

PHOTO GUIDE WORKFLOW

OK, so you took a whole bunch of photos of cool critters, now what? If you were careful you took more photos than you need. So the first step in your workflow is to **get rid of extra shots that you do not need**. Modern digital camera files are large, so storage is an issue when generating many thousands of photos. An abundance of photos also burdens the user to look at more than they need to. As a rule of thumb **keep 1-3 shots per orientation of your animal**, more if you need to cover the focal depth across a tall specimen. Make sure you **keep some photos with the labels** as well.

Once you are done with weeding out the extra photos, it is best to **rename your photos with unique identifiers**. As with the specimen and station numbers this is best done with a prefix, followed by a series of numbers. For our class projects, I used **dMBM_#####**. **Use enough digits to fit all photos – 5 digits allow you to catalog up to 99,999 photos from a project. Use all five digits, so programs can sort your photos alphanumerically in order – thus use dMBM_00011, not dMBM_11**. Several programs allow you to rename photo filenames, or you can write your own script to do so. I use **Adobe Bridge – a program coupled with Photoshop**. Bridge will recognize duplicate photos (like jpg and raw of same shot) and renumber them with the same number. In Bridge this is done with the Tools – Batch Rename command.

Next, **associate the file name of your photo with the specimen number of the subject in a spreadsheet**. This is the single essential association you need to make to use a photo – it **links to unique identifier of the photo to the unique identifier of the specimen**. A spreadsheet with this association is in the Field&Photo folder of the Dropbox: **dMBM_photo_data_AA.xlsx** (thanks to Abigail for associating the photo and specimen numbers). You can capture a lot of other metadata in this spreadsheet as well, but depending on the project this may be superfluous. If you are shooting only lab specimens, then all the other data with the specimen will be captured in the specimen spreadsheet, and you do not want to duplicate that. If however you include a lot of field photos of organisms that you did not collect, then the photo database is the place to record provenance, identification, etc information. Note that **digital cameras capture dates (based on what time zone etc you have your camera set to) and basic image parameters (exposure, f-stop, etc) as part of the digital photo file, so you do not need to capture this separately**. Visualize the photo metadata that are part of your image file to get a feeling for what is (and can be) stored there.

If you **process a photo** (Chris will give an intro to **photoprocessing using the freeware GIMP**), then save the processed photo as a copy; keep the original archival copy separately. A good way to do this, is to add a mark to the filename, such as a letter at its end: e.g. **dMBM_0011.jpg → dMBM_0011a.jpg**. Save the processed photo at native resolution and compress it minimally as a jpg. Later on if you need smaller files, you can batch process these to be more compressed (preferred) or lower resolution. A 5 MB jpg file at minimal (12) compression becomes a 500 KB jpg at mid compression (5) even at full resolution. All the photos on Dropbox are full resolution files compressed to jpg-5.

You can **rename photos with a more sensible file name if you desire**. In a spreadsheet you can first import fields from another page using the VLOOKUP function. Paste specimen number and ID into a second sheet in your photo database, and pull the taxonomic name into the photo page with this common. Follow this by creating a custom label using the CONCATENATE function – e.g. combining genus_species_photo-number_specimen-number into a string. Once done, copy and paste the two columns (original photo filename and new combined file name) into a separate spreadsheet and save that as a CSV file.

Francois Michonneau wrote an **R script to replace the original filenames with the combined file names**. Open R, load the script (renamePhotos.R), change directory to where photos are, and run the script. Ignore error messages (you get these unless you have a perfect match between all photos in the file and in the directory).

```
> renamePhotos(fileName="FILENAME.csv")
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Now that the **photos are renamed with taxonomic names, organize them into a taxonomic hierarchy of directories to make them more useful**. If you want you can create a printsheet from these, with the file (species) name under each with Photoshop.

Open Photoshop, under File, select Automate → Contact Sheet II. This opens a window in which you can specify parameters: source Folder, how many images and how arranged per page, size of font (important – as long file names will get truncated), etc. Play around with settings to get a feel for this function. Also, organize your hierarchy of folders in the order you want the photos to be assembled; you can add letters to change alphabetical position of folders if you want. E.g., if you want Porifera to come before Cnidaria, rename the Porifera folder as a-Porifera or some-such. You can save the Contact Sheets as pdf's and get high quality field guides printed from these.