

## Pre-Capture Workflow for Herbarium Sheets (NEVP-TCN)

### Background

#### **Purpose of pre-capture stage and pre-capture application:**

With the aid of a software application, this workflow is designed to create human and machine readable labels or slips of paper to accompany containers of collection objects (folders of herbarium sheets) into a digitization apparatus where the machine readable information can be extracted at the container level and applied to the digital records of each of the contained collection objects. The purpose of this is to reduce redundant capture of information. For example, all the herbarium sheets in a folder are likely to share a current filed under identification. An initial pre-data-capture pass through the collection can capture this current identification once, print it in machine readable form, and associate that printed information with the folder. Thus, when that folder is brought to a station in a workflow, the machine readable information can be scanned and associated with the image and database record of each specimen in the folder, without the current identification having to be retyped for each sheet. The focus of this workflow is on capturing the filed-as identification and geographic area in which the specimens were collected.

Download pre-capture application:

[http://sourceforge.net/projects/datashot/files/PreCaptureApp/Version\\_0.12/PreCaptureApp.jar/download](http://sourceforge.net/projects/datashot/files/PreCaptureApp/Version_0.12/PreCaptureApp.jar/download)

Instructions on installing the pre-capture application:

[http://nevp.org/sites/default/files/resources/preCaptureInstall\\_1.4.pdf](http://nevp.org/sites/default/files/resources/preCaptureInstall_1.4.pdf)

Instructions on using and configuring the pre-capture application:

<http://datashot.sourceforge.net/precapture/ApplicationHelp.html>. This information can also be found through the **Help** menu within the pre-capture application.

What follows is a basic workflow. Your institution may choose to vary the steps below or add steps to accommodate the particular needs of your collection. See the iDigBio Workflow Modules and Task Lists for detailed information covering all stages of the digitization process:

<https://www.idigbio.org/content/workflow-modules-and-task-lists>.

#### **Basic Pre-Capture Workflow (may be concurrent with Inventory Workflow)**

- 1) Within your collection there may be sorting, conservation, curatorial, and selection activities that precede the steps presented below. See the iDigBio Pre-Digitization Curation Tasks module (Module 1):  
[https://www.idigbio.org/sites/default/files/sites/default/files/Module\\_1\\_Pre-digitization\\_Curation\\_Tasks.pdf](https://www.idigbio.org/sites/default/files/sites/default/files/Module_1_Pre-digitization_Curation_Tasks.pdf).
- 2) Select cabinet for pre-capture<sup>†</sup>.
- 3) Select folder(s) to which collection-level information will be produced. Remove only a few

vers. 06/09/14 – [http://nevp.org/sites/default/files/resources/preCaptureInstall\\_1.3.pdf](http://nevp.org/sites/default/files/resources/preCaptureInstall_1.3.pdf)

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folders at a time.

- 4) On a folder-by-folder basis, decide if collection-level information will be attached to the folder or to sets of specimens within the folder.\*
- 5) Choose **Change to SplitPane** from the **Window** menu.
- 6) For a folder or a set of specimens, select appropriate filed-as taxon name from the pick-list (i.e., the **Taxon** field). The individual taxon name fields will fill in automatically.
  - To facilitate this process, use the Family or Genus filter.
  - If taxon name is not in pick-list, type the elements of the taxon into the appropriate fields (i.e., Genus, Specific Epithet, etc.).
    - For hybrids not listed in pick-list, refer to section below: “**Guidance for entering Hybrids**”.
- 7) Add additional information (e.g., state, collector) that applies to all sheets in the folder(s)/set.
- 8) If more than one folder contains the same information, increase the number of labels/slips\*\* to print using the **Number to Print** field.
- 9) Press **Add To Print List**. Continue with steps 2) through 6) until you are ready to print labels/slips.
- 10) When you are ready to print several different labels/slips, go to the **Print List** tab.
- 11) Adjust any information you wish to change.
- 12) Press **Print**. The labels/slips will be written to a PDF file named labels.pdf, and a printer dialog will be invoked.
- 13) Associate printed labels/slips with folder(s) or sets of specimens\*\*.
- 14) Press **Clear** to empty print list.
- 15) If during the course of the pre-capture workflow specimens are encountered that need conservation, route individual specimens to conservation stream, as necessary. Ideally, these specimens should be returned to their folder before primary digitization.
- 16) Return folder(s) to cabinet.

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17) Continue steps 3 through 16 until cabinet is complete.

† *The status of the specimens within a cabinet should be indicated. For example, a marking could indicate if a cabinet "contains NE material", another could indicate "contains pre-captured NE material", and another could indicate "imaged NE material". These markings could be differently-colored pieces of tape or some other marking system.*

*\*In many collections, a folder will often contain specimens all of one species. If multiple species are contained within a folder, the genus can be recorded for the folder, or information can be recorded for subsets of specimens within the folder that all belong to a particular species.*

*\*\*The NEVP-TCN distribution of the pre-capture application is pre-configured to print in the formats presented in the table below. Adhesive labels can be printed (e.g., 2.3x4" Dymo LabelWriter) and adhered to a folder when the data is applicable to the entire folder. Alternatively data can be printed to sheets of paper (e.g., Half Sheet), or "slips", that can be inserted above the top herbarium sheet of the folder. When the data is applicable only to a subset of specimens in a folder, data can be printed to sheets of paper ("slips") that can be inserted above the top-most specimen of the subset.*

Print Format	Columns	Label Height	Label Width	Printer	Medium
Full Sheet	1	10.0	7.5	standard	8.5 x 11" paper
Half Sheet	2	10.0	3.25	standard	8.5 x 11" paper
2.5x4 on Paper	2	2.5	3.5	standard	8.5 x 11" paper
2.3x4" Dymo LabelWriter	1	3.7	2.1125	Dymo LabelWriter 450	Adhesive Label
4x2.3" Label	1	2.1125	3.8		

### Guidance for entering Hybrids not in authority file

1. If a named hybrid species (nothospecies), place elements of name in genus, species, authorship fields, prepending the specific epithet with a multiplication sign × (Unicode 00D7). Likewise for named hybrids at other ranks.
2. If a hybrid other than a named hybrid:
  - (a) place the entire hybrid name including the × separator (or separators) and the authors in the scientific name field. Leave the authorship field blank.
  - (b) If all constituents of the hybrid are in the same genus, place the generic name in the genus field. If more than one genus is involved, leave the genus field blank.

***Do not use the letter x in place of the multiplication sign × .***

## Inventory Workflow

If the inventory functionality has been enabled in your pre-capture application (property `config.showinventorytab=true`), then a tab will show up in the main program screen labeled **Inventory**. This tab allows you to estimate the number of specimens that are to be imaged within a container. The default configuration is for herbarium cabinets, organized by family, with measurements of how many inches thickness of sheets are present for the folders covered by your project in this cabinet in this family, along with an estimate of how many sheets are found per inch in this family. Follow project protocols for how to use this inventory if your project includes an inventory estimation in the pre-capture phase.

- 1) Select cabinet for inventory.
- 2) Within the PreCaptureApp click **Inventory** tab.
- 3) Within the PreCaptureApp click **Add Row**.
- 4) Enter the cabinet identifier into the **Cabinet** field of the Inventory table.
- 5) For the family to be inventoried, enter the family name into **Taxon** field\*.
- 6) For a subset of specimens within the target family, count the number of sheets present within an inch thickness. If possible, count four to five inches of specimens, and average the number of specimens in an inch.
- 7) Enter the per-inch value obtained in the step above into the **Sheets per inch** field.
- 8) Measure the total number of inches of New England specimens within the family and enter this value into the **Inches of New England** field.
- 9) Continue steps 2 through 8 until cabinet is inventoried.
- 10) When cabinet is inventoried, mark outside of cabinet with marking indicating such.

\*Visually inspect the cabinet to determine the taxon-level at which specimen thickness varies. In many cases all specimens within a family will be of a similar thickness, for other groups this may vary at the genus or even sub-generic level. If specimen thickness varies at a sub-familial level, select the appropriate taxon-level and enter this into the "Taxon" field. In this case, this will be the Taxonomic unit at which values will be obtained for the "Inches of New England" and "Sheets per inch" fields.