Digitization Workflow

Created 15-July-2015
Updated 13-Aug-15

Creating MyCoPortal Records

1. Log in to MyCoPortal
   a. Go to "My Profile" → "Specimen Management" → Choose the collection you wish to add a record to → "Add New Occurrence Record."

2. Populate as many fields as possible using the specimen label information, but the MINIMUM is the Scientific Name (Genus and species) and Catalog Number (Barcode) fields.

3. Change "Processing Status" to "Stage 1."

4. Click "Add Record" (make sure "Follow-Up Action:" is set to "Go to New Record").

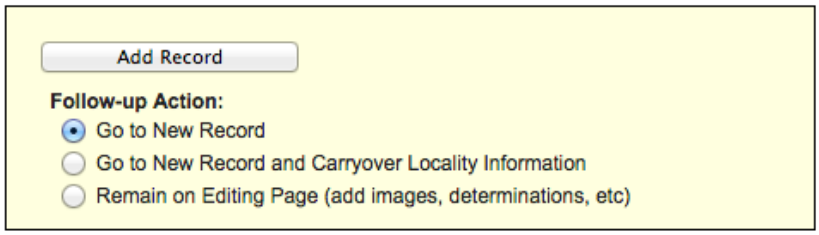


Image Capturing

1. Turn on the lights (give them a minute or two to get bright).

2. Turn on the camera (flip the camera switch to "on").

3. If it does not open automatically, open EOS Utility → click on "Camera settings/Remote shooting" → make sure images are being saved in correct folder. We save each day's images in a separate folder named with the date (i.e. "1 May 2015", "2 May 2015", etc.).

4. Open Digital Photo Professional → make sure the correct folder is being displayed in window
(select the folder from the menu on the right side of the screen)

5. Take the first specimen to be photographed
    a. Open the packet/box and remove any ancillary items (additional labels, notes, illustrations, spore prints, etc.)
    b. One at a time, place each item separately under the camera with the barcode and capture an image.
    c. After all the ancillary items have been photographed, the barcode can then be attached to the main specimen packet/box and photographed.
        - Some items may be very old and brittle- please, handle them carefully.
        - With folded items, gently unfold them to image. They do not need to be perfectly flat; the camera will autofocus and collect a clear image.

6. Repeat this process until you have about 80 images in the folder.

7. Rename the images with the barcode number according to the following protocol (barcode_1, barcode_C1, etc.).

Table 2. Image naming conventions for jpeg uploads to MyCoPortal

Image Type	Convention	Example
Main Label	Just the Barcode	ILL00042658
Additional Labels	Barcode_Integer	ILL00042658_1 ILL00042658_2
Field Notes	Barcode_C[Integer]	ILL00042658_C1 ILL00042658_C2

*for additional information (convention for photographs, spore prints, etc.), refer to pg 35-37 of the manual

8. Switch to a new, empty folder on EOS Utility and Digital Photo Professional and continue imaging.

[If images are not showing up in Digital Photo Professional, double check to make sure you (1) have them saving to the correct folder through EOS Utility (step 3 above) and (2) have the correct folder selected for display on the screen of Digital Photo Professional (step 4 above.)]

Image Editing: Setup

1. Open Adobe Photoshop.

2. Open a single image (make a duplicate of a file and use the duplicate, or use an image you do not need).

3. Go to "Window" → "Actions"
    a. Click "Create New Set" (folder icon) and name it (i.e. "Batch Edit")
    b. Making sure that your new set is highlighted, click "Create New Action" (rectangle next to the folder icon) and name it (i.e. Grayscale, Crop, Copyright.)
    c. Click "Record" (the circle should turn red.)
    d. Go to "Image" → "Mode" → "Grayscale"
    e. Go to "File" → "Automate" → "Crop and Straighten"
    f. Go to "File" → "File Info" → Add your Institution as the "Author" and select "Copyrighted" as the "Copyright Status." Click OK.
    g. In the Actions Window, hit stop (the rectangle) and the red circle will turn gray.

Image Editing: Batch Processing

1. Open Adobe Photoshop.

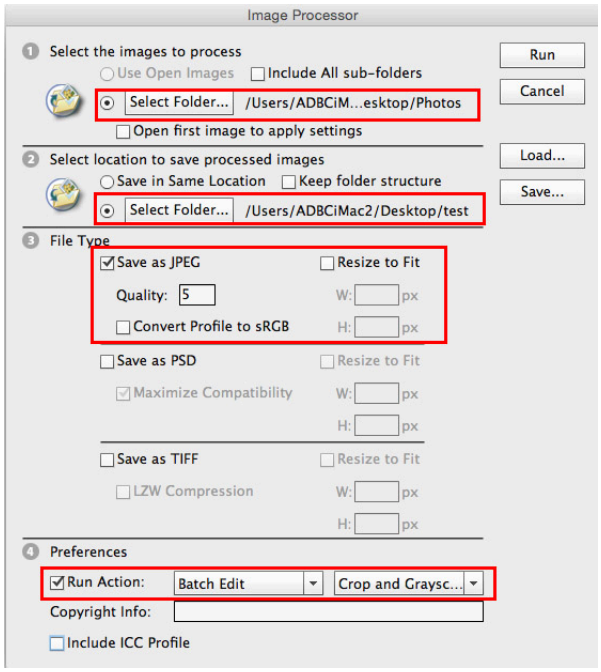
2. Go to "File" → "Scripts" → "Image Processor"

3. In Box 1, choose the folder containing your Raw Images (.CR2 files).

4. In Box 2, choose the folder you want the images to be stored (i.e. [dayMonthyear_JPG]).

5. In Box 3, make sure the "Save as JPEG" box is checked (do not resize or compress).

6. In Box 4, check "Run Action" and then choose the set and action you already set up.



7. Click “Run” (top right corner)

8. Let Photoshop do its thing…this may take a few minutes.

9. Repeat steps 2 through 7 until you have processed all of your raw images. Click File > Close All to close all the images in the program once they have been processed.

   [As way to keep track of the progress and make sure no images are getting left out, transfer raw image files (folders of about 80-90) into a single Raw images file as you process them. The number of items in the Raw folder and the JPG folder should always match up.]

10. Once all images have been processed, open the JPG folder and sort it by size. Images should be around 200-400 KB. Any images significantly smaller than that were probably cropped too much in Photoshop. Reopen these images in Photoshop and manually crop, straighten, and change to grayscale before saving them in the JPG folder, replacing the incorrectly cropped images.

Files are now ready to be uploaded through FTP (i.e. FileZilla).

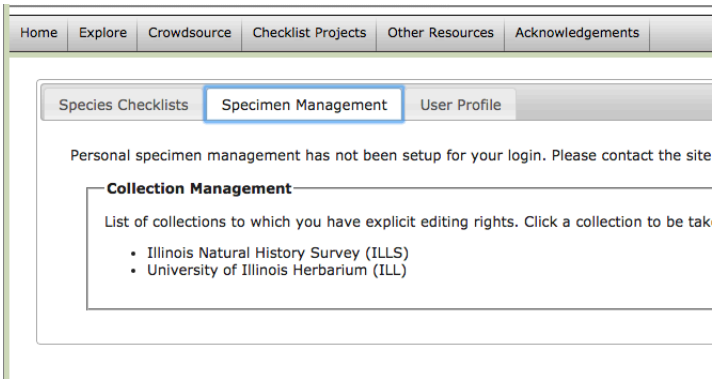
See document: Uploading_Images_Via_FTP

Uploading Skeletal Records Via Mycoportal

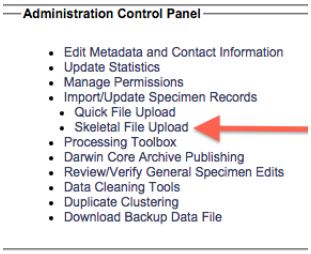
Created 13-July-2015

1. Log onto http://mycoportal.org/portal/index.php with credentials.

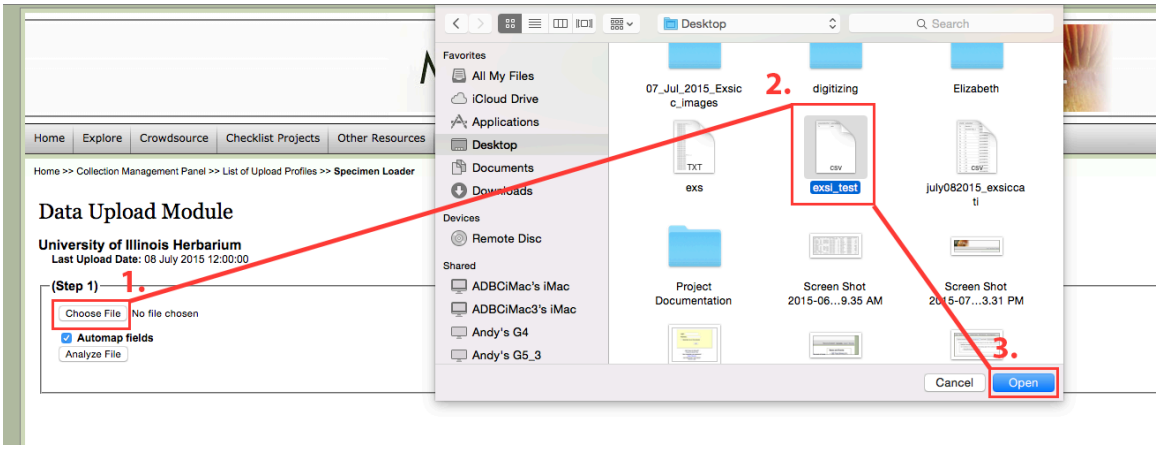
2. Go to My profile, select Specimen Management, and select collection related to upload.



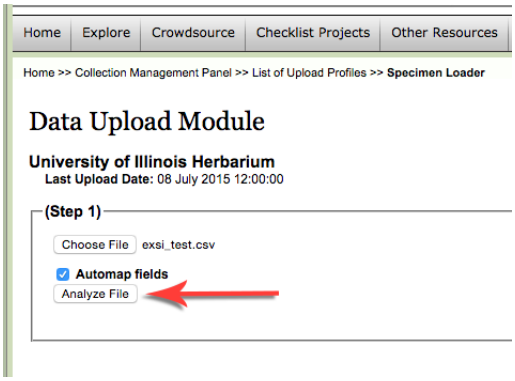
3. Underneath Administration Control Panel, select Skeletal File Upload.



4. Within the Data Upload Module, choose the .csv file you wish to upload.

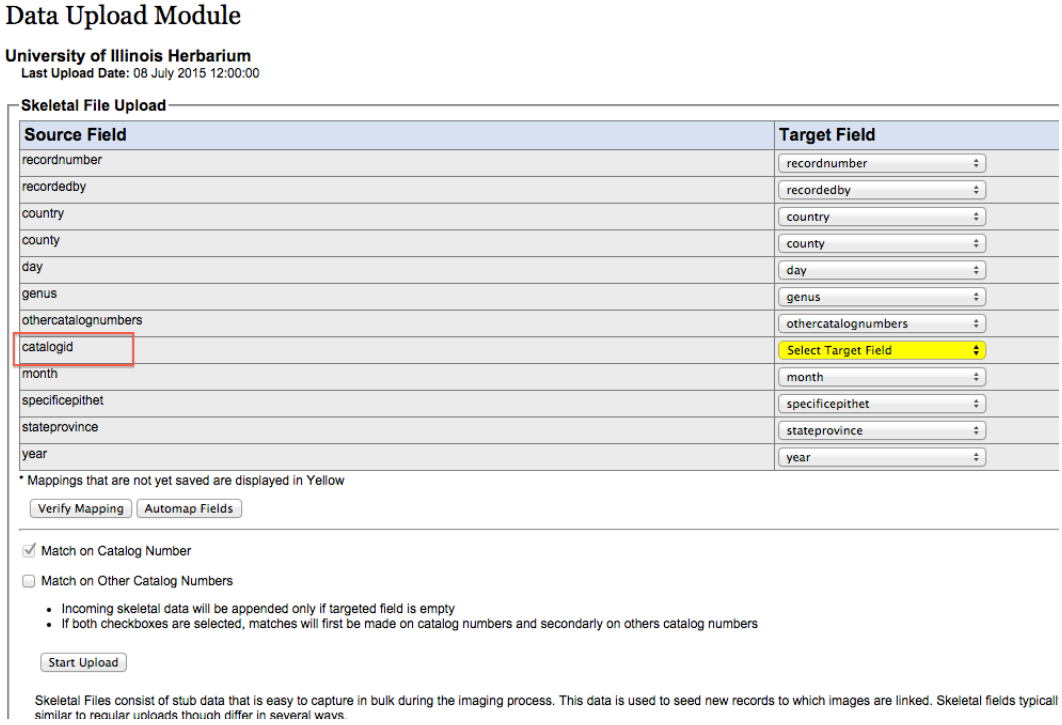


5. Hit Analyze File.



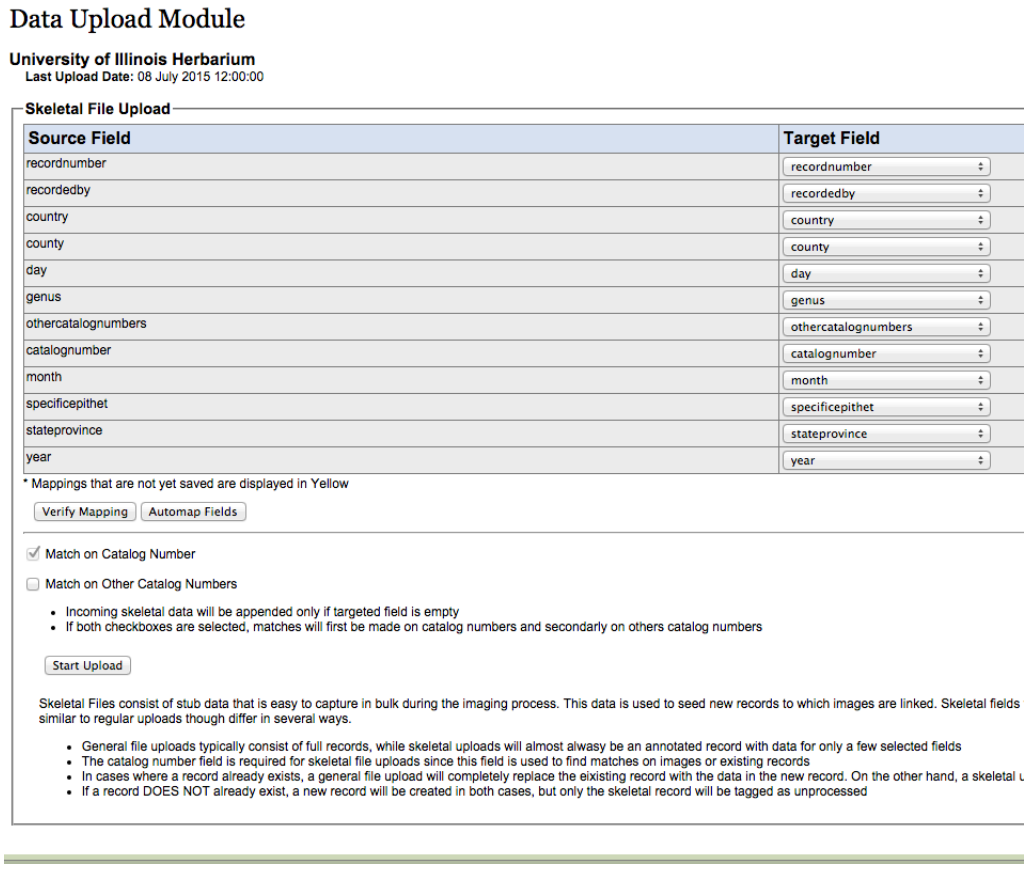
6. The following table maps the institution's .csv headers (Source Field) with the Symbiota headers (Target Field.)

   Fields highlighted in yellow indicate that the Source Fields do not automatically match with the Target Fields. This could be due to misspelling, mislabeling, or institutional preferences in the original .csv.



Example of field-mapping errors.

Go into the Target Field drop-down bar and select the corresponding header. Consulate http://symbiota.org/docs/wp-content/uploads/SymbiotaOccurrenceFields.pdf for aid in determining the correct Symbiota header.

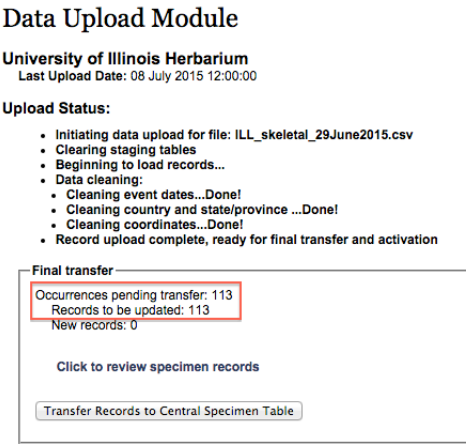


Example of good field mapping.

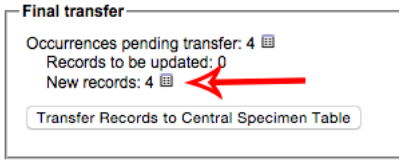
7. Hit Start Upload.

8. On the next page, Occurrence Pending reflects the number of records in the .csv sheet. Records to Updated reflects the number of records duplicated from the .csv sheet that will be uploaded into the portal. Both numbers *must* match [image 8a.]

   If the page lists New Records, click on the icon next the New Records number [image 8b], which will pull up a table of the "new records" [image 8c.] There is probably an error in the Catalog Number field. Open the .csv file, sort it by catalogNumber (go to Data→ Sort→ find catalogNumber in the column drop down and make sure "my list has headers" box is checked), locate and correct the error [image 8d.] Save the corrected .csv, replacing the old one. Go back to Step 4 and re-upload the file.



8a. Correct .csv; ready for Step 9.

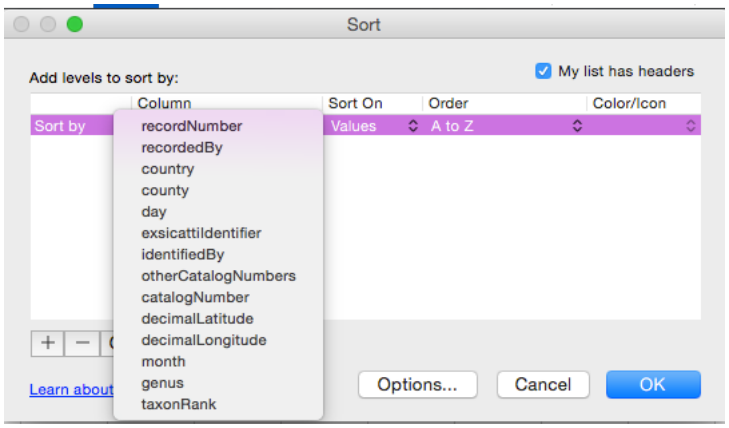


8b. Error in .csv, click the icon to the right of New Records, troubleshoot, and fix before proceeding.

Illinois Natural History Survey (ILLS)

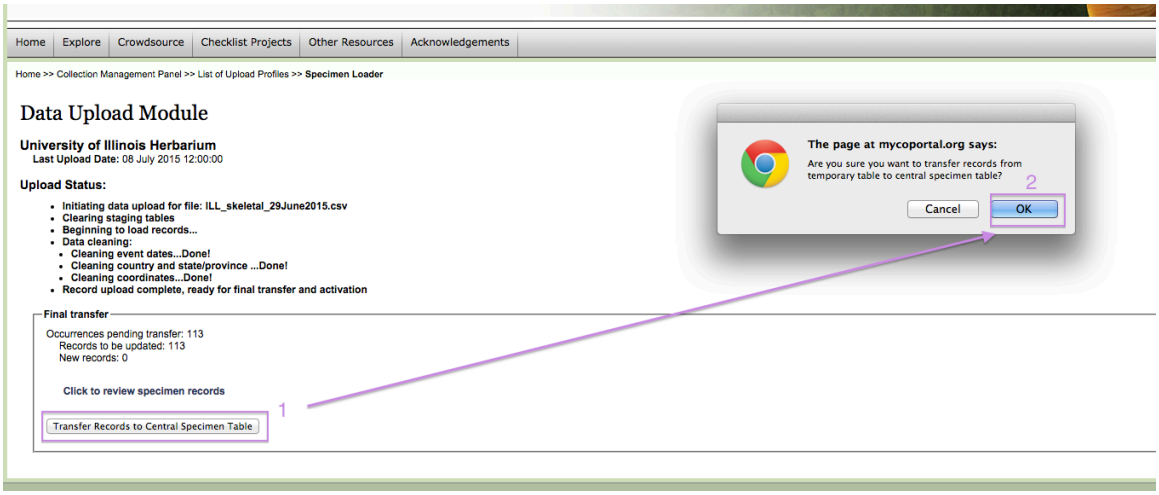
Catalog Number	Processing Status	Basis Of Record
ILL000085124	unprocessed	PreservedSpecimen
ILL00084964	unprocessed	PreservedSpecimen
ILL00085490	unprocessed	PreservedSpecimen
ILL00085491	unprocessed	PreservedSpecimen

8c. Table of New Records



8d. Sorting the .csv file

9. Hit “Transfer Records to Central Specimen Table” and then “OK”.



10. When the .csv file is done loading, double-check to assure that specimens were uploaded.

    a. Return to My Profile → Specimen Management → Collection Management and select the collection the file was uploaded to.
    b. Select Edit Existing Occurrence Records.
    c. Search a few of the specimens from the .csv by entering in the Catalog Number.
    d. Check that the fields are populated with info matching the images.

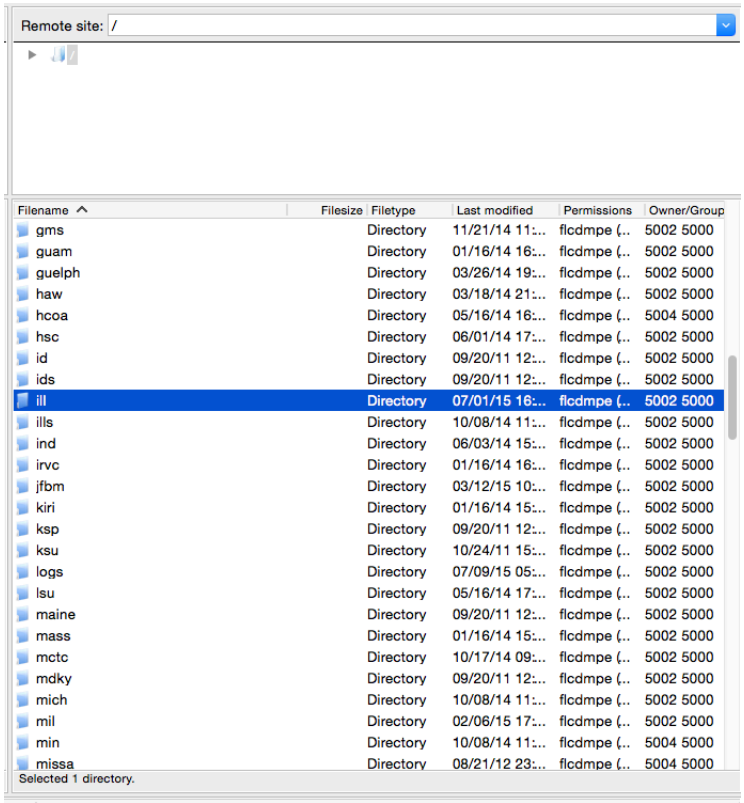
Uploading Images Via FTP

Created 10-July-2015

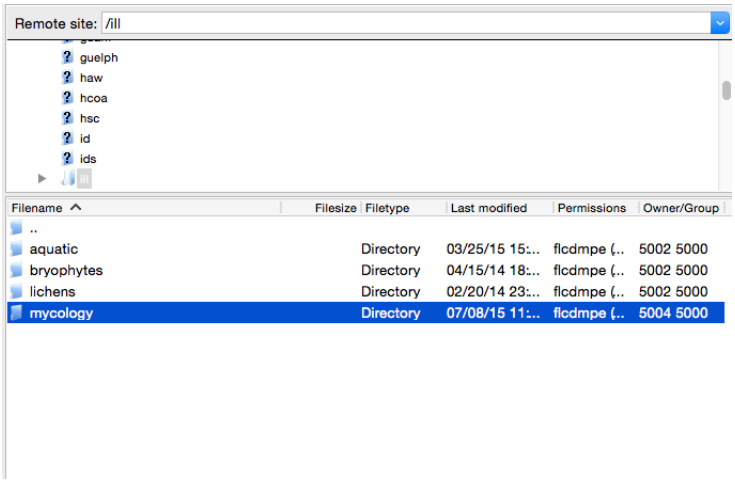
1. Open FileZilla and log into the idigbio server with the following credentials:
   Host: storage.idigbio.org
   Username: mfccstorage
   Password: macrofungi
   Port: 21
   Protocol: FTP [no encryption]

2. The directory on the left lists the files on your computer (Local Site) and the directory on the right lists the files on the iDigBio server (Remote Site.)

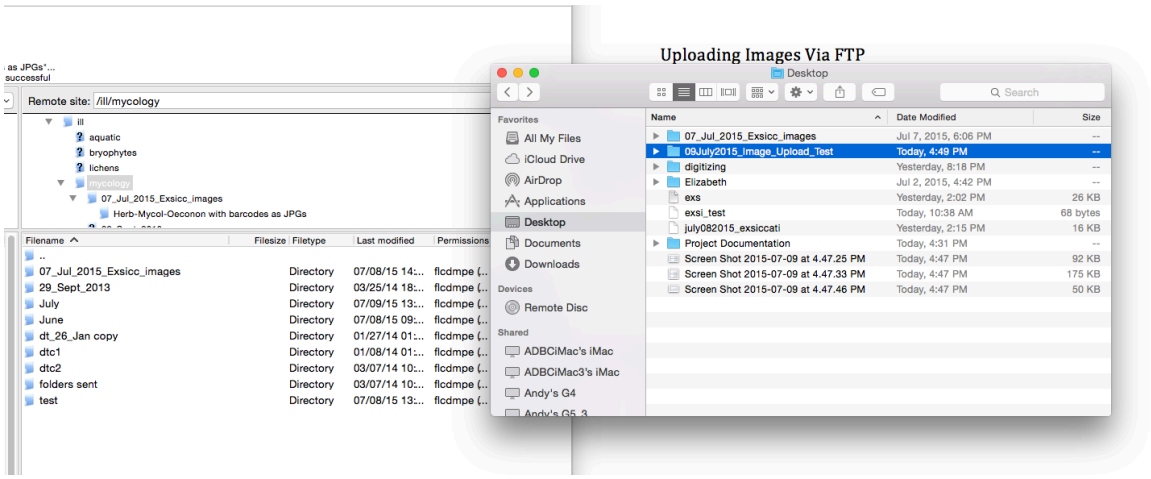
   Locate and open the Filename corresponding to your institution's code on the right.

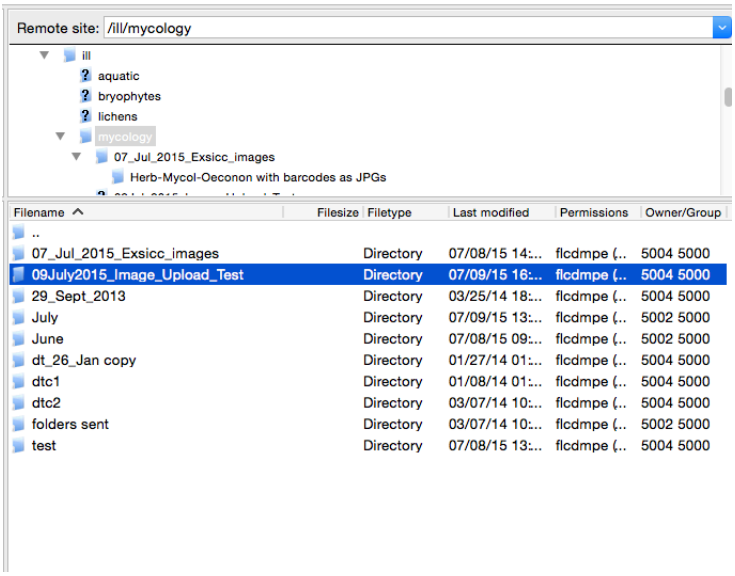


3. Locate and open the “mycology” folder.



Locate the folder of images and copy them over to this folder. The images will be automatically uploaded to iDigBio overnight.





Naming Conventions

Created 14-July-2015

Table 1. List of codes to be used before .csv file is uploaded to MyCoPortal

FileMaker Field	Excel Header
Collector Number	**recordNumber**
Collector	**recordedBy**
Country	**country**
County	**county**
Day	**day**
Det.	identifiedBy
Exsiccati	exsiccatiIdentifier
Genus	**genus**
Host/Substrate	substrate
Accession Number	**otherCatalogNumbers**
Barcode No.	**catalogNumber**
Latitude (decimal)	decimalLatitude
Longitude (decimal)	decimalLongitude
Month	**month**
Notes	notes
Species	**specificEpithet**
State/Prov.	**stateProvince**
Var. or Subsp. or Forma*	**taxonRank** **infraspecificEpithet**
Year	**year**

*note that "Var. or Subsp. or Forma" must split into two columns: v/f/t abbreviation (taxonrank) and actual name (infraspecificepithet)

****those in bold are more common to skeletal records**

***those in plain font are additional with Stage 2 records

Table 2. Image naming conventions for jpeg uploads to MyCoPortal

Image Type	Convention	Example
Main Label	Just the Barcode	ILL00042658
Additional Labels	Barcode_Integer	ILL00042658_1 ILL00042658_2
Field Notes	Barcode_C[Integer]	ILL00042658_C1 ILL00042658_C2

*for additional information (convention for photographs, spore prints, etc.), refer to pg 35-37 of the manual

Downloading Collection Back-Up

1. Log in to MycoPortal.

2. Go to My Profile → Collection Management and select your collection.

3. Underneath Administration Control Panel, click Download Backup Data File (image A) and select Perform Backup (image B.)

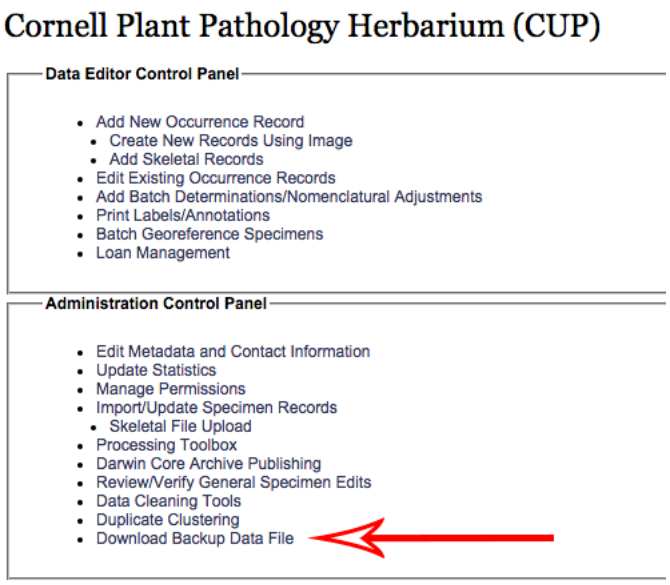


Image A

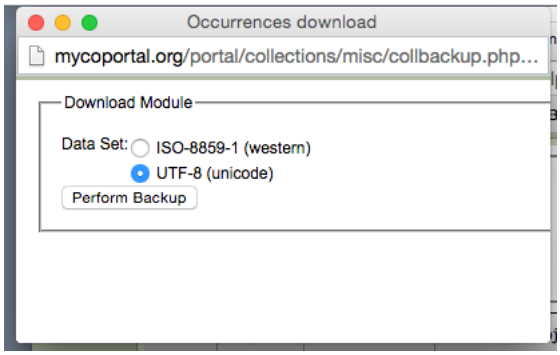
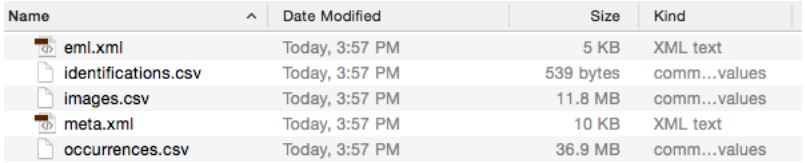


Image B

4. This will download a zip of .cvs files of: occurrence records and links to the image locations on the idigbio server. The files can be 1) used to save data in case of data-loss or iDigBio server issues 2) manipulated to be ingested into an institution's own database and 3) used for assigning and tracking batches of transcription work.

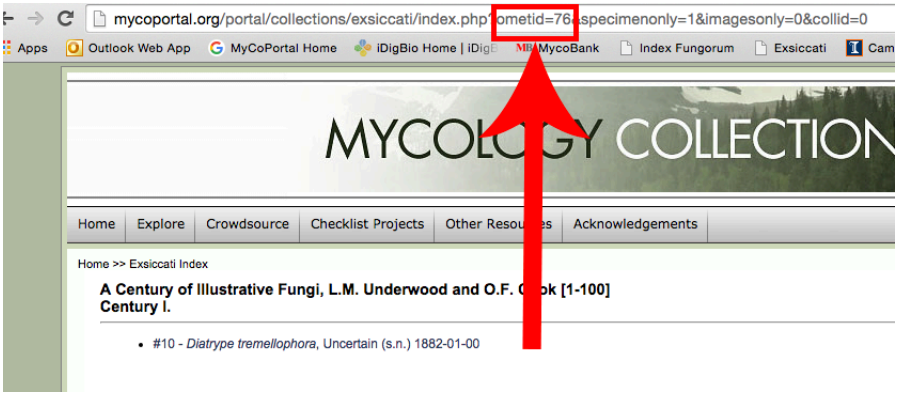


Uploading Exsiccati Skeletal Records

Created 12-October-2015

1. When constructing .csv files to upload exsiccate sets, include the columns *exsiccatiIdentifier* and *exsiccatiNumber*.

   ExsiccatiIdentifier refers to a database number assigned individually to each exsiccati title. This can be found by selecting the title, looking at the website address, and locating the ometid= code in the address. The number following "ometid=" is the exsiccatiIdentifier.



   Ex: The exsiccatiIdentifier is 76 for this exsiccati.

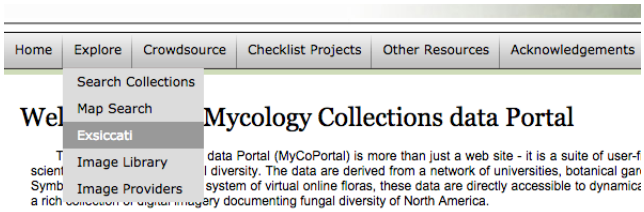
   ExsiccatiNumber refers to the number assigned to the specimen within the exsiccati.

2. Follow the steps in the Uploading Skeletal Records workflow guide.

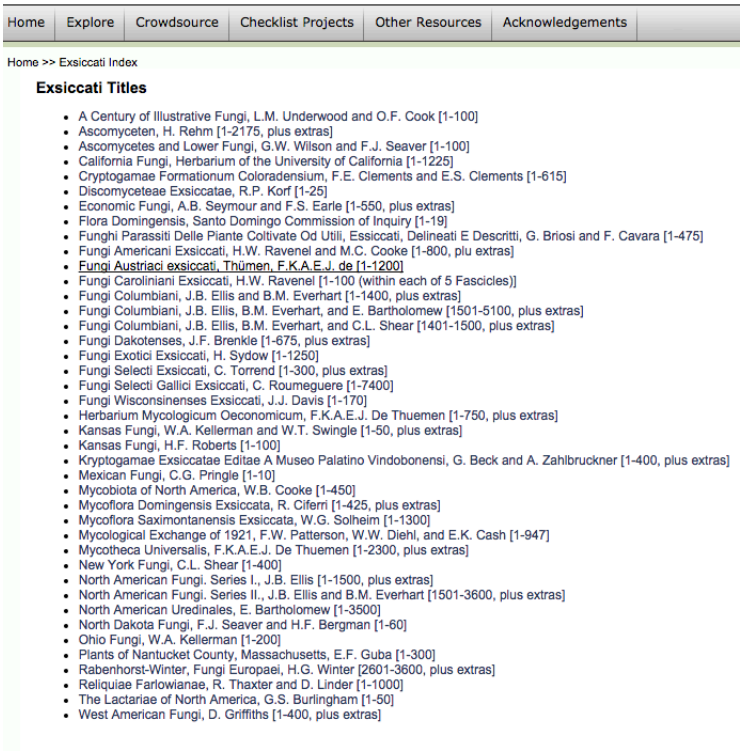
Transcribing Exsiccati

1. Log onto http://mycoportal.org/portal/index.php with credentials.

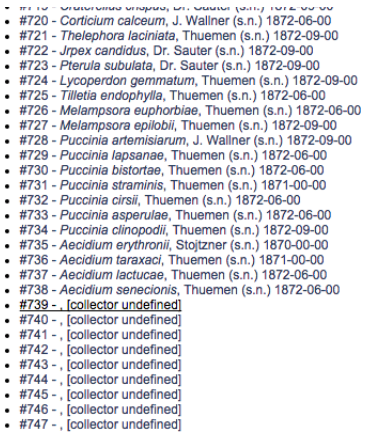
2. Go to Explore → Exsiccati



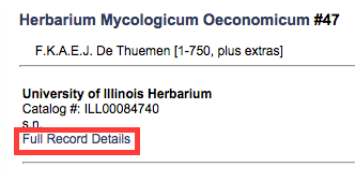
3. Select the Exsiccati Title you wish to work from.

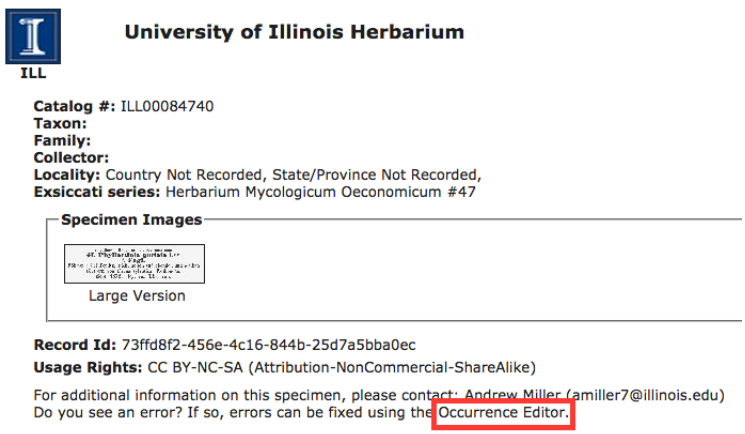


4. Select the individual exsiccate record you wish to transcribe.



5. Click Full Record Details and then in the next window click Occurrence Editor.





6. Transcribe the exsiccati record. Please refer to the Exsiccati Transcription Guidelines below.

7. If you wish to add another exsiccate record to this exsiccati, then go to Add New Occurrence Record in the Data Editor Control Panel, enter data into the necessary fields (Exsiccati Title, Exsiccati Number, Collector, Date, Notes, etc.), and save new occurrence record.

Exsiccati Transcription Guidelines

- Collector
  - usually marked as "legi _____" on the label, or some variant.
  - "Ipse legi" refers to the exsiccati collection author as the collector.

- Date
  - formatted in year/month/date.
  - Use 0's as placeholders for unknown data, leave blank if completely unknown.
  - Latin: vere – spring; aestate – summer; autumn – autumn; hieme – winter.

- Scientific Name
  - As you type the name, the list of species within the portal's dictionary will generate. Select the correct name.
  - Oftentimes the name will not be in the dictionary; type the name out as best as possible, anyway.

- Author & Family
  - If either of these are not auto-generated with the scientific name, then do not worry about them. They will be automatically filled in after we implement the MycoBank taxonomic thesaurus in the near future.

- Country
  - Use current country names. For example, Bohemia is now an area within the Czech Republic, so use the Czech Republic.
  - These, like the scientific names, will generate a list with the correct spelling as you type, select the name from the list.
  - United State is entered as "USA."

- Locality
  - Enter in the locality as it appears on the label. The georeferencer will have to determine the correct coordinates from your transcribed locality.

- Habitat & Substrate
  - Substrate = item the specimen was on (usually a plant, "rotting log"); Habitat = environment descriptor where the specimen was found ("grassy field")
  - Enter in the habitat and substrate as in appears, in the original language. If you are competent in the original language, include a translation [in brackets] if time allows.

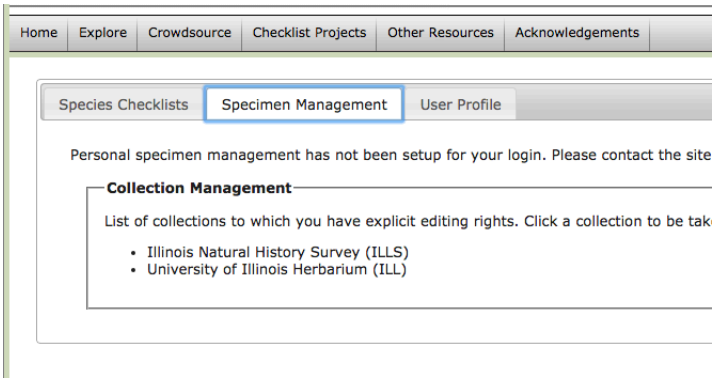
- Transcription vs. translation
  - Enter in the data exactly as it appears on the label (this is transcription). If you also choose to translate from the foreign language into English, then please include your translation in brackets after the transcribed data. Example: something in German [translated phrase in English]

Batch Georeferencing

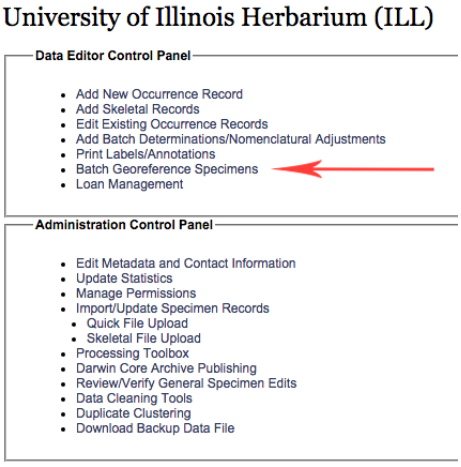
Batch Georeferencing should be done after images have been uploaded and fully transcribed.

1. Log onto http://mycoportal.org/portal/index.php with credentials.

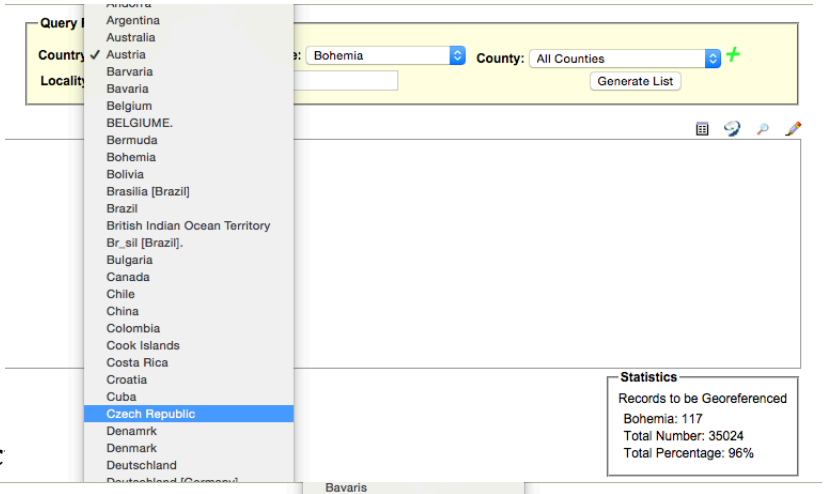
2. Go to My profile, select Specimen Management, and select your collection.



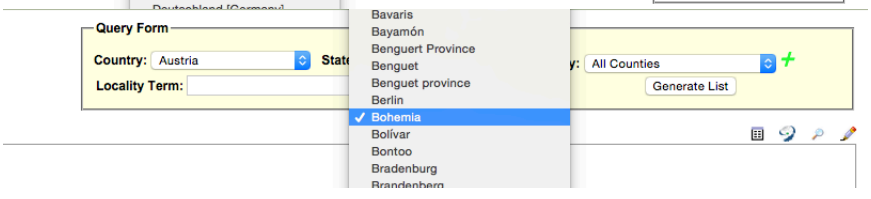
3. Underneath Administration Control Panel, select Batch Georeference Specimens.



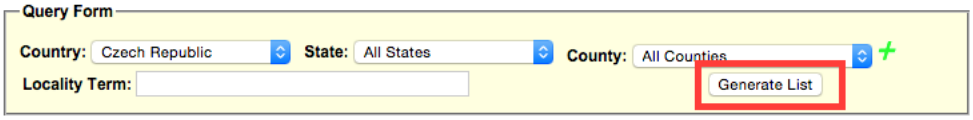
4. Select the country you wish to batch georeference.



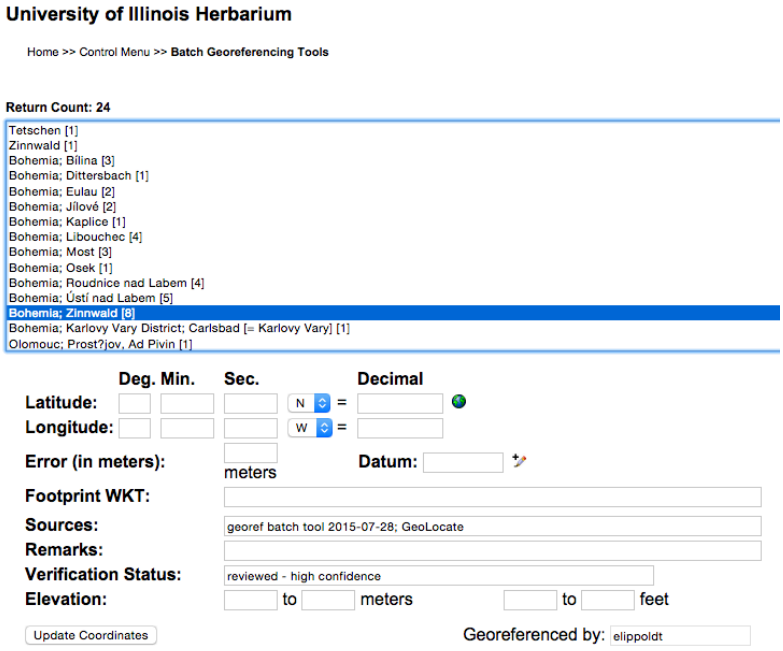
5. Selec



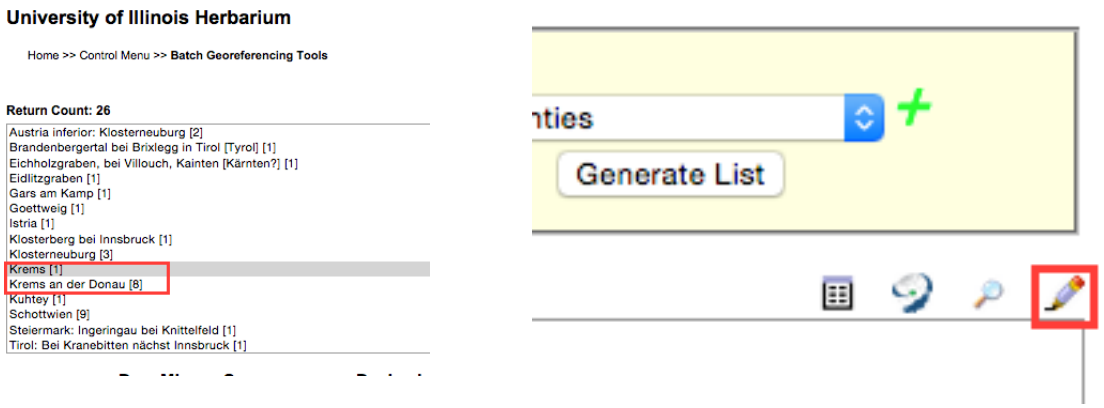
6. Hit "Generate List."



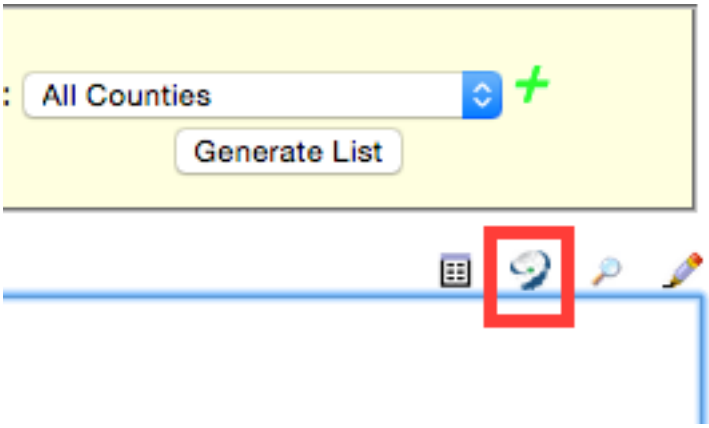
7. Select the locality you wish to georeference.



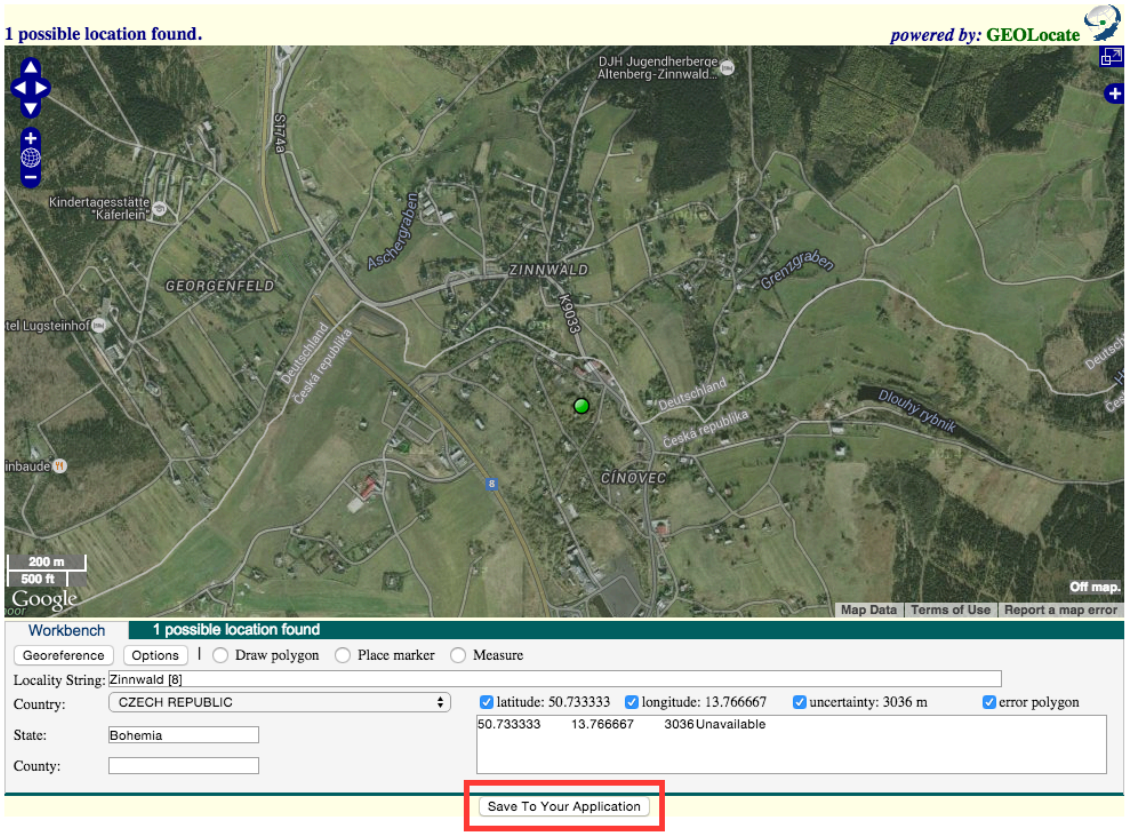
7a. Occasionally there are multiple locations that have been transcribed differently. You can go back and edit the occurrence records so that they are transcribed correctly by hitting the pencil button.



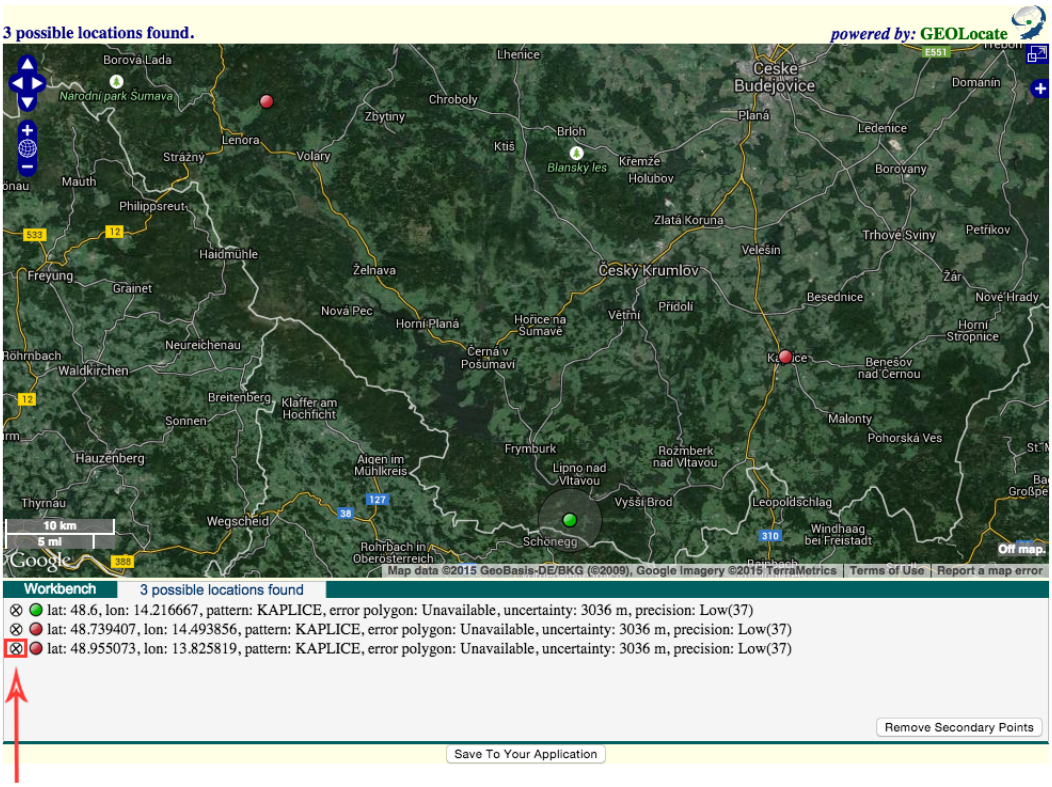
8. Hit the swirled Geolocate Locality button from the bar on the upper right.



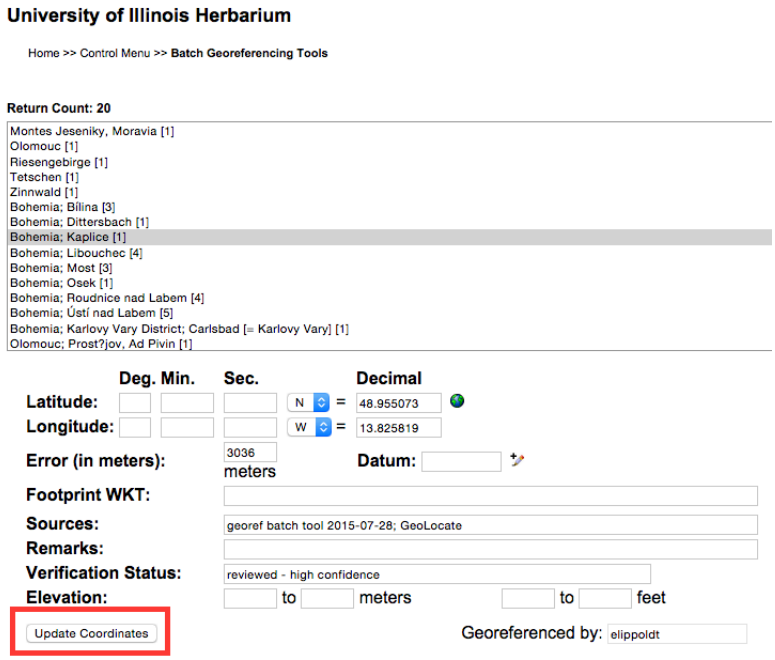
9. This will open a new window with Google Maps. Once you have determined that this location matches the locality of the specimens, hit Save to Your Application.



9a. Occasionally there will be multiple locations. Select them one by one and view it on the map to determine if they are plotted near the locality. If they are incorrect, hit the circled X button to remove them from the list. Do this until you have your determined correct locality.



10. Hitting Save to Application will plot the coordinates into the previous page. Hit Update Coordinates to apply this location to all the specimens of the selected locality.



11. You've successfully batch georeferenced specimens!