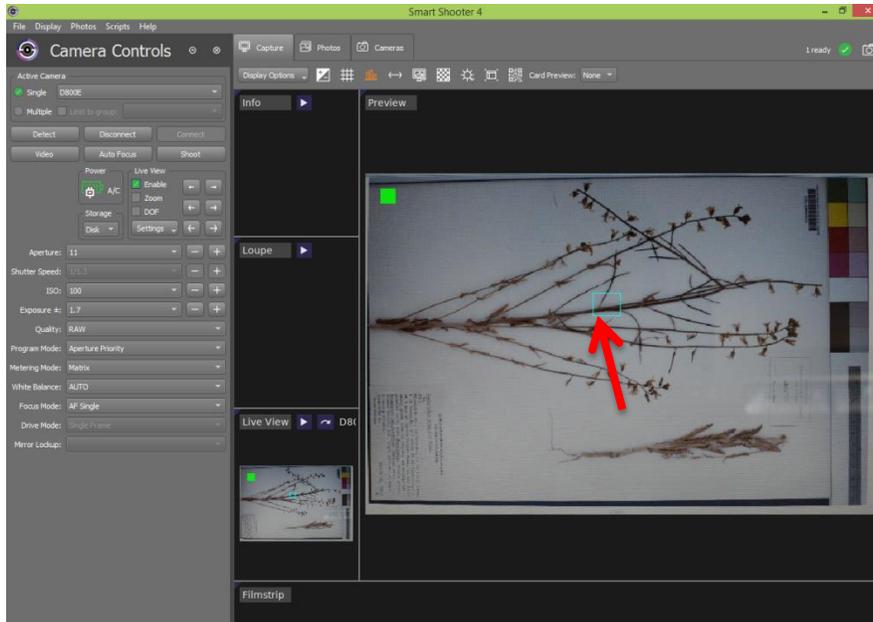
22. Click the "Auto Focus" button once you are satisfied with your choice of focal point.
23. Click the "Shoot" button in Smart Shooter 4.
24. Uncheck the box next to "Enable."
25. View the image you just captured. It should have appeared on the screen after you unchecked "Enable." If not, click the appropriate image in the Filmstrip window at the bottom.

26. Check the quality of the image you just took.
    - Is the whole label and barcode visible?
    - Is the specimen straight and aligned with the edges of the specimen platform?
    - Is the focus sharp? Place your mouse over several parts on the specimen to zoom in and check the focus.
        i. If there are any problems with focus:
            a. Return to the Display tab.
            b. Re-focus the camera by repeating steps 20-21.
            c. Instead of clicking "Shoot", click the Photos tab (circled below) and right click the name of the problematic image.
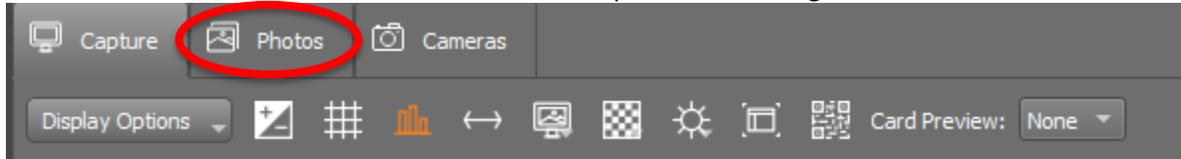
            d. Select "Reshoot with same name" from the dropdown menu and repeat steps 23-25 with this new photo.
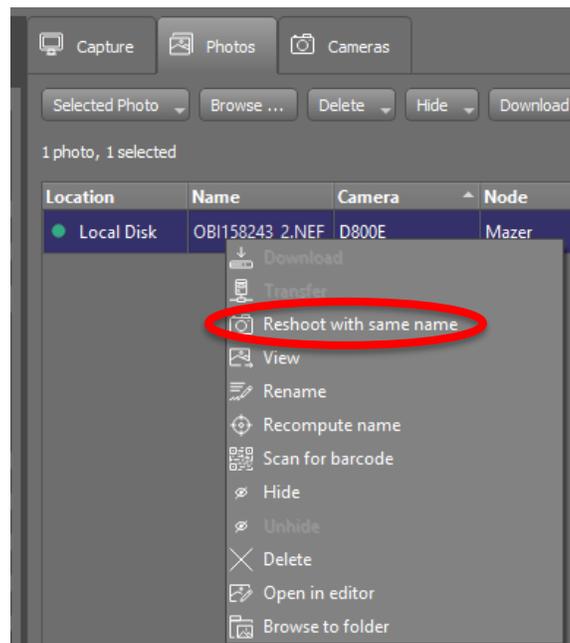
27. If you are happy with the focus, switch the camera from Autofocus (AF) mode to Manual (M) mode by flipping the switch left side of the camera body. Do NOT touch the M/A / M switch on the lens.
28. Carefully remove the specimen from the lightbox and place it in your "imaged" pile or to the right of the imaging station.
29. Get a new specimen and place it in the lightbox like you did in step 19.
    - For the remaining specimens in this stack, you do NOT need to refocus and check for quality! (i.e., you can skip steps 21-27)
30. Image the remaining specimens in your stack by placing each specimen in the lightbox individually and clicking "Shoot." Make sure to quickly check each image for alignment and focus.

31. When you have finished imaging your stack, ensure that it is in the correct order (i.e., alphabetical according to genus, then species. Rearrange if necessary.
32. Return the stack of imaged specimens to its cubby.
33. Switch the camera back to Autofocus (AF) by flipping the switch on the camera body.
34. Repeat steps 17-32, switching to Autofocus at the beginning of each cubby and checking the quality of the first specimen of each cubby as instructed.
35. At the end of your shift, navigate to the Photos tab.
36. Check that all the images have names in the expected format: the institution code of your collection followed by a set number of digits (e.g., OBI100259).
    - **Note:** Pay particular attention to barcodes that are longer than expected (e.g., OBI100259_1). This may indicate that Smart Shooter was unable to recognize the barcode in that image or that the image is a duplicate of the same specimen.
    - If any images are not named correctly:
        i. View the image by right clicking on it and selecting "Open in editor" in the dropdown menu. If no editor opens, click "View".
        ii. Rename the image according to the barcode by right clicking on the record in the Smart Shooter 4 table, selecting "Rename" in the dropdown menu, and manually entering the barcode number. Make sure to keep the .NEF file extension.
        iii. Double check that you have entered the entire barcode correctly, including the institution abbreviation (e.g., OBI) at the beginning.
37. In the Photos tab, randomly select one of the images in the table. Double click to open it in the Display tab.
38. Check that the barcode number in the image matches the image name.
39. Repeat steps 37-38 for at least four additional specimens.
40. Turn off the camera and lightbox and replace the lens cap on the camera.
41. Complete your Imaging Log entry by indicating your ending cabinet/cubby and the number of specimens you imaged. You can find the number of images you created by right clicking on the folder into which you imaged the specimens, clicking Get Info (PC: Properties), and looking for the number of files.

9. Combined Barcoding & Imaging Protocol

Goals: This example protocol describes how to barcode and image specimens using the Ortery lightbox setup and Smart Shooter. For specimens that already have data in the database, the assigned barcode numbers are added to their respective specimen records in CCH2.

1. Turn on the lightbox using the switch labeled "Front & Rear." Do not turn on the "Back" switch.
2. Ensure that the camera is correctly plugged in to a power source and the computer. The cord that connects to the computer is plugged in to the left side of the camera, and the cord that connects to the power source is plugged in to the right side of the camera, where the battery pack usually is (see image below).

3. Turn on the computer (if necessary) and camera, in that order. The camera's "on" switch is located to the right of the lens on the top of the camera (circled in photo above).
4. Remove the camera lens cap.
5. Ensure that the dial on the left side of the camera body, below the lens, to AF and the switch on the lens, if present, is set to M/A (see photo below).

6. Start an Imaging Log entry by writing the date, your name, and the starting cabinet/cubby numbers in the appropriate fields on the Imaging Log (see Section 3.2).

7. Create a folder on the desktop with the date (YYYYMMDD) and your last name separated by an underscore. Include a zero before single-digit days or months (e.g., if Katie Pearson made a file on October 1st, 2020, the filename should be 20201001_Pearson).

8. Open the application Smart Shooter 4. If you have already turned on the camera, it should automatically be connected (the "Connect" button will be greyed out, as shown below). If not, click the "Detect" button, then the "Connect" button.

If the Camera Controls toolbar is not visible, click "Display" in the menu bar at the top of your screen and click "Camera Controls" in the dropdown menu.

If the camera does not connect, close Smart Shooter 4, turn off the camera, and unplug the camera from the computer. Then plug the camera in to the computer, turn on the camera, and re-open Smart Shooter 4.

9. Press the Cmd and comma keys simultaneously (PC: Ctrl and comma) or, in the menu bar at the top of your screen, click "Smart Shooter 4" followed by "Preferences" (PC: "File" followed by "Options").

10. In the Preferences (PC: Options) window, open the General tab, if it isn't already open.

11. In the box labeled Photo Download Directory, click "Browse" and navigate to the folder that you created in step 7. Click "Open."

12. Open the "Name Policy" tab. Ensure that the text in the "Filename Expression field" is "[Z]" with no quotation marks and no spaces before or after.

13. Open the "Barcode" tab. Ensure that the "Autoscan for Barcodes" box is checked.

14. Click "OK" to close the Preferences (PC: Options) window.
15. Ensure that all the camera settings match those shown in the example below (but see first time set up note). Select the correct values from the dropdown menus as necessary. Don't worry about changing the greyed-out fields. You will not be able to change these values.

First time set up note:
- Appropriate values of ISO and Exposure may differ depending on your ambient lighting conditions. You will want to experiment with what settings make clear and relatively bright (but not overexposed) images.
    i. Lower values of ISO means that the camera will be less sensitive to light. If you find that your images are **overexposed** (i.e., too bright), decrease this value. If you find that your images are **underexposed** (i.e., too dark), increase this value.
    ii. Lower values of exposure means that the shutter is open for a shorter amount of time, letting in less light. If you find that your images are **overexposed** (i.e., too bright), decrease this value. If you find that your images are **underexposed** (i.e., too dark), increase this value.
- You can also experiment with Shutter Speed. The longer the shutter speed, the brighter the image will be. We have found that it can be helpful to try changing the Program Mode to Manual and selecting 1/13 for Shutter Speed, especially when imaging small or thin specimens, like grasses.
16. Click the checkbox next to "Enable" in the Live View portion of the Camera Control toolbar (indicated in the photo below). You should now be able to see camera's view in the viewscreen. Increase the size of the Preview window by dragging the left edge of the Preview box left. The image will look grainy on the screen, but don't worry, the pictures will not!

17. Open a browser window and navigate to the CCH2 portal (http://www.cch2.org).
18. Log in to your account and click My Profile followed by the Specimen Management tab, then the Robert F. Hoover herbarium link.
19. Select "Edit Existing Occurrence Records" from the Data Editor Control Panel. This will open the CCH2 Record Search Form (see screenshot below).

20. Arrange the windows on your computer screen so that the Smart Shooter window and browser window are side-by-side.
21. Determine where imaging was most recently left off by looking at the Cabinet Logs attached to the herbarium cabinet doors (examples in Section 3.1).
    - The last imaged cubby will be indicated by initials and a date under the word "Imaged," while the cubbies that follow on the diagram will not have initials or a date.
22. Remove all the specimens from the next cubby to be imaged and bring them to your workstation, taking care to initial and date on the corresponding cubby of the cabinet log.
23. Place the first/next specimen on a level surface by itself.
24. Apply a barcode 1/8 inch (NO CLOSER) from the bottom left corner of the first specimen (see following image).
    - DO NOT apply a barcode sticker on top of anything else (e.g., herbarium stamp, piece of the specimen, or a label).
    - If there is not space in the bottom left corner, place the barcode somewhere else along the bottom of the specimen. If there is not space at the bottom of the specimen, you may use the top edge of the specimen.
    - If a sheet has an indication that there are two different species on a single sheet, set this sheet aside and notify a supervisor, making sure to record the folder in which the specimen had been filed.
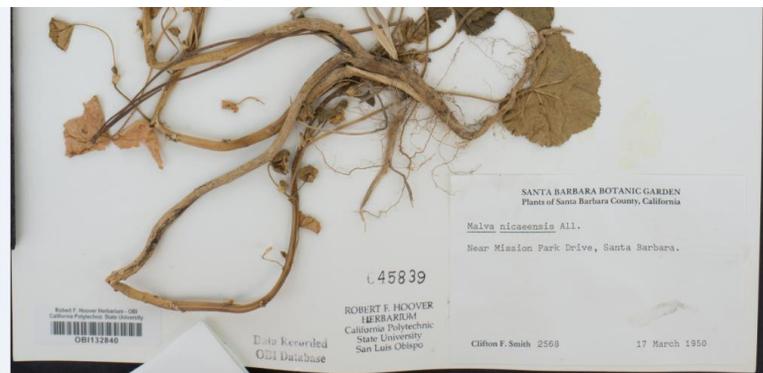
25. Look for a stamped number ("accession number") on the specimen. This is sometimes (but not always) located near the Robert F. Hoover Herbarium stamp. Some examples are shown below.
   - If a stamped number exists, continue to step 26.
   - If a stamped number does not exist, proceed to step 28.
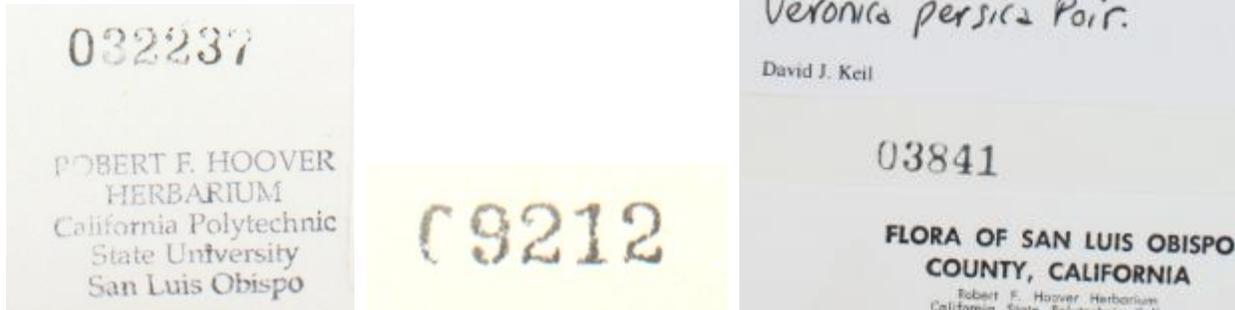
26. Look for a stamp on the specimen that says "Data Recorded OBI Database."
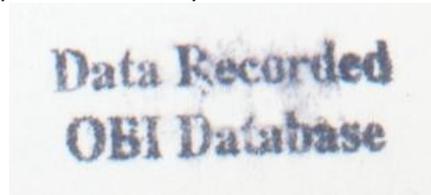
   - If there is such a stamp on the specimen, continue to step 27.
   - If you do not find this stamp on the specimen, proceed to step 29.

TIP: You can zoom in to the image by pressing Command (Mac) or Control (Windows) and clicking on the image where you want to zoom in. Alternatively, you can hold Shift, click on the area where you want to zoom in, and move the mouse up (to zoom in) or down (to zoom out).

27. Enter the stamped number into the Other Catalog Numbers field. Do not include leading zeros (e.g., if the stamp is 01499, enter 1499). Click Display Editor.
   - If no record is returned, double check that you entered the accession number correctly into the Other Catalog Numbers field and that there are no extra spaces before or after the numbers you typed. If the number is correct, proceed to step 28.
   - If a record is returned, check that the data on the specimen record match the data on the label of the specimen in front of you, particularly collector, collector number, and date.
      i. If these data match, place your cursor in the Catalog Number field (top left) and scan the barcode of the specimen in front of you. The barcode number will then appear in this field. Press Tab on your keyboard, followed by Enter. Proceed to step 29.
      ii. If these data do NOT match, notify your supervisor, change the processing status of the problematic record to "Expert required", and proceed to step 28.

TIP: To re-open the Record Search Form after you have performed a search, click the magnifying glass icon at the top right side of the specimen record.

28. In the CCH2 Record Search Form, enter the last name of the collector preceded by a percent sign (%), the collector number, and the date (in YYYY-MM-DD format) into the top three fields (see example below) and click Display Editor.

- If no record is returned, double check that you entered data correctly into the appropriate fields. If everything looks correct, continue to step 29.
- If a record is returned, check that the data on the specimen record match the data on the label of the specimen in front of you, particularly collector, collector number, and date.
    - i. If these data match, place your cursor in the Catalog Number field (top right) and scan the barcode of the specimen in front of you. The barcode number will then appear in this field. Press Tab on your keyboard, followed by Enter. Proceed to step 29.
    - ii. If these data do NOT match, notify your supervisor, change the processing status of the problematic record to "Expert required", and proceed to step 29.

29. Place the specimen inside the lightbox, aligning the top left corner of the specimen to the inside corner of the raised pieces of foamboard.
- The ruler and color guide should be at the top of the specimen. If the label is on the bottom right corner of the specimen, like most are, the label should be closest to you and on your right side.

Image credit: Ben Legler, Consortium of Pacific Northwest Herbaria

30. Make sure the entire specimen, ruler, and color guide are visible in the viewscreen and that the specimen does not appear crooked.
- If the specimen does not appear aligned, the specimen platform or camera may have been jostled or shifted. Adjust the camera and/or specimen platform if necessary. Do NOT untape the specimen platform or unscrew the camera from its mount. Contact a supervisor if you cannot fix the problem without doing so.

31. Adjust the focal point by clicking and dragging the blue square in the Preview window (indicated by the arrow below). The best focus can be achieved by selecting a focal point that is relatively flat and contains mostly vegetation and/or text with little white space. Some examples of good focal points are shown below the screenshot.
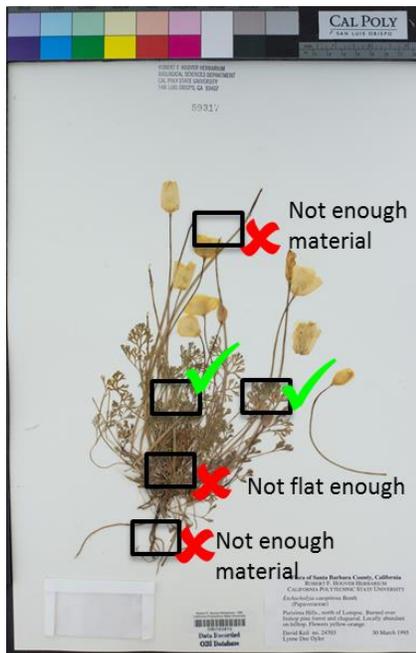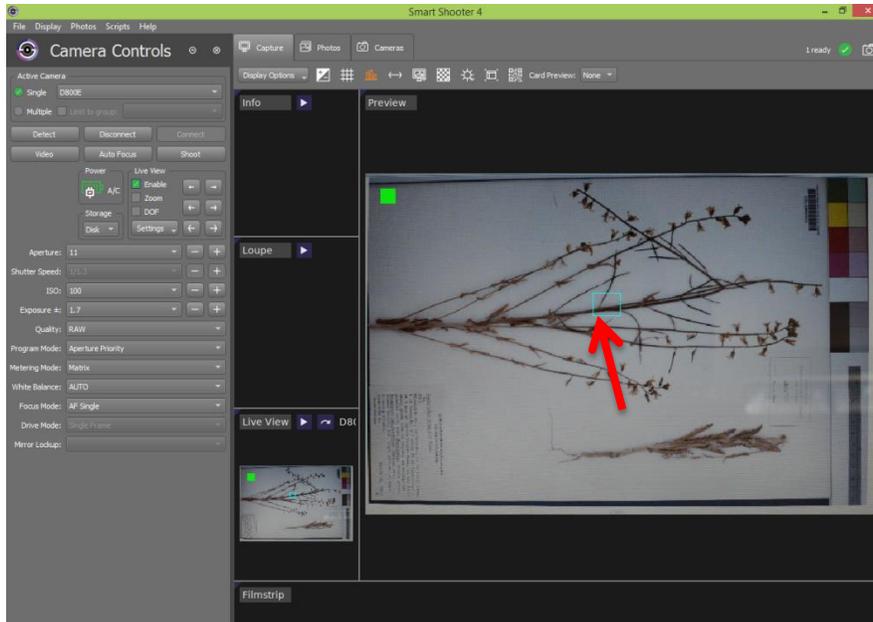
32. Click the "Auto Focus" button once you are satisfied with your choice of focal point.
33. Click the "Shoot" button in Smart Shooter 4.
34. Uncheck the box next to "Enable."
35. View the image you just captured. It should have appeared on the screen after you unchecked "Enable." If not, click the appropriate image in the Filmstrip window at the bottom.

36. Check the quality of the image you just took.
    - Is the whole label and barcode visible?
    - Is the specimen straight and aligned with the edges of the specimen platform?
    - Is the focus sharp? Place your mouse over several parts on the specimen to zoom in and check the focus.
        i. If there are any problems with focus:
            e. Return to the Display tab.
            f. Re-focus the camera by repeating steps 31-32.
            g. Instead of clicking "Shoot", click the Photos tab (circled below) and right click the name of the problematic image.

            h. Select "Reshoot with same name" from the dropdown menu and repeat steps 35-36 with this new photo.
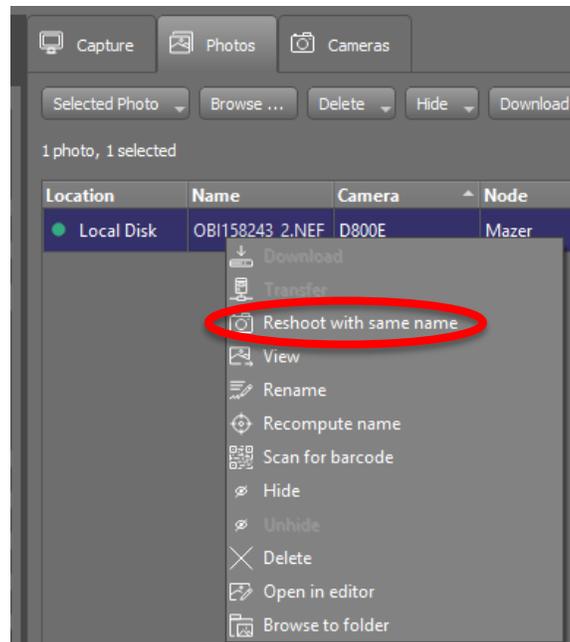
37. If you are happy with the focus, switch the camera from Autofocus (AF) mode to Manual (M) mode by flipping the switch left side of the camera body. Do NOT touch the switch on the lens.
38. Carefully remove the specimen from the lightbox and place it in your "imaged" pile or to the right of the imaging station.
39. Get a new specimen and place it in the lightbox like you did in step 29.
    - For the remaining specimens in this stack, you do NOT need to refocus and check for quality! (i.e., you can skip steps 31-37)
40. Image the remaining specimens in your stack by placing each specimen in the lightbox and clicking "Shoot." Make sure to quickly check each image for alignment and focus.

41. When you have finished imaging your stack, ensure that it is in the correct order (i.e., alphabetical according to genus, then species. Rearrange if necessary.
42. Return the stack of imaged specimens to its cubby.
43. Switch the camera back to Autofocus (AF) by flipping the switch on the camera body.
44. Repeat steps 23-43, switching to Autofocus at the beginning of each cubby and checking the quality of the first specimen of each cubby as instructed.

At the end of your shift:

45. Navigate to the Photos tab.
46. Check that all the images have names in the expected format: the institution code of your collection followed by a set number of digits (e.g., OBI100259).
    - If any images are not named correctly:
        iv. View the image by right clicking on it and selecting "Open in editor" in the dropdown menu. If no editor opens, click "View".
        v. Rename the image according to the barcode by right clicking on the record in the Smart Shooter 4 table, selecting "Rename" in the dropdown menu, and manually entering the barcode number. Make sure to keep the .NEF file extension.
        vi. Double check that you have entered the entire barcode correctly, including the institution abbreviation (e.g., OBI) at the beginning.
47. In the Photos tab, randomly select one of the images in the table. Double click to open it in the Display tab.
48. Check that the barcode number in the image matches the image name.
49. Repeat steps 47-48 for at least four additional specimens.
50. Turn off the camera and lightbox and replace the lens cap on the camera.
51. Complete your Imaging Log entry by indicating your ending cabinet/cubby and the number of specimens you imaged. You can find the number of images you created by right clicking on the folder into which you imaged the specimens, clicking Get Info (PC: Properties), and looking for the number of files.

Supervisor Notes:

Specimens with multiple specimens on a single sheet should be barcoded once for every specimen on that sheet. Then, when imaging, one image will be taken for each barcode on that sheet (i.e., 3 barcodes = 3 identical images, each with a different image name corresponding to one of the barcodes on the sheet).

Note that the program we are using to rename images at the time of imaging, Smart Shooter will not be able to automatically name specimens with multiple barcodes on the sheet! Therefore, during imaging, the technicians should make a note of which barcodes belong to this anomalous specimen, they will have to manually rename the images accordingly.

Specimens that consist of multiple sheets or items should be treated as a set of botanical duplicates, with each sheet or item receiving its own barcode. Each sheet or item should then have a corresponding record in the database.

10. Image Processing

10.1 Image Processing Protocol

Goals: This protocol should be used by supervisors or trained technicians to process folders of raw images. Processing steps include adding metadata, cropping, adjusting highlights and light values, adjusting sharpening, and exporting raw images as DNG and JPEG files.

Notes
- **Instructions are based on a Mac OSX; Windows/PC directions are provided in parentheses.**
- **Some material adapted from Skema & Barber 2018**
- **Once the supervisor/technician is trained and has practiced this protocol, s/he should refer to the Image Processing Checklist (section 10.2) when processing images.**

1. Create a folder on the desktop that mimics the name of the folder of images you will process plus "_Processed" (e.g., 20181001_Pearson_Processed). Within this folder, create a subfolder called "JPEGs."
2. Open Adobe Lightroom.
3. Click the Import button at the bottom left of the Lightroom window.
4. Drag the folder of images you wish to process from its location (e.g., on the desktop) into the Lightroom library. (Or navigate to the folder in the Source menu on the left side of the window.)
5. In the menu on the right side of the window, click the triangle next to "Apply During Import." Select the preset metadata settings from the dropdown menu.
    First time set-up note:
    Upon first use, set up a metadata standard for your institution that can be applied to all images during processing by doing the following:
    a. From the metadata settings in "Apply During Import," select "New" from the dropdown menu.
    b. Name the Metadata preset something recognizable (e.g., your herbarium acronym).
    c. Under the heading "IPTC Copyright," type your herbarium/institution name in the "Copyright" box followed by "- funded by National Science Foundation award number" followed by your NSF award number.
    d. Select "Copyrighted" in the Copyright Status dropdown list.
    e. In the Rights Usage Terms field, enter "CC BY-NC-SA." This means that users of your images must credit your institution when using the image, the image cannot be used for commercial means, and the image and its derivatives must be shared using a copyright license that is no more restrictive than the copyright license you provide.
    f. Click "Create" (or "Done"). Now you should be able to select that metadata preset in the Metadata drop down menu, and that copyright will be applied to every photo you import into your catalog.
6. Make sure all of the images in the folder you wish to process are checked (upper left corner of each thumbnail), then click the "Import" button at the bottom right corner of the window.
7. Select all the images in the resulting Library page by clicking one thumbnail image and pressing the Cmd and A keys simultaneously (PC: Ctrl and A). Hover your cursor over one of the

thumbnails and rotate the images so that the labels are right-side-up by clicking the arrow keys to the bottom left or right of the thumbnail you are hovering over (circled in white below).
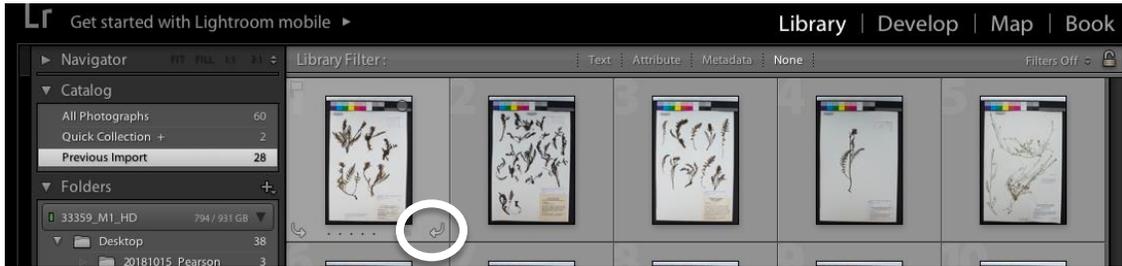
8. Click on a single specimen image in the Library tab so that only that specimen is highlighted. Click the "Develop" tab in the menu at the top right side of the screen (see below). If this menu is not immediately available, click the top right side of the Lightroom window.
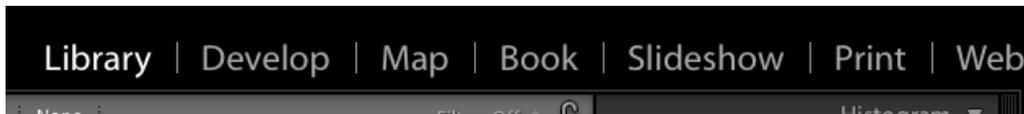
9. In the editing toolbar on the right side of the window (shown below), click the Crop Overlay tool symbol (circled in white below). This will open a new menu for the Crop & Straighten Tool.
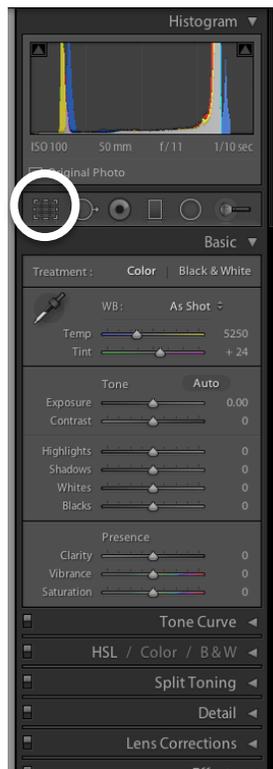
10. Crop the image by adjusting the edges of the cropping rectangle to remove unwanted empty space. Make sure that all edges of the specimen sheet **and the color separation guide and ruler** remain inside the cropped image.
11. Click "Close" at the bottom right of the Crop & Straighten Tool.

Note: Steps 12-16 are optional, but recommended, adjustments to increase the visual appeal and clarity of the specimen images.

12. In the editing toolbar, open the Tone Curve panel by clicking the triangle to the right of the words "Tone Curve." If this panel is already open, you do not need to click the triangle.
13. To the right of the "Highlights" slider, enter 10 in the text box and press Return (PC: Enter) on your keyboard.
14. To the right of the "Lights" slider, enter 25 in the text box and press Return (PC: Enter) on your keyboard.
15. In the editing toolbar, open the Detail panel by clicking the triangle to the right of the word "Detail." If this panel is already open, you do not need to click the triangle.
16. Under "Sharpening" in the Detail menu, click the number to the right of the "Amount" slider. Enter 50 into the text box and press Return (PC: Enter). Once you have made these three adjustments, your editing toolbar will look like that shown on the right.
17. Click on the thumbnail image at the bottom left of the window (circled below) and press Cmd and "A" (PC: Ctrl and A) simultaneously to select all of the recently imported images.
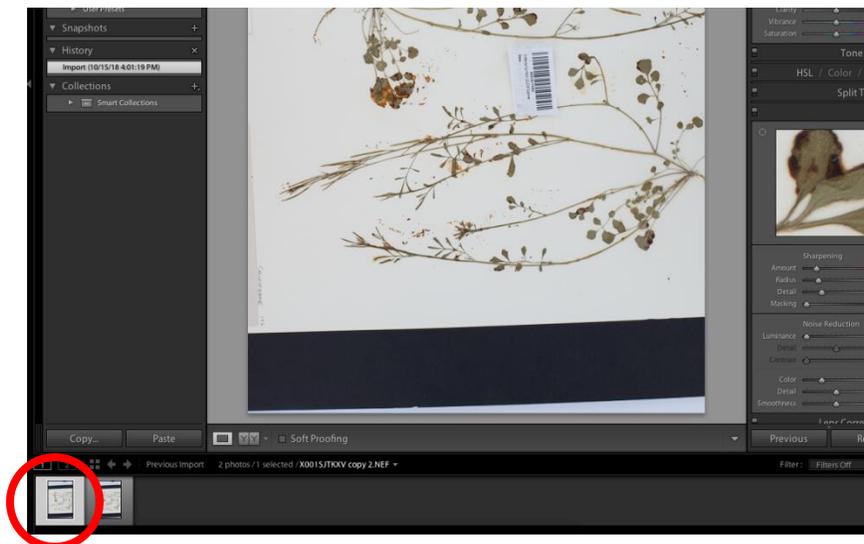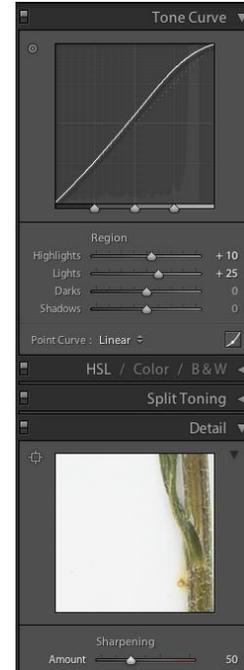
18. Press Shift, Cmd, and "S" simultaneously (PC: Shift, Ctrl, and "S") or, in the menu bar at the top of the screen, click "Settings" > Sync Settings…. Make sure that the box next to "Crop" is checked in the Synchronize Settings window. Click "Synchronize." This will apply all the edits that you made to the first image to all subsequent images.
19. Click the Library tab and select all the images by pressing Cmd and "A" (PC: Ctrl and "A") simultaneously.

20. Click the "Export" button in the bottom left corner of the window. The following dialogue box will open:
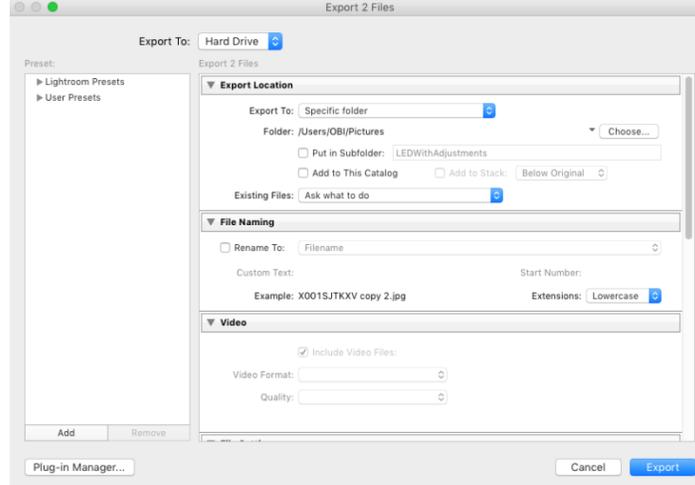
First time set-up note:

Upon first use, set up two User Presets that can be used for future exports by doing the following:

      a. On the left side of this window, click the "Add" button. Enter DNG as the preset name. Click Create.

      b. In the export settings, make sure the "Rename To:" checkbox is unchecked.

      c. Scroll down. Under File Settings, change the Image Format to DNG.

      d. Right click on the name of the preset (DNG) in the menu on the left. Select Update with Current Settings.

      e. Click the "Add" button on the left side of the window. Enter JPEG as the present name. Click Create.

      f. In the export settings, make sure the "Rename To:" checkbox is unchecked.

      g. Scroll down. Under File Settings, change the Image Format to JPEG.

      h. In the Color Space dropdown menu, select sRBG.

      i. Check the Limit File Size box and enter 7000 in the text box.

      j. Scroll down. Make sure the Include: field in the Metadata box says "All Metadata"

      k. Uncheck the "Remove Person Info" and "Remove Location Info" boxes.

      l. Right click on the name of the preset (JPEG) in the menu on the left. Select Update with Current Settings.

21. Select the JPEG preset from the menu on the left side of the window

22. Change the Export Location to the JPEGs subfolder within the "_Processed" folder that you created on the desktop in step 1.

23. Click "Export." Note that this may take a while if you are processing many images at one time.

24. Repeat step 20 and select the DNG preset from the export window.

25. Click "Export." Note that this may take a while if you are processing many images at one time.

26. Ensure that both DNGs and JPEGs are found in the "_Processed" folder that you created in step 1 and that the number of DNG files and number of JPEG files are both identical to the "Number of Images" listed in the Imaging Log entry for the file you are processing.

27. Write your initials and the date in the imaging log under "Processed" on the corresponding entry.

10.2 Image Processing Checklist

The quick-reference checklist on the following page was developed to expedite the process of image processing for supervisors.

Image Processing Checklist

Print this checklist and post it next to the image processing computer.

☐ Import with appropriate metadata

☐ Rotate

☐ Crop

☐ Adjust Highlights and Lights

☐ Sharpen

☐ Sync settings

☐ Export as JPEG

☐ Export as DNG

Once images are processed:

☐ Upload DNGs and JPEGs to institutional storage

☐ Upload JPEGs to CyVerse using Cyberduck

☐ Link images to CCH2

The last two steps are explained in the Set Up and Upload of Images to CyVerse and Loading into CCH2.

11. Protocol for Set Up and Upload of Images to CyVerse and Loading into CCH2

Goal: Section 11.1 of these directions describes how to set up the system that will be used to make images web-accessible and linked to the CCH2 portal. Once the system is set up once, you can refer only to Sections 11.2 and 11.3 of this protocol. Part 2 describes how a supervisor or trained technician can upload specimen images to CyVerse, which will then make these images web-accessible. Section 11.3 describes how to link the URLs for these images to the specimen records in the CCH2 portal.

11.1 Setting up Cyberduck to upload JPEGs (one time only)

Adapted from the CyVerse User Manual, also available here:
https://cyverse.atlassian.net/wiki/spaces/DS/pages/241869843/Using+Cyberduck+for+Uploading+and+Downloading+to+the+Data+Store

Step 1: Create a CyVerse account and request access to BisQue

1. Go to www.cyverse.org and click on the ⬤ in the top right corner of the page.
2. Click Sign Up and follow the provided instructions for creating a CyVerse account.
3. Email your portal manager (kdpearso@calpoly.edu) with your CyVerse account name so that you can be given permission to edit your institution's folder.
4. Log in to your CyVerse account (https://user.cyverse.org/).
5. Click the AVAILABLE tab (see screenshot below).

6. Find the BisQue tool in the resulting list and click Request Access**.**
    Note: You may not be instantaneously given access to BisQue. Please wait at least six hours after requesting access before uploading images to CyVerse.

Step 2: Install or update Cyberduck
- **If Cyberduck is already installed,** check if you need to update (this allows you to be compatible with iRODS 4.1):
    1. Click the **Cyberduck** menu.
    2. Click **Check for Updates**.
    3. Determine if your installed version requires an update:
        - If using **< 4.7.0**, the update is required.
        - If using **> 4.7.0 and < 5.0.0**, the update is recommended.
        - If using **5.0.0 and later**, the update is optional.
    4. Depending on your version, click **Install Update**.

- **To install Cyberduck for your operating system for the first time:**
    1. Go to the Cyberduck installation page at https://cyberduck.io/ .
    2. Follow the steps for your OS (not available for LINUX users):
        - **For Mac OS:**
            a. Click **Download Cyberduck for Mac**.
            b. Move the downloaded file (either a zip file or the unzipped application file, depending on your browser) to your **Applications** folder.
            If the zip file is listed, unzip the file in your Applications folder.
            IMPORTANT: The file **must** be located in your Applications folder.
        - **For Windows:**
            a. Click **Download Cyberduck for Windows**.
            b. Locate the downloaded file and double-click to begin installation.
            c. Go through the install process.

Step 3: Configure Cyberduck for use with the Data Store

1. Click ![duck icon] to open Cyberduck.
2. Click this link to download the **Connection Profile**, which contains preconfigured settings for using Cyberduck with the CyVerse Data Store.
3. Click to open the downloaded CyVerse Data Store.cyberduckprofile file.
4. Verify **CyVerse Data Store** is displayed in the first field.
5. In the Nickname field, enter **data.cyverse.org – iRODS**.
6. Create the connection:
    - In the **Server** field, enter **data.cyverse.org**.
    - In the **Port** field, enter **1247.**
    - **To create the connection with your CyVerse user account for login:**
        a. Enter your CyVerse user name in the Username field.
        - Verify your username is added to the URL field, as shown above.
        Example: irods://*yourusername*@data.cyverse.org.
    - **To create an anonymous connection so you can access public data without a CyVerse user account:**
        . Click the **Anonymous Login** checkbox.
        a. Verify **anonymous** is displayed in the **Username** field.
The remaining fields are populated.
7. Click in the **Transfer Files** drop-down list and select **Open multiple connections**.
8. Close the window.

11.2 Uploading JPEGs to CyVerse

Goal: This protocol describes how a supervisor or trained technician can upload specimen images to CyVerse, which will then make these images web-accessible. The URLs for these images will then be linked to the specimen records in the CCH2 portal in Part 3.

1. If necessary, click ![duck icon] to open Cyberduck (or find the Cyberduck program in your applications or programs list).

2. In the Cyberduck window, click the bookmark icon ![bookmark icon] and then click **Open Connection**.

3. In the drop-down list, click the repository to use (data.cyverse.org – iRODS if you set it up as instructed above)

4. Log in to Cyberduck by entering your CyVerse username and password.

5. Click **Connect**.

6. Click the image of the hard drive that now appears in your bookmarks page (see example below).

data.cyverse.org – IRODS
data.cyverse.org
kdpearson

7. You will be brought to your home folder, which may look something like that below. Notice that the folder you are currently viewing is your personal CyVerse home folder with the path name: /iplant/home/username
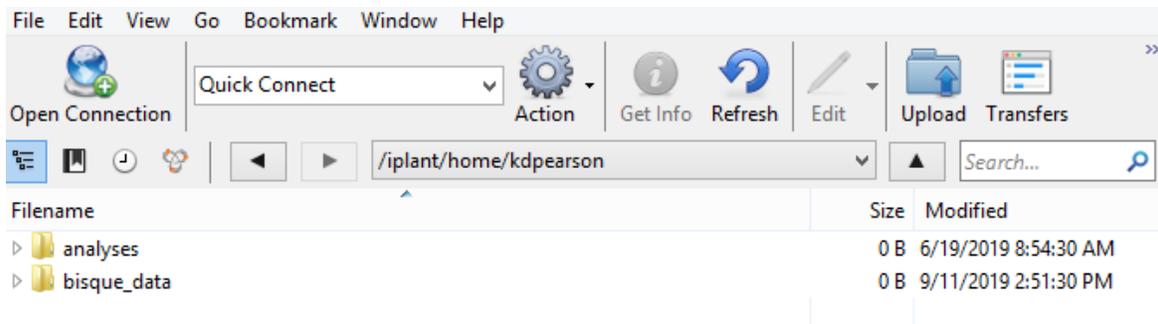
8. You now need to navigate to the shared folder where we store CAP TCN images. At the top of the window, click **Go** and select **Go to Folder...** from the dropdown menu.

9. In the pop-up window, enter the following path: /iplant/home/shared/CAP_TCN . Click **Go.**

10. Click the folder with the acronym of your institution. If there are many files in this folder, just wait; it may take some time to list the directory.

11. Click Upload at the top of the window and navigate to the folder that you intend to upload. Select the folder and click the Choose button. Let the uploader run until the whole folder has been successfully transferred.

    - Alternatively, you can drag and drop the folder you intend to upload into the Cyberduck window. Note that, if you intend to put that folder within a new folder, **you will need to click on that folder and open it up before dragging and dropping**.

Note: In case of an unsuccessful or partial transfer, or if incorrect files are uploaded, contact your portal manager to delete the appropriate files. You will not be able to delete files from CyberDuck.

11.3 Loading JPEGs into CCH2

The user conducting this protocol must have administrator permissions in CCH2.*

Notes:

- **After uploading your images to CyVerse using Cyberduck as described above, wait at least 30 minutes before doing the next step.**
- **If the process is not successful after 30 minutes, try again on the following day.**
- **Note that the servers often undergo maintenance on Tuesdays, which can cause a delay in processing or unexpected errors.**

1. Log in to your account in CCH2 and navigate to the collection management page (My Profile > Specimen Management tab > name of collection).
2. In the administration control panel, click **Processing Toolbox**.
3. Select the Image Loading tab and select **iPlant Image Processing** from the Saved Image Processing Profiles box.
4. Ensure that the Processing start date is the same as the Last Run Date. This means that the API will search and load your folder for all the images that were uploaded since you last loaded JPEGs into CCH2.
5. Click the Process Images button. Examine the resulting log file to ensure the expected number of images was loaded into CCH2.

Understanding the Log File

The image linking algorithm will work chronologically to load all the images uploaded each day since the last day you ran the algorithm. For each day, the log will list how many images were recognized and linked (see screenshot on next page).

Images will be recognized and linked only if they have been (1) uploaded to the appropriate folder in CyVerse and (2) processed by BisQue. Processing in BisQue happens automatically once you have uploaded the images; however, the BisQue server can get busy at times, which can delay the processing of your images. This is why we recommend waiting 30 minutes or longer after uploading images to CyVerse before conducting steps 1-5 above.

- Linked image to existing record (OBI158185.jpg; #3823923)
- Linked image to existing record (OBI158121.jpg; #3823970)
- Linked image to existing record (OBI158135.jpg; #3823985)
- Linked image to existing record (OBI158108.jpg; #3823939)
- Linked image to existing record (OBI158109.jpg; #3823928)
- Linked image to existing record (OBI158134.jpg; #3823988)
- Linked image to existing record (OBI158120.jpg; #3823968)
- Linked image to existing record (OBI158136.jpg; #3823984)
- Linked image to existing record (OBI158122.jpg; #3823975)
- Linked image to existing record (OBI158123.jpg; #3823987)
- Linked image to existing record (OBI158133.jpg; #3823990)
- Linked image to new "unprocessed" specimen record (#3973642)
- Linked image to existing record (OBI158127.jpg; #3823991)
- Linked image to existing record (OBI158126.jpg; #3823983)
- Linked image to existing record (OBI158132.jpg; #3823995)
- Linked image to existing record (OBI158118.jpg; #3823967)
- Linked image to existing record (OBI158124.jpg; #3823986)
- Linked image to existing record (OBI158130.jpg; #3823993)
- Linked image to existing record (OBI158131.jpg; #3823989)
- Linked image to existing record (OBI158119.jpg; #3823972)
- Linked image to existing record (OBI158125.jpg; #3823996)
- No images were loaded on this date: 2020-08-04
- No images were loaded on this date: 2020-08-05
- No images were loaded on this date: 2020-08-06
- No images were loaded on this date: 2020-08-07
- No images were loaded on this date: 2020-08-08
- No images were loaded on this date: 2020-08-09
- No images were loaded on this date: 2020-08-10
- Updating collection statistics...
  - Updating collection statistics...
  - Populating recordID UUIDs for all records...
- Image upload process finished! (2020-08-10 10:56:19 AM)

The log shows you what happened to each image we uploaded. You will see one of the following messages for each image that was recognized and loaded:

- **Linked image to new "unprocessed" specimen record** - this means that CCH2 did not find an existing record for this image, so it created a skeletal record (i.e., record with just the barcode number and image) for that image. The Processing Status of this specimen will be "unprocessed," and you can use this fact to search for these skeletal records in the future.
- **Linked image to existing record** - this means that CCH2 found an existing record for the image and added the image to it. This happens when you have already entered barcode numbers into CCH2 *or* when you upload multiple images for a single record at one time (i.e., a skeletal record was created for the first image for that record, then CCH2 linked the second image to that skeletal record as well).
- **Replacing previously mapped image with new input; Linked image to existing record** - this means that an image with the same name already existed in the portal, so CCH2 is replacing the old image with the most recently uploaded one.
- **NOTICE: Imaging mapping skipped; image identifier already in system** – the means that an image already exists for the specimen for which you were uploading an image; CCH2 does not replace images if they already exist on the server. To replace an image, you will need to delete the previous image from the CCH2 occurrence record first. See the Section 9.1 of the Symbiota Guide (https://www.capturingcaliforniasflowers.org/symbiota.html) for instructions on deleting previous images.

Note that the number following each line of the log is the SymbiotaID number, rather than the catalog number of the specimen. The first time you view the log, you can click the SymbiotaID number to navigate to that record. When you download the log later, these links do not exist. Instead, you can look up a specimen by copying the SymbiotaID number and pasting it after **occid=** in the following URL:

http://cch2.org/portal/collections/editor/occurrenceeditor.php?occid=

12. Protocol for Associating Barcode Numbers with Accession Numbers

Goal: This protocol describes how to update your old accession number with the specimen's new barcode number. You can do this only after you have uploaded specimen images to the iDigBio server and linked them to your database in CCH2.

1. Log in to your CCH2 account and click My Profile on the right side of the menu bar.
2. Click the Specimen Management tab.
3. Click the name of the collection that you will be imaging.
4. In the Data Editor Control Panel, click Edit Existing Occurrence Records.
5. In the Record Search Form, click the Processing Status field select "Unprocessed" from the dropdown menu.
6. Click the "Display Table" button.
7. Select a specimen from this list by clicking the Symbiota ID number in the far left column. This will take you to the Occurrence Editor form (see screenshot below).
8. Locate the accession number (the stamped number, rather than the barcoded number or the collector number) on the specimen in the image to the right of the Occurrence Editor form (screenshot below). You can zoom in by pressing Command (Mac) or Control (Windows) and clicking on the image where you want to zoom in. Alternatively, you can hold Shift, click on the area where you want to zoom in, and move the mouse up (to zoom in) or down (to zoom out).
9. Enter the accession number, without leading zeros (e.g., if the number reads "0145", you will enter "145"), into the Other Cat. #s field (circled below).

10. Click outside of the Other Cat. #s field. A message should show up under the "Dupes?" button. Make sure that your browser's pop-up blocker is disabled so you can see these messages.
    a. If the message shows "No Dupes Found" (see below):

      i.   Check that the specimen sheet is not stamped "Databased" or has any other indication that it SHOULD have a record in the database. If it is, try adding a leading zero to the accession number and repeat step 9.

     ii.   Press the Save Edits button (or press Tab and Enter on your keyboard)

    iii.   Move on to step 11.

    b.   If a message shows up that says "Record(s) using the same identifier already exists. Do you want to view this record?":

        a.   Click OK.

        b.   Check that the data of the identified duplicate matches the data on the label of the specimen image you were viewing. You need not check every field, just two or three important fields such as Scientific Name, Collector, and Locality.

        c.   If the data match up, click "Merge Records" and exit the duplicate window. If the data do not match up, scroll down to the Processing status field in the Curation box and select "Expert Required" from the dropdown menu.

11. Return to the table of specimens you opened in step 6 by clicking the back button on your browser.

12. Click the refresh button on your browser.

13. Repeat steps 7-12.

14. When you are done with your shift, make sure to log out of your account and close the browser window.

13. Guide to Transcribing Label Data in CCH2

Goal: This protocol describes how to transcribe specimen data from images of skeletal records in the CCH2 portal.

13.1 Navigating to records to transcribe

1. Log in to your account in CCH2 (cch2.org).

2. Click My Profile.
3. Click the Specimen Management tab.
4. Click the name of the collection for which you will transcribe specimens (there will likely only be one).
5. In the Data Editor Control Panel, click Edit Exiting Occurrence Records.
6. In the resulting Record Search Form, select "Unprocessed" from the dropdown list in the Processing Status field.
7. For Custom Field 1, select "Other Catalog Numbers" from the first dropdown list and "IS NOT NULL" from the second dropdown list.
   - Note: this step applies to institutions that associate barcode numbers with accession numbers in a separate step; if you are not sure whether this is true, ask a supervisor or omit this step

8. Click the Display Editor button.

13.2 Transcribing records

Answers to common transcription questions can be found on our FAQ page here:
https://www.capturingcaliforniasflowers.org/faq

> If you find that you are unable to transcribe part of a specimen label, set the processing status of the specimen to Expert Required, explain the reason you had trouble transcribing the record in the Notes (Occurrence Remarks) field, and move to another specimen record.

1. When you have a specimen record in front of you, scroll down to the bottom of the page to the Status Auto-Set field, which is right above the Save Edits button. Select Pending Review from the dropdown menu (an explanation for the Processing Status field is provided in Appendix 1).

Note: Beware of the Status Auto-Set field. Setting this field to anything other than Not Set will apply that processing status to the specimen that are working on, regardless of whether you change the Processing Status of the specimen itself. Furthermore, if you switch to another task besides transcription, the Status Auto-Set will continue to function, potentially auto-setting the statuses of specimens that you do not intend to change.

2. Scroll back up to the top of the specimen record. Zoom in to the specimen label on the image on the right by clicking and holding on the image, holding the Tab key on your keyboard, and moving the mouse up. Hold shift, click, and move the mouse down to zoom back out. Alternatively, you can hold the Control (or Command) button and click somewhere on the specimen image to zoom in.
   - The specimen label is usually on the bottom right of the specimen.
   - If the label is too blurry to read, click the High Res. button above the image.
3. Type the name of the primary collector into the Collector field.
   - Type the name exactly as it appears on the label
   - If there are multiple collectors, use the first collector name or the collector name that is associated with the collector number.

4. Type the collector number in the Number field.
   - A collector number is a personal, consecutive number that collectors assign as they collect. This is not the same as the catalog number, barcode number, or accession (stamped) number.

- This number will almost always be typed or written on the label rather than stamped onto the herbarium sheet.
- Collector numbers will occasionally include letters, dashes, or other characters. Enter these as they appear on the label. You do not need to enter "no." or #.

5. Type the collection date in the following format: YYYY-MM-DD. For example, if the label says 5 August 2017, the correctly formatted date would be 2017-08-05.
   - For single-digit months and days, include a preceding zero (e.g., 08, 09, 01).
   - If the date does not include a year, month, or date value, enter zeros for that value (e.g., if the label says "August 1987" you would enter 1987-08-00; if the date says "Summer 1950" you would enter 1950-00-00)
   - If no date is provided on the label, leave this field blank.

6. Click the Dupes? button (or, if Auto search is checked, the next step will happen automatically). For more information about the Dupes? tool, watch this video: https://youtu.be/XyYPYJ1guMY?t=268
   - If you see the "No Dupes Found" message, continue to step 7.

   - If a duplicate is found, a pop-up window will show up. (Make sure that your pop-up blocker is disabled to allow this). Examine the results of this pop-up window.
     - o If you see the "Possible Matching Duplicate EVENTS" message, exit out of the window and proceed to step 7 *unless you are trained to georeference specimens and can evaluate whether to import any duplicate coordinates*.

Possible Matching Duplicate EVENTS

     - o If you see the "Possible EXACT Duplicates" message, look at the record listed in the pop-up window.

Possible EXACT Duplicates

       Check to see whether the scientific name, collector, date, and general details about the potential duplicate record(s) are the same as those on the label of the specimen you are transcribing. It may help to view the label and the potential duplicate record side-by-side as shown by the following screenshot.

   o If the records are the same, make sure the "Link as Dupes" box is checked in the pop-up window and click "Transfer to Empty Fields Only."

     ▪ If there are multiple potential duplicates, select the one that matches the specimen you are transcribing AND has georeferenced (latitude/longitude) coordinates, if possible.

     ▪ **Check that the information imported into the data entry form matches the label exactly and that the data have been imported into the correct fields.** You may have to re-type or move information around so it is stored in the correct fields (see step 11).

     ▪ Data that originated from the duplicate specimen will be highlighted in blue on the data entry page.

   o If the records are not the same, double check that you have correctly entered the collector name, number, and date in the original occurrence editor form. If you are sure these values are correct, notify a supervisor that you have found a potential data quality issue. Make sure you report the catalog numbers of the potentially problematic records to your supervisor.

7. On the record editor form, enter any collectors other than the primary collector in the Associated Collectors field. Separate names in this field by a semicolon and do not include words like "with" or "and."

8. If any part of the date information was not clear in the Date field above (e.g., if the label said "Spring 2019"), type in the date EXACTLY as it is shown on the label into the Verbatim Date field.

9. Begin to type the ORIGINAL scientific name of the specimen into the Scientific Name field. If there are annotations (i.e., a more recent name for the specimen), you will add these in Section 13.3. Once the field begins to auto-populate, **select the appropriate scientific name from the dropdown menu**.

  • The ORIGINAL scientific name is the one that is on the original label. If there is no scientific name on the original label, leave this field blank.

  • Note that you do not need to enter authorship (e.g., the last names and abbreviations after the genus and specific epithet); these will be auto-populated.

  • You also do not need to enter the family name, since it will also be auto-populated.

10. Start typing the Country, State, and County into the appropriate fields and **select the appropriate values from the dropdown menus** as they appear.

  • Always select from the dropdown menus whenever possible.

  • Enter any reference to the USA as "United States"

  • The State/Province field primarily applies to states or provinces of the United States, Canada, and Mexico. If you are unsure about what to enter here, leave it blank.

11. Look at the label to see what further information is provided on the label. The most common fields for which there are label data are described below. See section IV for examples of specimen labels and how they would be transcribed into CCH2.

- **Locality** – geographic description of where the plant was collected
  - o 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").
  - o This field should include directions to the collection location, city names, road names, names of parks, etc.
  - o Some habitat information may be included in this field if it would help someone be able to re-locate the specimen's locality. This information can be entered into this field AND the habitat field.
  - o Note that you can check the "Locality Security" box if the locality information should be protected (e.g., protected species location).
- **Verbatim Coordinates** – the latitude and longitude for the collection location of the specimen
  - o Enter the latitude and longitude coordinates and click the double arrows (<<) .
  - o If coordinates were provided on the sheet, enter "coordinates from collector" in the GeoreferenceRemarks field.

NOTES: If coordinates are provided in degrees minutes seconds (e.g., 36° 11' 45" N, 120° 12' 06" W), township-range-section (e.g., T4N, R12W, sec. 7), or UTMs (e.g., 3572309E 1340983N), these can be entered by clicking the F button to the right of the Latitude and Longitude fields. Clicking this button will reveal fields where you can enter these data (in yellow boxes below). For more information about degrees, minutes, seconds; UTM, or township-range-section coordinate systems, watch this short video: https://youtu.be/twR1o_CR1tw?t=167

The C button will open the Coordinate Cloning Tool which will look for other specimens that have a locality similar to that which you entered in the locality field. If there are good-quality (i.e., accurate and precise) coordinates that match your locality, you can import these data into your data form by clicking the georeferenced point on the pop-up map and selecting Use Coordinates. For more information about the Coordinate Cloning Tool, watch this short video: https://youtu.be/XyYPYJ1guMY?t=413.

Note: Only import coordinates from the Coordinate Cloning Tool if you are familiar with our georeferencing protocols and can evaluate the quality of the coordinates that you import. Some coordinates that you can import are of low quality, and we do not want to propagate these in our data.

- **Verbatim Elevation** – elevation or altitude of the collection location of the specimen
    - ○ Enter the elevation value and units provided on the specimen label and click the double arrows (<<) to standardize to meters.
- **Habitat** – environmental conditions in which the plant was found (e.g., marsh, grassy field, roadside)
- **Substrate** – technical definitions given for substrate (e.g., soil type/series or rock formation)
- **Associated Taxa** – other plant taxa listed as growing with the collected specimen.
    - ○ Begin to type scientific names into this field and a dropdown list will appear. Make sure to select the appropriate name from this dropdown list.
    - ○ Separate multiple associated taxa with a comma. Once you have placed a comma, the field will "understand" that you are about to type in a new associated taxon and will clear the dropdown menu.
- **Description** – information specific to the individual plant (e.g., condition, flower color, leaf shape, height of the plant)
- **Notes (Occurrence Remarks)** – population characteristics (rare, common, frequent, 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 records that require further review.
- **Phenology** – information about whether the plant is flowering or fruiting; only enter information into this field if it is written on the label or if you are instructed otherwise.

12. Once you have filled out the above fields as appropriate, check to see that any additional information is visible on the specimen label.
    - If the specimen is noted to be cultivated or planted, check the Cultivated/Captive box.
    - You do not need to include label headers (e.g., "Flora of California") or the name of the herbarium.
    - If there are additional notes about the specimen having been collected for a specific study, enter this information in the Notes field.
    - For additional explanations of the Occurrence Data Fields, see Section 16.7.2.
13. Click the Save Edits button or press Enter on your keyboard.
14. If your specimen has an annotation label (see Section 13.3), move on to part III. Otherwise, return to the beginning of Section 13.2.

13.3 Transcribing annotation labels

15. On the image that you just transcribed, check to see if there are any annotation labels on the specimen (see the example image)
    - Annotation labels are usually above the specimen label but may be beside the label or elsewhere on the specimen. Make sure you view the full specimen for annotations before you move on.

ANNOTATION—ROBERT F. HOOVER HERBARIUM
Boechera glaucovalvula (M.E.Jones) Al-Shehbaz

David J. Keil   2011

Plants of   California   **Herbarium of David Keil**
                CRUCIFERAE
                Arabis glaucovalvula Jones

County: Inyo
Location: Death Valley, road to Wild Rose , 0.4 miles
                southeast of junction to Aguereberry Point.

Habitat: Chaparral hillside.
                D. J. Pinkava, George Batchelder, Jan Lewis,
                Jan Velasco, David Keil and
Collector: Elinor Lehto 12451   **Elevation:**
Determiner: David Keil   Date:11-IV-1968

16. If there are annotation labels, click the Determination History tab at the top of the occurrence editor form.

Robert F. Hoover Herbarium, Cal Poly State University (OBI)
Home >> Collection Management >> Public Display >> Editor |< << | 1 of 49 | >> >| >*

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

17. Start to type the scientific name of the specimen annotation into the Scientific Name field. Select the appropriate scientific name from the dropdown menu once it appears.
    • If there is an identification qualifier (for example: cf., aff., or ?), enter this in the Identification Qualifier field above the Scientific Name field.
18. Enter the name of the determiner (the person making the annotation) exactly as it appears on the annotation label into the Determiner field.
19. Enter the determination date in the YYYY-MM-DD format in the Date field.
20. If any references by which the specimen was identified or other notes occur on the annotation label, enter them in the appropriate fields.
21. If this is the most recent annotation, make sure the "Make this the current determination box" is checked. If there are more recent annotations after the annotation you are entering, uncheck this box.
22. Click Submit Determination.
23. Repeat steps 16-21 for any remaining annotation labels on the specimen.

13.4 Example diagrammed specimen labels

State
County
Scientific Name
Locality
Habitat
Associated Taxa
Notes
Collector

FLORA OF CALIFORNIA
Santa Cruz County
California Polytechnic State University
Brassica geniculata (Desf.) Ball
(Brassicaceae)
Soquel Demonstration State Forest off of Highland Ave. Redwood-Douglas Fir forest dominated by Sequoia sempervirens, Pseudotsuga menziesii, Lithocarpus densiflora, Arbutus menziesii, Acer macrophyllum, Quercus agrifolia, and Quercus wislizenii. Understory of ferns, Oxalis oregana, Toxicodendron diversilobum, and Rubus spp. Occasional in disturbed habitats.
Larry Kelly no. 603
1 July 1991

Number
Date (1991-07-01)

Scientific Name
County
State
Country
Locality
Habitat
Substrate
Associated Taxa
Verbatim Coordinates
Verbatim Elevation

PLANTS OF THE WHITE MOUNTAINS
Boechera pendulina W. A. Weber
USA CA Mono County
(W&I) White Mountains: .33 air-mile s Golden Siren Mine, .88 air-mile wsw UC White Mountain Research Center Crooked Creek Station; crevices in steep e-facing blue-gray rock outcrop, calcareous substrate (Deep Spring Fm); with Monardella odoratissima subsp. glauca, Castilleja applegatei
37.49619 -118.18732 GPS
Elev 3197 meters
Petals pinkish-white, siliques wide-pendent; ca. 50 plants in population; uncommon
Dylan M. Neubauer 181
15 June 2015

Collector
Number
Description
Notes
Date (2015-06-15)

14. Georeferencing Protocol

For an online course on Georeferencing in CCH2, visit
https://www.capturingcaliforniasflowers.org/georeferencingcourse.html

Section 14.1 describes how to georeference (assign latitude, longitude, and error to a specimen given the textual locality information) individual specimens in the occurrence editor. Section 14.2 describes how to georeference specimens using the batch georeferencing tool. Section 14.3 contains the quick guide for georeferencing using the point-radius method. Section 14.4 contains helpful georeferencing resources.

14.1 Georeferencing individual specimens in CCH2

1. Log in to your account in the CCH2 portal, click "My Profile," navigate to the "Specimen Management" tab, and click the name of the institution for which you will be georeferencing.
2. In the Data Editor Control Panel, click "Edit Existing Occurrence Records."
3. In the Record Search Form, specify your search to include the specimens that you are interested in georeferencing and have not already been georeferenced. For example, if you wanted to georeference all the *Eschscholzia californica* in San Luis Obispo county, your record search form should look like this:

   Notice that we specify "Decimal Latitude" IS NULL because we are specifically searching for specimens that have not already been georeferenced.
4. Click either Display Editor (to see one specimen at a time) or Display Table (to see a table of all the specimens).
5. Select the specimen you wish to georeference (if it is not already open) and click the Dupes? button at the top right hand corner of the page (circled below).

6. If you see a No Dupes message, proceed to step 7. If a window pops up (make sure you do not have a pop-up blocker activated) that says Possible EXACT Duplicates or Potential Duplicate EVENTS, do the following:
   * In the search results, look for any records that have latitude/longitude coordinates (see example window below). If none of the potential duplicates have latitude/longitude coordinates, close the pop-up window and proceed to step 7.

- Compare the location information on your specimen record (in the Locality field) to the location information for the potential duplicate record(s) that has latitude/longitude coordinates. If both location descriptions indicate the exact same place, click Transfer to Empty Fields Only. If none of the location descriptions for the potential duplicates match the location description of your specimen, close the pop-up window and proceed to step 7.
- If you transferred information into the specimen record, double check ALL blue highlighted fields to make sure that the data match your specimen record. Delete any data that was imported into fields that are not in the Locality box.

  The example below shows an instance when you would NOT "transfer to empty fields only" because the locations are not the same. Although the SD specimen has latitude/longitude, the locality description ("East end of El Monte Road, El Capitan...") does not match the original record's locality description ("Near hwy 101 in SLO").

7. Click the C button to the left of the latitude and longitude fields in the Locality box. In the pop-up window (make sure your pop-up blocker is disabled for CCH2), select the Contains radio button and click Search. If you see the message "Search failed to return specimen matches", proceed to step 8. If otherwise, do the following:
   - View the potentially matching localities in the resulting map (see next page). If any of them seem to match the location of your specimen (judging from the location description on your specimen), click that coordinate and click Use Coordinates.
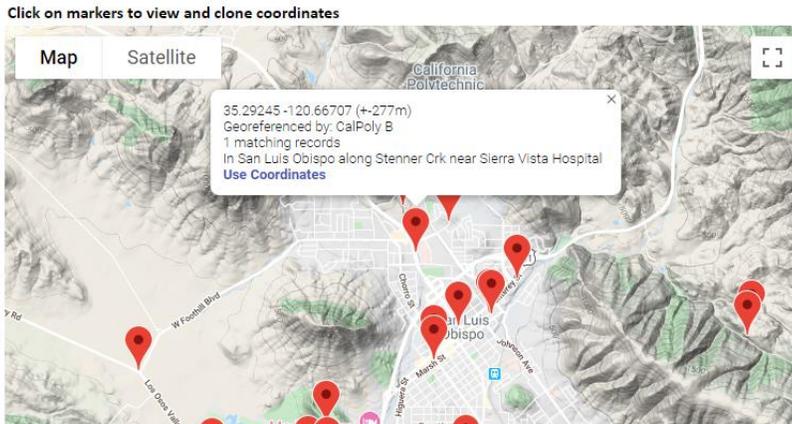
- • Click the globe icon to the right of the uncertainty field. In the resulting window, adjust the point and the uncertainty radius according to the point-radius method (read through the remainder of the protocol for instructions on how to do this accurately).

8. Click the Geolocate (🌀) icon to the right of the latitude, longitude, and uncertainty fields. This will open a new GeoLocate window (see screenshot below) 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.

9. 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.
10. Make sure that all of the boxes (latitude, longitude, uncertainty, and error polygon) near the bottom right of the window are checked.
11. 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.

12. 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 screenshot on next page).

    - **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, look back at the specimen record to 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 and you think someone else may be able to georeference this record in the future, move on to another record. If you think the specimen data are insufficient for anyone (even an expert) to georeference the specimen, add a note in the Georeference Remarks field (click the pencil at the bottom right corner of the Locality box) that begins with "cannot georeference."
    - ▪ If only a county is provided, enter "locality imprecise; cannot georeference" in the Georeference Remarks field.

13. 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 Section 14.3 when deciding where to place the dot.**
14. Set the error radius and/or create an error polygon to indicate the uncertainty of the specimen's locality. **Follow the guidelines provided in Section 14.3 when deciding how large of an error radius to use for a given point 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.
15. 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 specimen record page.
    - The coordinates and error will now show up below the search results in the appropriate Latitude, Longitude, Uncertainty fields, and Georeference Remarks. If you created an error polygon, its coordinates will be listed in the Footprint Polygon field.
16. Explain your reasoning for setting the error radius in the Georeference Remarks field (indicated by the arrow below). For example, if you were georeferencing a named place that did not have clear boundaries, explain how you determined a suitable error radius.

17. Add your CCH2 username to the Georeferenced By field.
18. Click the Save Edits button at the bottom of the page.

14.2 Batch georeferencing

1. Log in to your account in the CCH2 portal, click "My Profile," navigate to the "Specimen 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 screenshot below).
   - 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 screenshot on next page) 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.
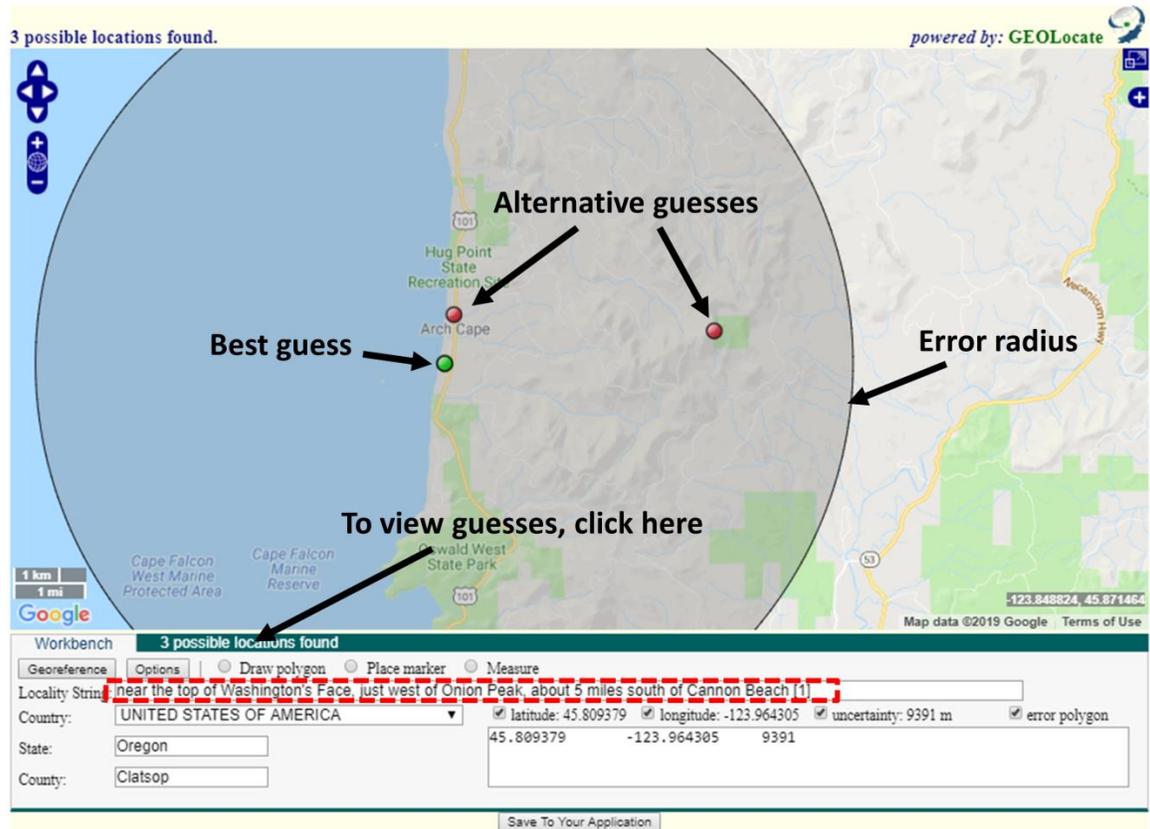
5. Click the "Options" button on the bottom left of the GeoLocate window and ensure the "Do Uncertainty" box is checked. Close the Georeferencing options window.

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 screenshot on next page).

- **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 first page) 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, return to the batch georeferencing window (see screenshot on first page). If you think someone else may be able to georeference this record in the future, just move to another record. If you think the specimen data are insufficient for anyone (even an expert) to georeference the specimen, add a note in the Remarks field that begins with "cannot georeference."
    - ▪ If only a county is provided, enter "locality imprecise; cannot georeference" in the Remarks field.
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 Section 14.3 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 Section 14.3 when deciding how large of an error radius to use for a given point 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."
      - 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 first page).
    - 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.

14.3 Quick guide for georeferencing from different types of locality information

Adapted from Wieczorek et al. 2012 "Georeferencing Quick Reference Guide" (https://www.idigbio.org/wiki/images/1/1e/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 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.
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 point on the feature nearest to 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.

Locality type	Example	How to place coordinates	How to measure error radius/polygon
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, where the nearest named place to use is 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
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.

Locality type	Example	How to place coordinates	How to measure error radius/polygon
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.

14.4 Helpful georeferencing resources

CAP georeferencing guides: https://www.capturingcaliforniasflowers.org/georeferencing.html

CAP georeferencing online course: https://www.capturingcaliforniasflowers.org/georeferencingcourse.html

(Non-CAP) videos about georeferencing: https://vimeo.com/showcase/2163673

For georeferencing township, range, section (TRS coordinates): https://www.earthpoint.us/TownshipsSearchByDescription.aspx and https://www.randymajors.com/p/township-range-on-google-maps.html

USGS Topographical Maps: https://ngmdb.usgs.gov/topoview/ and https://store.usgs.gov/map-locator

15. Phenological Scoring Protocol

This guide describes the general use of three tools in CCH2 that enable scoring of phenological traits from specimen images. Taxon-specific protocols will be developed and published separately.

15.1 Scoring phenology from images (using trait coding tool)

This is the most efficient method of scoring phenology from images. To access and use this tool:
1. In the Data Editor Control Panel (see Section 16.3.1), click Occurrence Trait Coding Tools.
2. Select "Trait Coding from Images" from the two provided options.
3. In the Filter box, select Angiosperm Phenological Traits from the Trait dropdown menu.
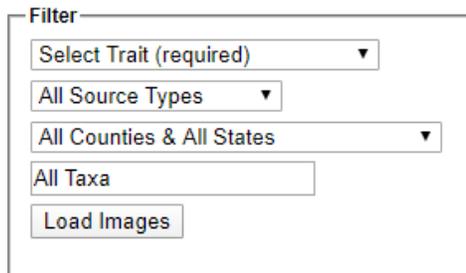
4. Type the name of the taxon for which you wish to score phenological traits in the **All Taxa** box. A dropdown list will appear, and you should select the appropriate taxon from that list. You can also refine your search using the following fields:
    *   **All Source Types:** this field allows you 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.
5. 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 as well.
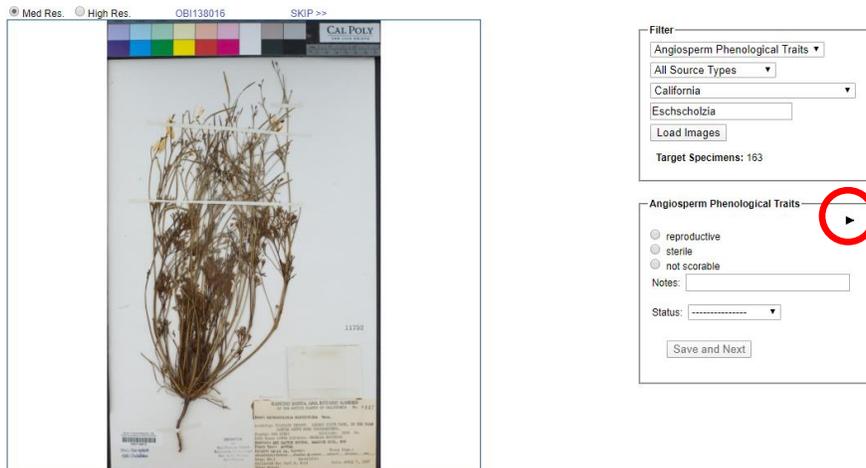
6. If you wish to score the specimen with more detail than just "reproductive" or "sterile", click the black triangle inside the Action Panel to show the finer-scale phenological scoring options (circled in previous image).

7. From this list, select which reproductive structures are present or absent on the specimen. If you are not sure about the presence or absence of a structure, leave the radio buttons for that structure unfilled.

    - If the image cannot be scored (e.g., the majority of plant is obscured or damaged), select "not scorable."
    - If you are unsure about your scoring, write a note about your uncertainty in the Notes field and change the Status to Expert Needed. Click Save and Next. Alternatively, you can skip the image by clicking SKIP >> at the top right of the image.

8. Once you are satisfied with your scoring, click Save and Next.

15.2 Scoring phenology from images (using occurrence editor)

You can also score the phenology of a specimen from that specimen's occurrence editor page by clicking the Traits tab (circled below).

If you wish to score the specimen with more detail than just "reproductive" or "sterile", click the black triangle inside the Action Panel to show the finer-scale phenological scoring options.

From this list, select which reproductive structures are present or absent on the specimen. If you are not sure about the presence or absence of a structure, leave the radio buttons for that structure unfilled.

- If the image cannot be scored (e.g., the majority of plant is obscured or damaged), select "not scorable."
- If you are unsure about your scoring, write a note about your uncertainty in the Notes field and change the Status to Expert Needed.
- If you need to redo your scoring, press the Delete Coding button.

Click the Save Edits button when you are satisfied with your scoring.

15.3 Scoring phenology from text fields

It is also possible to score the phenology of batches of specimens that have a particular string of text in a certain database field. For example, all specimens with a value of "flowering" in the reproductive condition field could be mapped to "flowers present." To access and use this tool:

1. Navigate to Data Editor Control Panel (see Section 16.3.1).
2. Click Occurrence Trait Coding Tools and select "Trait Mining from Verbatim Text".
3. For the "Occurrence trait" field in the resulting Harvesting Filter box, select Angiosperm Phenological Traits from the dropdown menu.

4. 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.
5. 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, you could search for "fowering" or "fwrr" as well as "flowering" and "fwr".
6. 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.
7. 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.

8. To score the phenology of specimens with these values in the specified database field, select the value or values that your wish to score from the list.
   - 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.
9. Select the appropriate score from the phenological traits list at the bottom of the lower box. If you wish to score the specimens with more detail than just "reproductive" or "sterile", click the black triangle inside the Action Panel to show the finer-scale phenological scoring options. From this list, select which reproductive structures are present or absent on the specimen. If you are not sure about the presence or absence of a structure, leave the radio buttons for that structure unfilled.
   - If the image cannot be scored (e.g., the majority of plant is obscured or damaged), select "not scorable."
   - If you are unsure about your scoring, write a note about your uncertainty in the Notes field and change the Status to Expert Needed.
   - If you need to redo your scoring, press the Reset Form button
10. When you are satisfied with your scoring(s), click the Batch Assign State(s) button.

16. CCH2 Portal Guide

16.1. 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 Sections 16.2 and 16.3).

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

16.1.1 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 in screenshot on next page). 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)

16.2 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 Section 16.16).

16.3 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. Species in the checklist can be linked to voucher specimens, enabling you to download custom checklists of specimens for the species on your list. This function will not be described in detail in this guide.

The "Specimen Management" tab is where you will manage your specimen 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 and you know who the administrator(s) for the collection is(are), contact them directly so they can grant you appropriate permissions. If you do not know an administrator for the collection or you believe you are the administrator, contact Katie (kdpearso@calpoly.edu) for assistance.

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.

16.3.1 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 Section 16.16). The Data Editor Control Panel can be accessed by logging in to the portal, clicking "My Profile," and clicking the "Specimen Management" tab. Each of the tools in this panel is described briefly below.
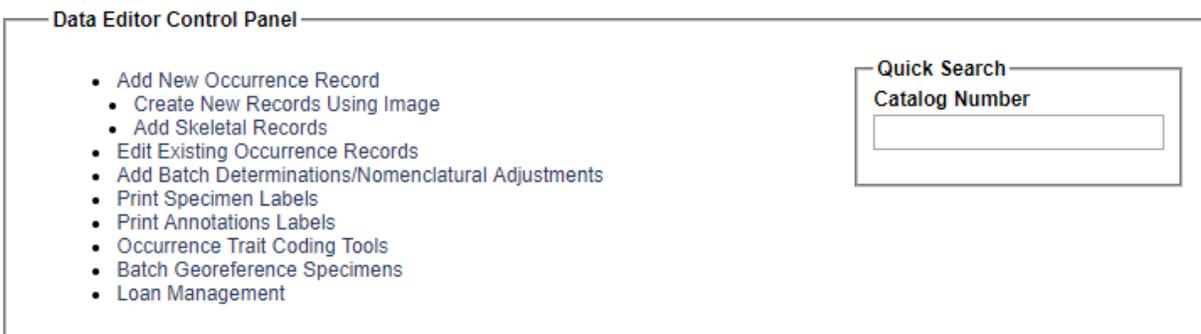
Add New Occurrence Record – This tool is used to create new specimen records from label data. See Section 16.4.

Create New Records Using Image – This tool is used to create new specimen records by uploading an image then entering specimen data. This tool will not be used for the CAP TCN and therefore will not be described in this guide.

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 Section 16.6.

Edit Existing Occurrence Records – This tool is used to add or edit data of records that already exist in the portal. See Section 16.7.

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 Section 16.8.

Print Labels/Annotations – This tool can be used to print specimen labels or barcodes for records with data entered in the portal. It 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 tool also 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. See Section 16.11.

Occurrence Trait Coding Tools – These tools enable scoring of specimen traits, such as phenological status, from images or label text of specimens. See section 15.

Batch Georeference Specimens - This tool can be used to update the geographic coordinates of a number of specimens all at once. See Section 14.2.

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 Section 16.12.

16.3.2 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 Section 16). It can be accessed by logging in to the portal, clicking "My Profile," and clicking the "Specimen Management" tab. The tools available in the Administration Control Panel are described below.

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 Section 16.14.

Edit Metadata and Contact Information – This navigates to the "Edit Collection Information" page where you can change your institution name, description, contact information (contact person, email address, etc.), homepage, license, GUID source, or other information. See Section 16.15.

Manage Permissions – This tool can be used to manage which users have which permissions. See Section 16.16.

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, and others. See Section 16.17.

Processing Toolbox – This link navigates to a set of tools for processing specimens (see tabs below). See Section 16.18.

Darwin Core Archive Publishing – This tool allows the user to publish occurrence data to an aggregator by uploading a Darwin Core Archive. See Section 16.19.

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 Section 16.20.

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 Section 16.21.

General Maintenance Tasks

Data Cleaning Tools – Available tools include a duplicate record identification tool for discovering accidental duplicate catalog numbers (section 16.22.1); a political geography tool to help fix and standardize country, state/province, and county designations (Section 16.22.2); and a taxonomy tool that aids in locating and fixing taxonomic errors and inconsistencies (Section 16.22.3).

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 Section 16.23.

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 Section 16.24.

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 Section 16.25.

16.4 Adding specimen records

New specimen records can be added by navigating to Add New Occurrence Record (Section 16.4) or Add Skeletal Records in Data Editor Control Panel (see Section 16.6).

16.5 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 Section 16.3), then click "Edit Existing Occurrence Records" in the Data Editor Control Panel. You will see a screen like that shown on the next page.

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 box 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 drop down 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 Section 16.7) 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 on next page). 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 page).

16.6 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 Section 16.3.1). 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.

- 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.

16.7 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 "Specimen 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 Section 16.5 for help with searching and sorting specimen records).
3. 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 13. See Section 16.7.1 for an explanation of the tabs on the Record Editor page, and see Section 16.7.2 for an explanation of the relevant fields in the "Occurrence Data" tab. You can click on the green question mark next to any field to get further explanation of its use.
4. 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.

16.7.1 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.
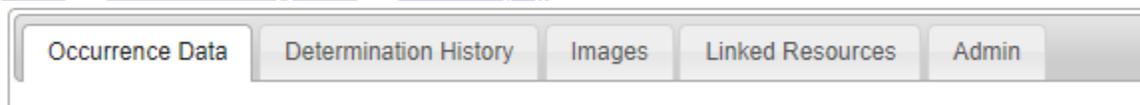
Occurrence Data – See explanation of fields in Section 16.7.2.
Determination History – where annotations are shown and can be entered. Annotations can also be batch uploaded from separate files. See Section 16.8 for instructions for using this tool.
Images – provides information on image(s) associated with the record. See Section 16.9.
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 Section 16.16) can delete specimen records.

16.7.2 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/.

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.

16.7.3 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 Download Backup Data File on page 48 of this guide) prior to making batch edits**

For batch editing of scientific names, see Section 16.8.

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 Section 16.5), 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 Section 16.5). 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."

16.7.4 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 Section 16.3.2). 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 Section 16.8 for instructions on how to use this tool.

16.8 Adding determination/annotation data

Navigate to this tool by accessing the Data Editor Control Panel (see Section 16.3) 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. If the latter option is used, a table of specimens of the indicated taxon will appear below the "Define Specimen Recordset" box, demonstrated in the image on the next page. 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" to uncheck all the boxes if you would prefer to select specimens one by one rather than eliminating those that do not need to be annotated.

	Catalog Number	Scientific Name	Collector/Locality
✔		Nemophila menziesii	David Keil 34384; United States, California, San Luis Obispo, Highway 41 between Creston and Shandon at 3220 Highway 41
✔	83127	Nemophila menziesii	Viola C. Call 22; USA, California, San Luis Obispo, North-facing rocky slope near entrance to Routzahn park in Arroyo Grande canyon.
✔	48660	Nemophila menziesii	Michener & Bioletti s.n.; United States, California, San Francisco, Lake Merced
✔	31240	Nemophila menziesii	Julie M. Vanderwier 102; United States, California, San Luis Obispo, Indian Knob Tar Sands
✔	64941	Nemophila menziesii	Greg Wilvert 34; United States, California, San Luis Obispo, SE half of the Caliente Range. Approx 1.6 km NNW of Wells Cyn
✔	66647	Nemophila menziesii	D. R. Miller 494-162; USA, California, San Luis Obispo, Pine Mt Region. from slope along Ridge Rd between Ridge meadows, Tobacco Crk drainage

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 name will not be changed. You can also print determination/annotation labels by checking the "Add to Annotation Print Queue" box and using the label manager tool (described below).

16.9 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 (Section 16.18.1), 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 Section 16.7) 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 page), 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

16.9.1 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 introduction to Section 16.9). NOTE: If you wish to move the image to a different specimen record rather than delete it entirely, see Section 16.9.2.

16.9.2 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.

16.10 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 Section 16.3). The following resources are currently linkable to a specimen record:
1. Checklists for which the specimen is a voucher (Checklist Voucher Linkages box)
2. Duplicate records, even those housed at collections other than your own (Duplicate Specimens box)
3. Genetic data such as sequences listed on GenBank (Genetic Resources box)

16.11 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 Section 16.7) 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 Section 16.9) prior to deleting the record. If there are no warnings at this point, click the Delete Occurrence button.

16.12 Printing labels or annotations

To print specimen labels, navigate to the Data Editor Control Panel (see Section 16.3) and click "Print Labels/Annotations." 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.

At the bottom of the page in the "Label Printing" box, 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.

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. 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
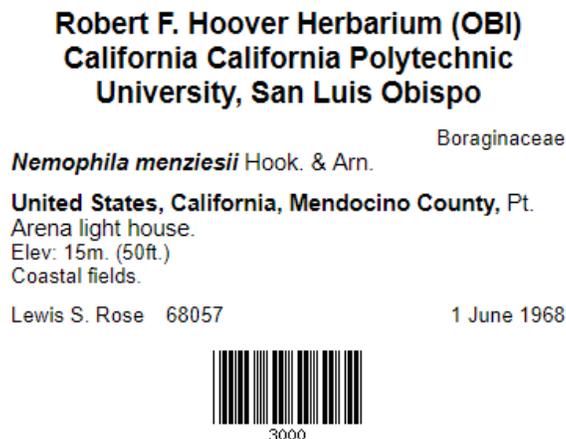
An example label for the Symbiota guide

16.13 Managing loans, gifts, and exchanges

Navigate to the loan management tool by accessing the Data Editor Control Panel (see Section 16.3) and clicking "Loan Management." You will see the following tabs:

| Outgoing Loans | Incoming Loans | Gifts/Exchanges |

Outgoing Loan Records   ╋
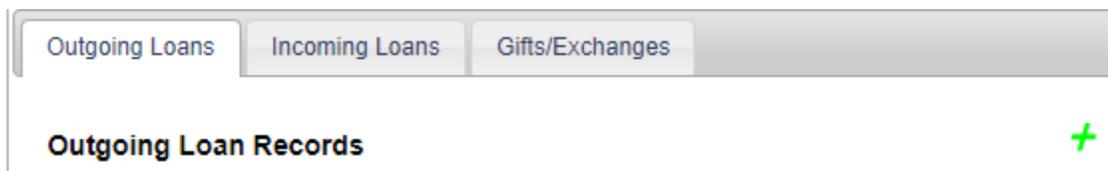
To add a new outgoing loan, click the green plus sign near the right side of the "Outgoing Loans" page. You will be prompted to enter a Loan Identifier (a unique number to mark the identity of the loan) and select an institution to which the loan is being sent from the dropdown list. If the institution 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 screenshot below).
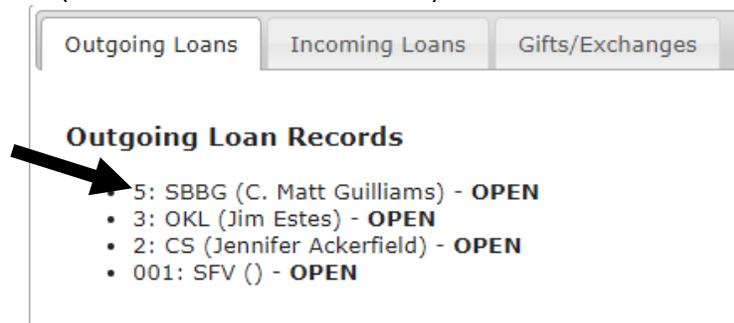
To add a new incoming loan, repeat the procedure outlined above using the "Incoming Loans" tab. Note that specimens cannot be linked to incoming loans.

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.

16.14 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 16.3) 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.

16.15 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 16.3) and clicking "Edit Metadata and Contact Information." A number of fields will be available for editing (see screenshot on next page). Unless you have special reason to do so, the following fields should not be changed: I*nstitution Code, GUID source, Dataset Type, Management*.

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

Edit Collection Information

Institution Code:	OBI ℹ
Collection Code:	ℹ
Collection Name:	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
Homepage:	http://bio.calpoly.edu
Contact:	Jenn Yost, Director and Assistant Professor
Email:	jyost@calpoly.edu
Latitude:	35.302189 🌐
Longitude:	-120.659350
Category:	Vascular Plants ▼
Allow Public Edits:	☐ ℹ
License:	CC0 1.0 (Public-domain) ▼ ℹ
Rights Holder:	ℹ
Access Rights:	ℹ
GUID source:	Symbiota Generated GUID (UUID) ▼ ℹ
Publish to Aggregators:	GBIF ☑ ℹ
Source Record URL:	ℹ
Icon URL:	http://www.portal.capturingcaliforniasflowers.org/portal/content/colli Upload Local Image ℹ
Dataset Type:	Preserved Specimens ▼ ℹ
Management:	Live Data ▼ ℹ
Sort Sequence:	ℹ
Global Unique ID:	3818d95b-b6a4-11e8-b408-001a64db2964 ℹ
Security Key:	3a095a57-b6a4-11e8-b408-001a64db2964

Save Edits

This page is also where you can update your mailing address for loans at the bottom of the page. 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.

16.16 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 Section 16.3.2).
- **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 16.3) 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

16.17 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.

NOTES

- 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 Section 16.3.2). Click "Full Text File Import."
- 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 note on next page), 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 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: ...
   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!**

16.18 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.

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

Specimen Processor Control Panel

This management module is designed to aid in establishing advanced processing workflows for unprocessed specimens using images of the specimen label. The central functions addressed in this page are: Batch loading images, Optical Character Resolution (OCR), Natural Language Processing (NLP), and crowdsourcing data entry. Use tabs above for access tools.

16.18.1 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.

16.18.2 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 screenshot on next page), 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.

Robert F. Hoover Herbarium, Cal Poly State University

Introduction	Image Loading	Crowdsourcing	OCR	Reports	Exporter	GeoLocate CoGe

Robert F. Hoover Herbarium, Cal Poly State University (OBI)
This module can be used to submit and manage records for data entry by the general public. For more information, see the Symbiota documentation on crowdsourcing.
    Instructions: This is a test

Total Counts:

    Records in Queue: 9 ✕
    Pending Approval: 1 (Review)
    Closed (Approved): 0
    Available to Add: 12161 (Add to Queue)

Volunteers

User	Score	Pending Review	Approved
Test, Iam	0	1 (Review)	0

Approved Editors

User	Score	Pending Review	Approved
No records processed			

Visit Source Board

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 Section 13).

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

16.18.3 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.

16.18.4 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 screenshot below).

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 screenshot below).

16.18.5 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 Section 16.18.6).

16.18.6 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

16.19 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.

16.20 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 Section 16.3). 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 Review Status: LEAVE AS IS ▼
- ○ Revert Edits

[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 cannot serve as a gateway to vetting edits before they are made public.

16.21 Duplicate clustering

The Duplicate Clustering dashboard can be accessed through the Administration Control Panel (Section 16.3). 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 Section 16.22.2.3 for more information on using this tool.

16.22 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 Section 16.3) under Data Cleaning Tools. The Data Cleaning dashboard will look like the screenshot below.

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...

16.22.1 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(see screenshot on next 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.

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.

16.22.2 Geographic cleaning tools

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

16.22.2.1 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 page), or you can search for those records using the record search form and batch edit them (see section 16.7.3).

16.22.2.2 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).

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 <u>not</u> 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 page).

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.

16.22.3 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 screenshot below:

16.22.3.1 Analyze taxonomic names

This function analyzes the values that exist in the Scientific Name field in your database and recognizes 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.

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

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

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.

16.22.3.2 Taxonomic distributions

Much like the Geographic Distribution viewer (Section 16.22.2.1), 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 page), or the user can search for those records using the record search form and batch edit them (see section 16.7.3).

- 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)

16.22.3.3 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 Section 16.21) 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.

.

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

16.23 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 (Section 16.3) and select Download Data Backup File.

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. UTF-8 is recommended. 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

16.24 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 (Section 16.23) with which you can replace your current database.

To replace your database, navigate to the Administration Control Panel (Section 16.3) 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 page), 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 page). 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!**

16.25 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 (Section 16.3) 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).

16.26 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.

16.26.1 Creating a checklist

A video tutorial of this process (on a general Symbiota site) is available here:
http://symbiota7.acis.ufl.edu/temp/2-checklists_create.mp4
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.

16.26.2 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.

16.26.2.1 Adding individual taxa

A video tutorial of this process (on a general Symbiota site) is available here, beginning at minute 7:15: http://symbiota7.acis.ufl.edu/temp/2-checklists_create.mp4

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.

16.26.2.2 Batch uploading taxa

A video tutorial of this process (on a general Symbiota site) is available here: http://symbiota7.acis.ufl.edu/temp/3-checklists_batch_load.mp4

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 section 16.26.2.1 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.

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

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

16.26.3 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.

16.26.3.1 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 screenshot on next page), 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.

16.26.3.2 Adding specimens from any collection (Manage Linked Voucher tool)

A video tutorial of this process (on a general Symbiota site) is available here:
http://symbiota7.acis.ufl.edu/temp/4-checklist_voucher.mp4

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 Section 16.26.1, 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 Section 16.26.1, 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)
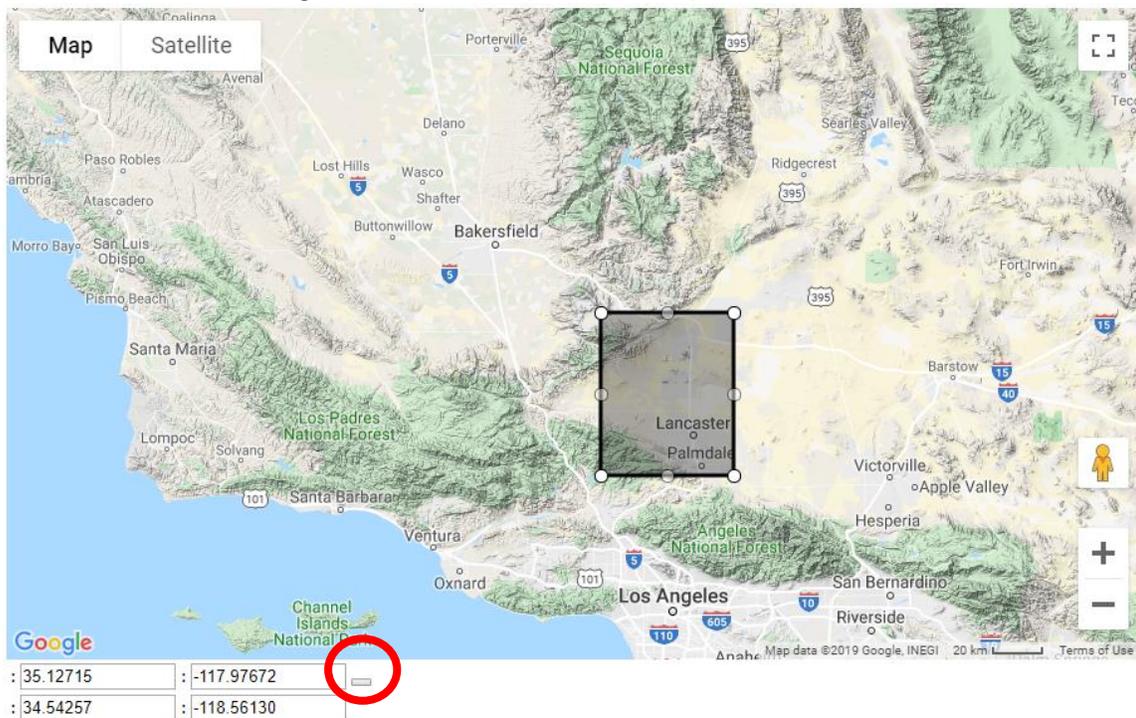
- There are a number of important **checkboxes** below the Lat/Long fields that you can use to refine your search. For example, you can allow the search to return specimens with the desired search terms OR within certain latitude and longitude coordinates.
- You can use any combination of the above options 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 Section 16.26.2) 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.

16.26.4 Other checklist tools

16.26.4.1 Voucher conflicts tab

In the Manage Linked Vouchers tool (see section 16.26.3.2), 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.

16.26.4.2 Reports tab

You can generate a number of useful reports using the Reports tab in the Manage Linked Vouchers tool (see section 16.26.3.2), 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 scientific name only)
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)

References

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