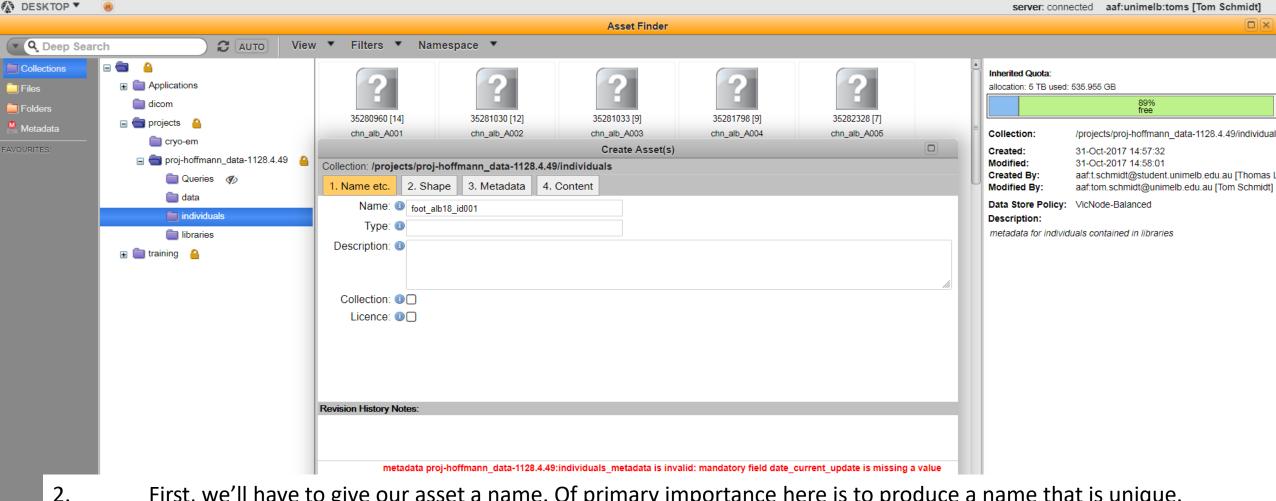


server: connected aaf:unimelb:toms [Tom Schmidt]

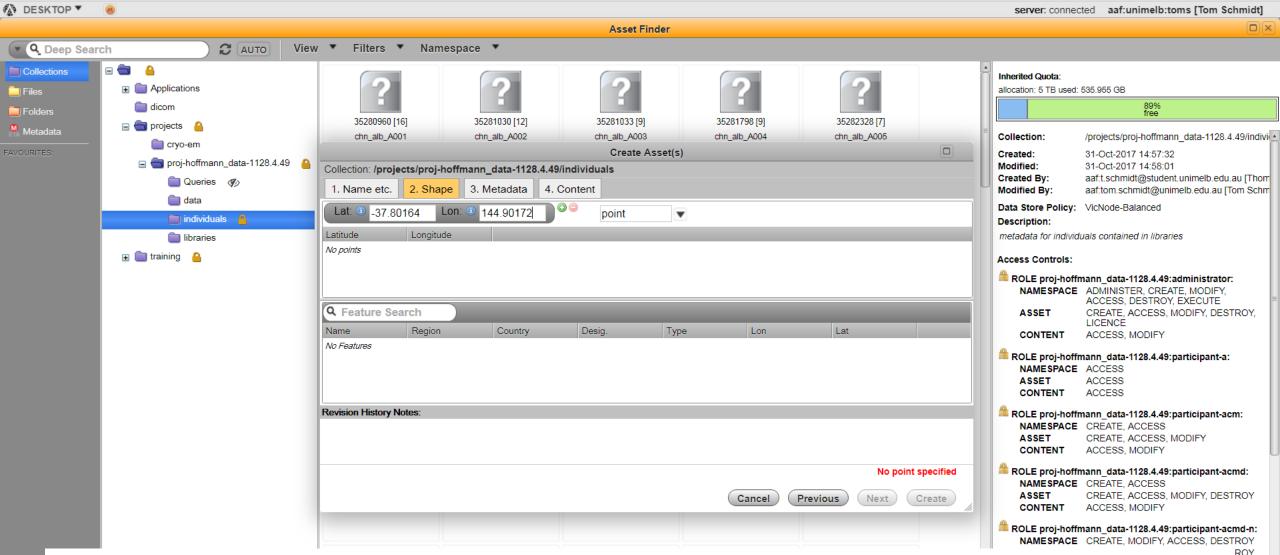
DESKTOP ▼

1. We can now try creating a new asset in the **individuals** namespace. Right click **individuals** and select "Create Asset(s)".



First, we'll have to give our asset a name. Of primary importance here is to produce a name that is unique. There are various ways in which this can be achieved. One way is to incorporate the project of which the individual is part into its name.

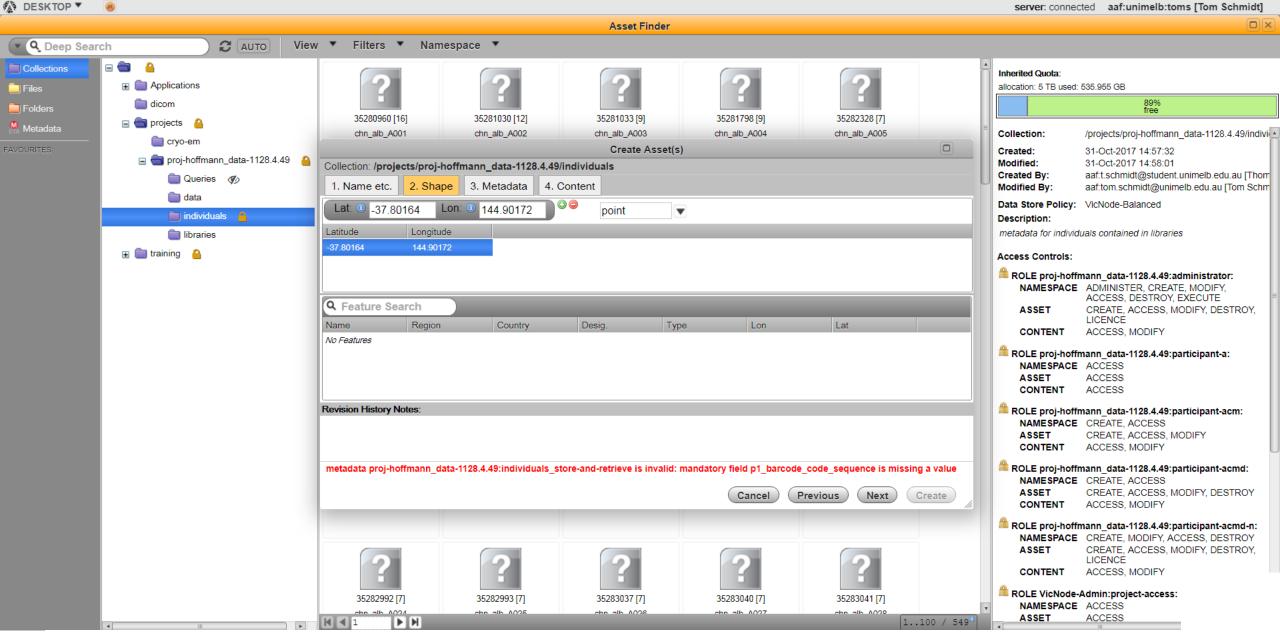
In this example, we are adding a dummy individual – an imaginary *Aedes albopictus* collected from Footscray in 2018. Thus we have called it "foot_alb18_id001". All individuals within this project can be assigned the same prefix of "foot_alb18", while the "id001" delineates between this individual and others within the project.



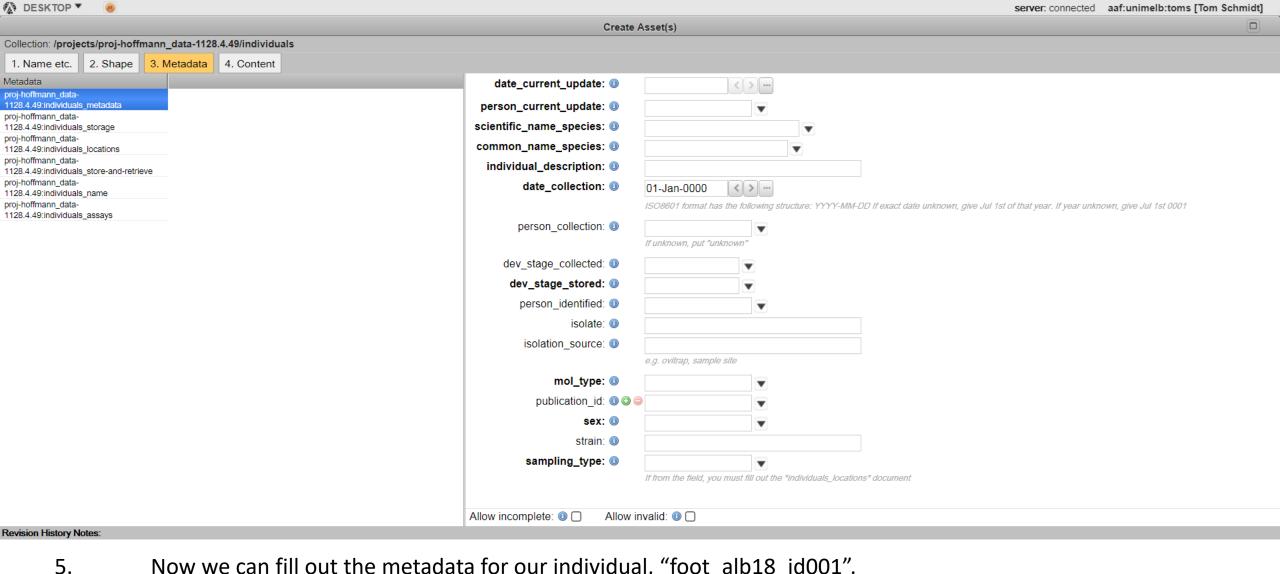
Next, move to then **2. Shape** tab. If the individual was collected from the field, it should be georeferenced, and here you can enter its location in decimal degrees (to five decimal places). If the individual was from the lab, leave this tab blank.

Remember that, in decimal degrees, North and East are positive, South and West are negative.

3.

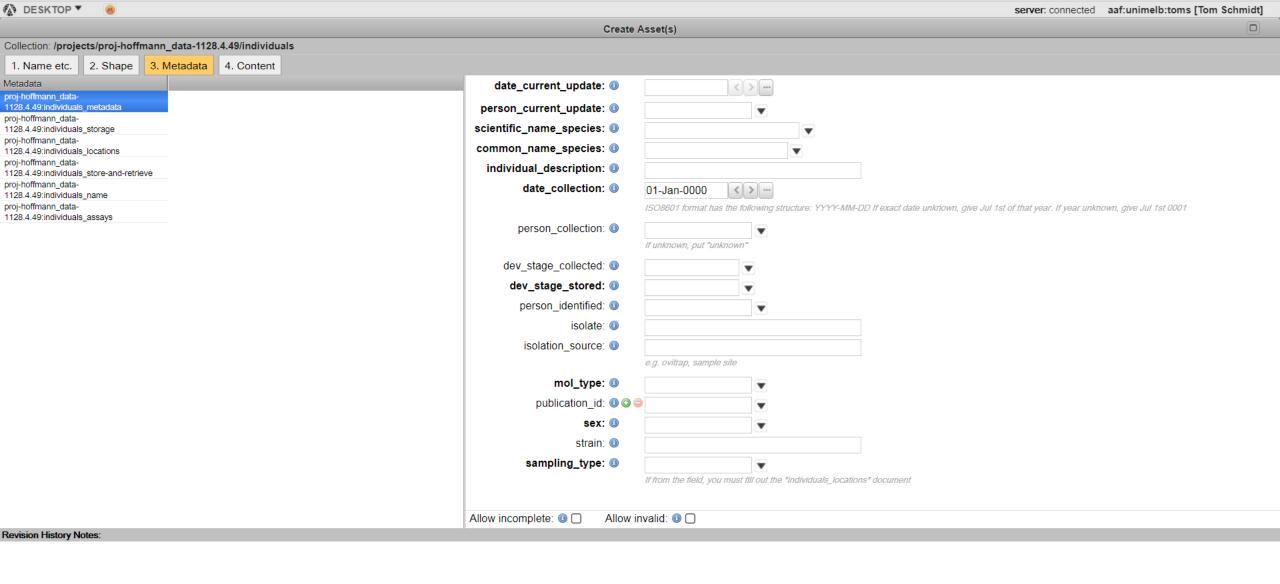


4. After entering the location, press the green "+" on the right, then select the value from the list below. It should automatically recognise this as 'point' data.



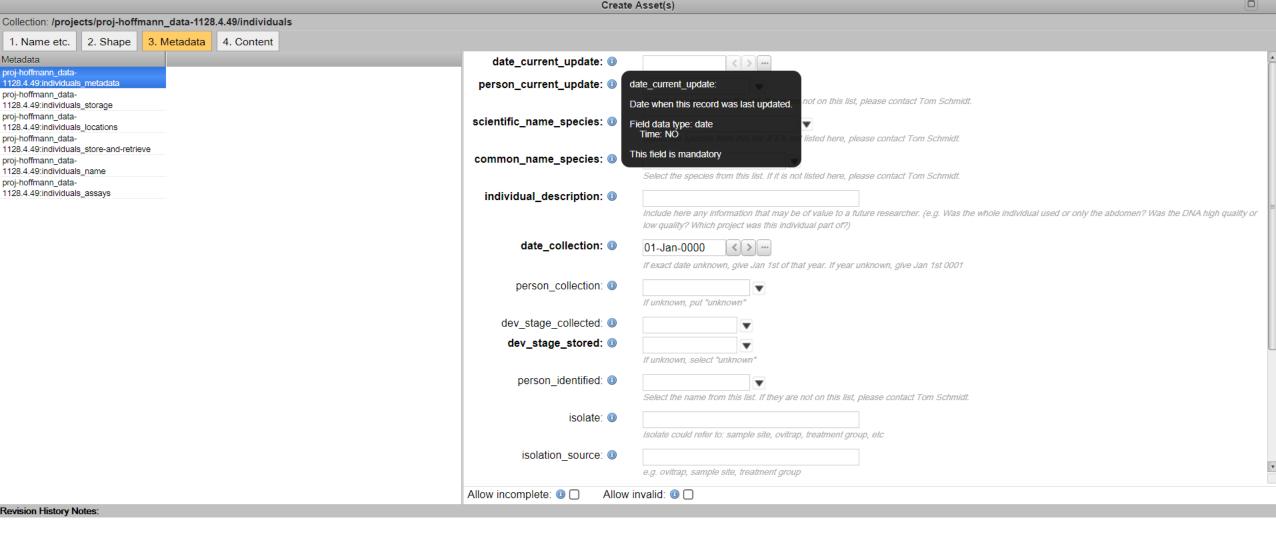
Now we can fill out the metadata for our individual, "foot_alb18_id001".

Click on the 3. Metadata tab. We can now see two windows. On the left, there is a list of six document types: individuals_metadata, individuals_storage, individuals_locations, individuals_store-and-retrieve, individuals_name, and individuals_assays.



metadata proj-hoffmann_data-1128.4.49:individuals_metadata is invalid: mandatory field date_current_update is missing a value

In the individuals_metadata document, we see 17 metadata elements (on the right hand side). Some of these are in **bold**, some are not. Those in bold are mandatory to fill out, those not in bold are optional. If you still have mandatory elements to complete, you will see a warning in red at the bottom of the page.

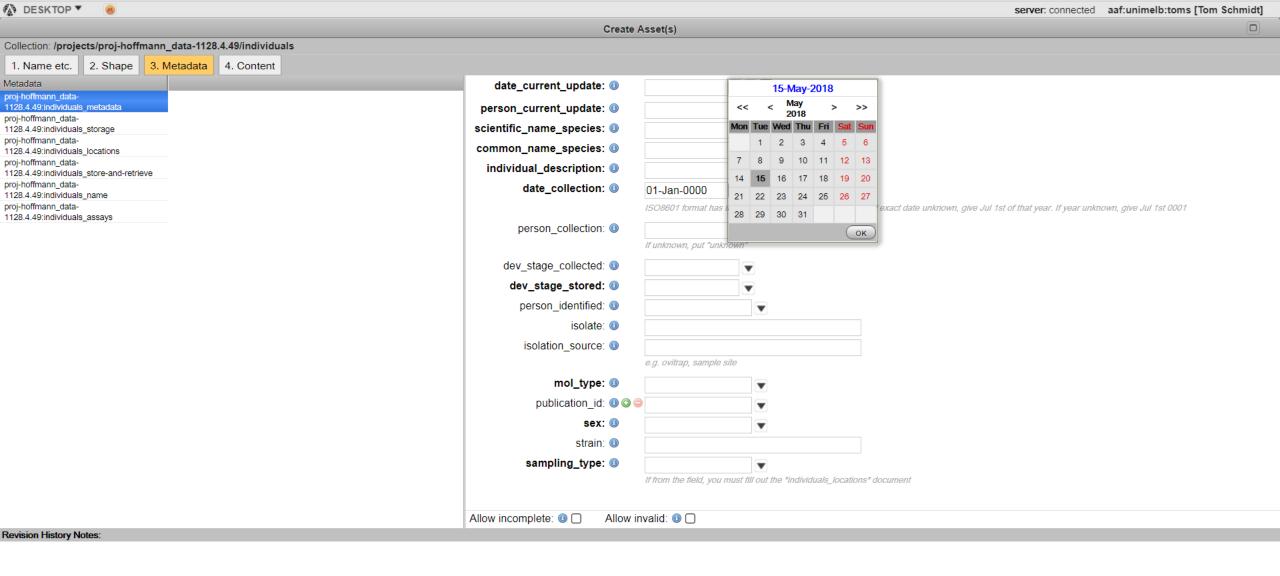


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On the left of each element, there is a little (i) symbol. If you hover the mouse over the (i) symbol, a description of the metadata element will appear. This will help explain how to fill out each element.

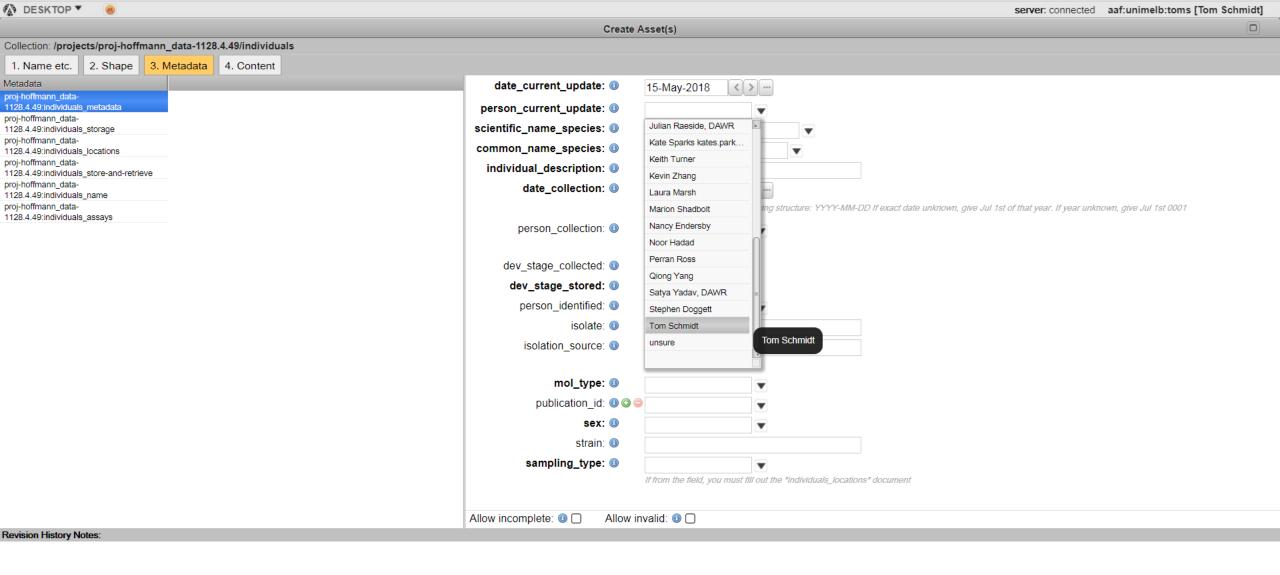
Additional information is also listed in grey beneath many of the elements.

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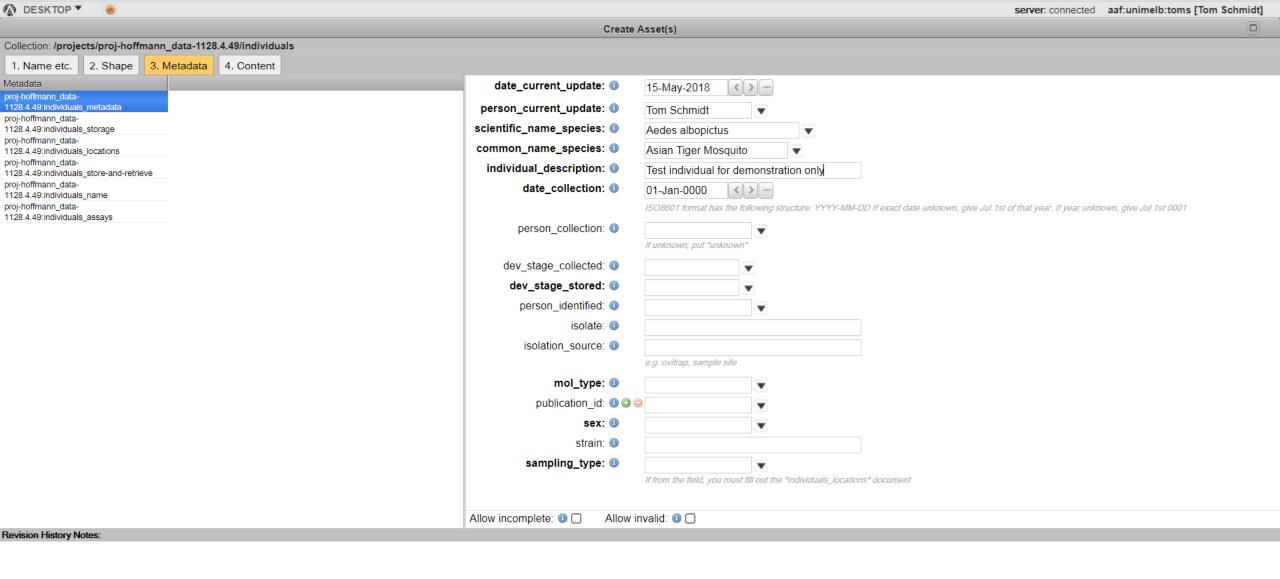
metadata proj-hoffmann_data-1128.4.49:individuals_metadata is invalid: mandatory field date_current_update is missing a value

8. You can also see that some elements have a drop-down list to choose from entries (a dictionary), while some use calendars to select dates, and others you fill out manually (a string). Clicking on the calendar next to date_current_update allows us to select today's date as the entry for this element.

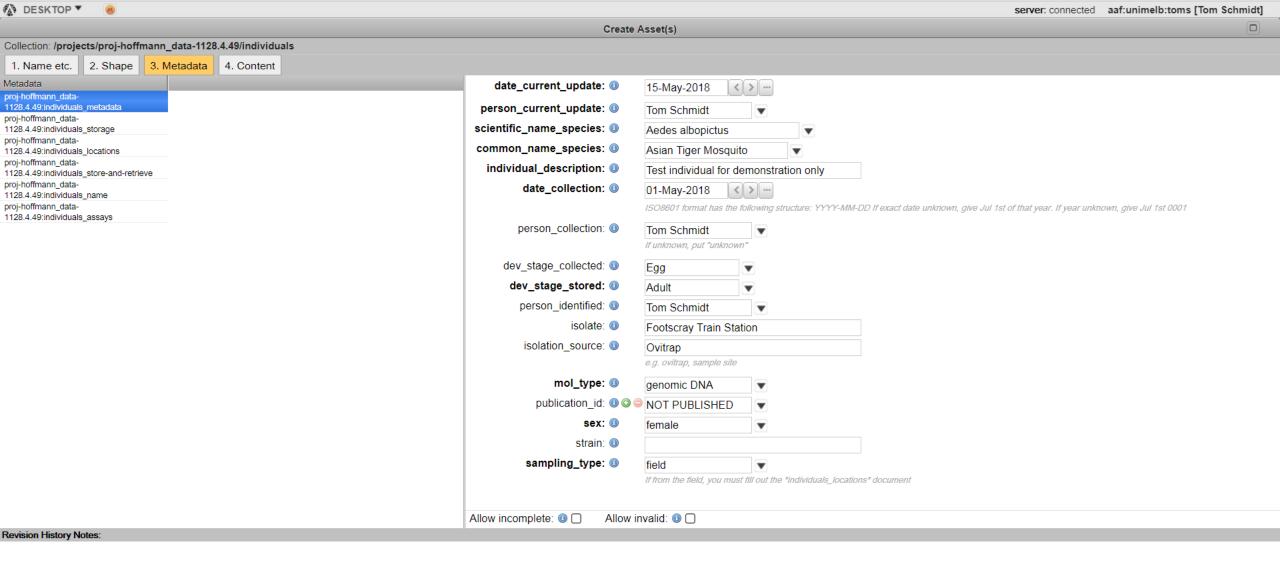


metadata proj-hoffmann_data-1128.4.49:individuals_metadata is invalid: mandatory field person_current_update is missing a value

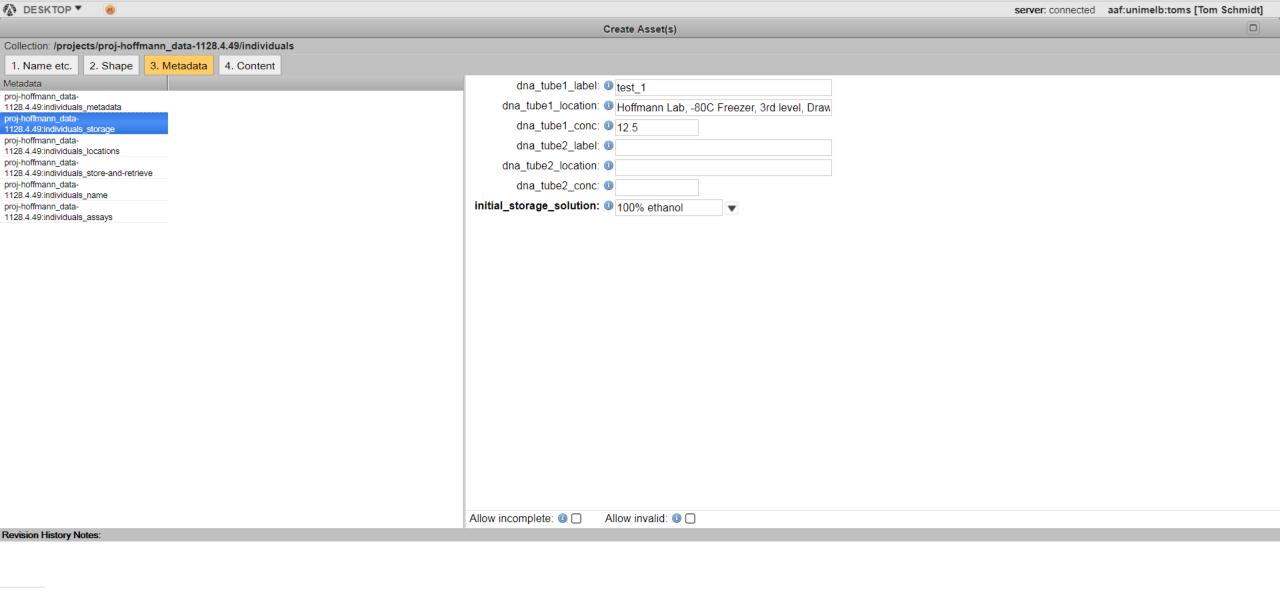
9. We can now fill out the remaining elements of metadata. Click the tab next to **person_current_update** and select your name. If you are not listed here, contact Tom Schmidt to get it added. Same goes for any time your entry is not listed within one of our metadata dictionaries.



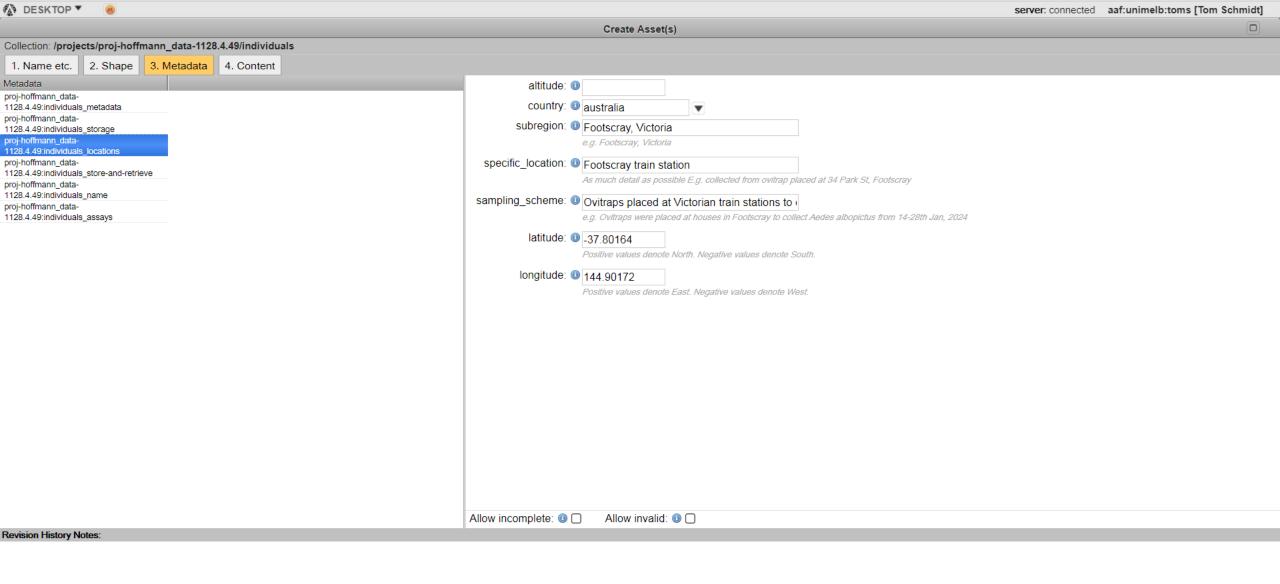
10. Some of the elements must be filled out manually. For instance, in **individual_description** you should provide any information that is not listed elsewhere, but that might yet be useful for a researcher to know. This might be information common to all individuals in that library (e.g. "Only abdomens were used for DNA extraction.") or specific to this individual alone (e.g. "Lightcycler assay confirmed individual is non-Aegypti."



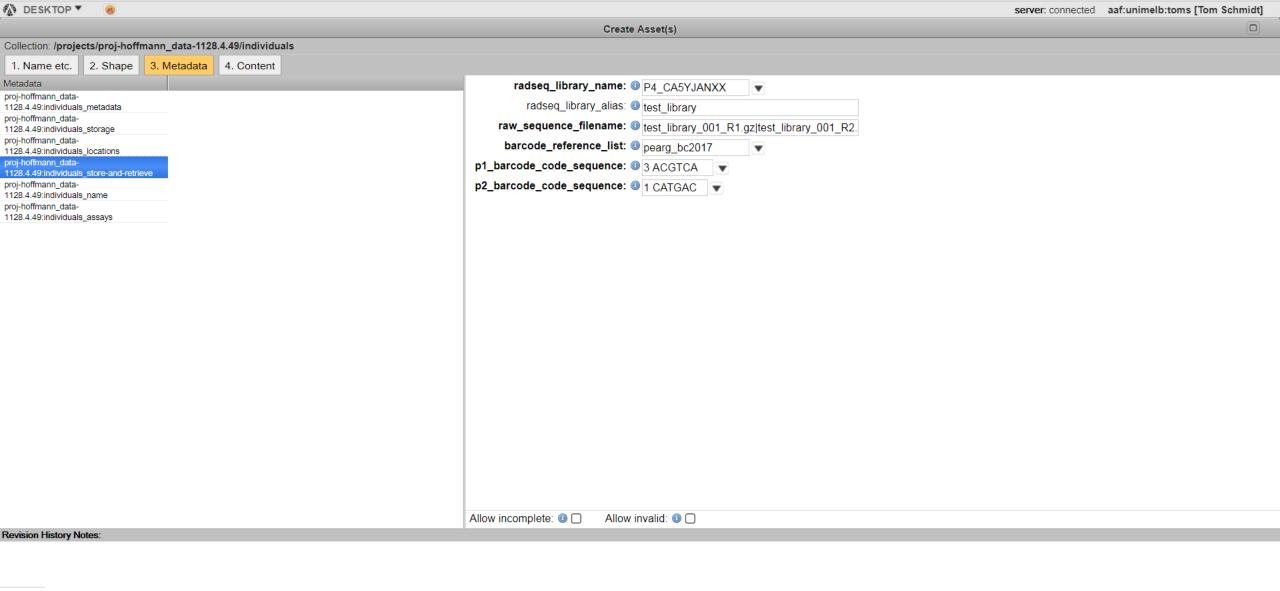
We have now filled out the rest of the individuals_metadata document for "foot_alb18_id001". Note we left blank the entry for strain, as this is not relevant information for this field-collected individual. As we selected "field" for sampling_type, we must enter locational information in the individuals_locations document.



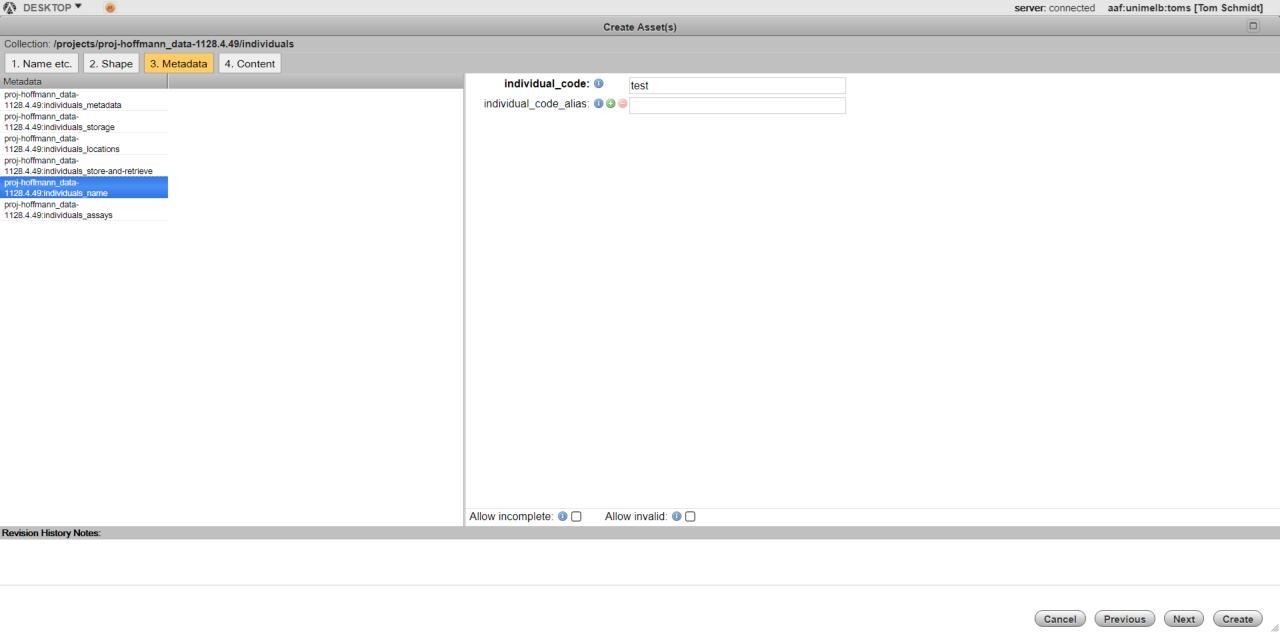
We can now fill out each document listed on the left. The individuals_storage document holds metadata concerning the physical tube(s) containing DNA from this individual. Among the elements here, tube1 and tube2 refer to cases in which multiple elutions may have been taken from an individual. For "foot_alb18_id001" only a single elution was taken, so we can leave the tube2 entries blank.



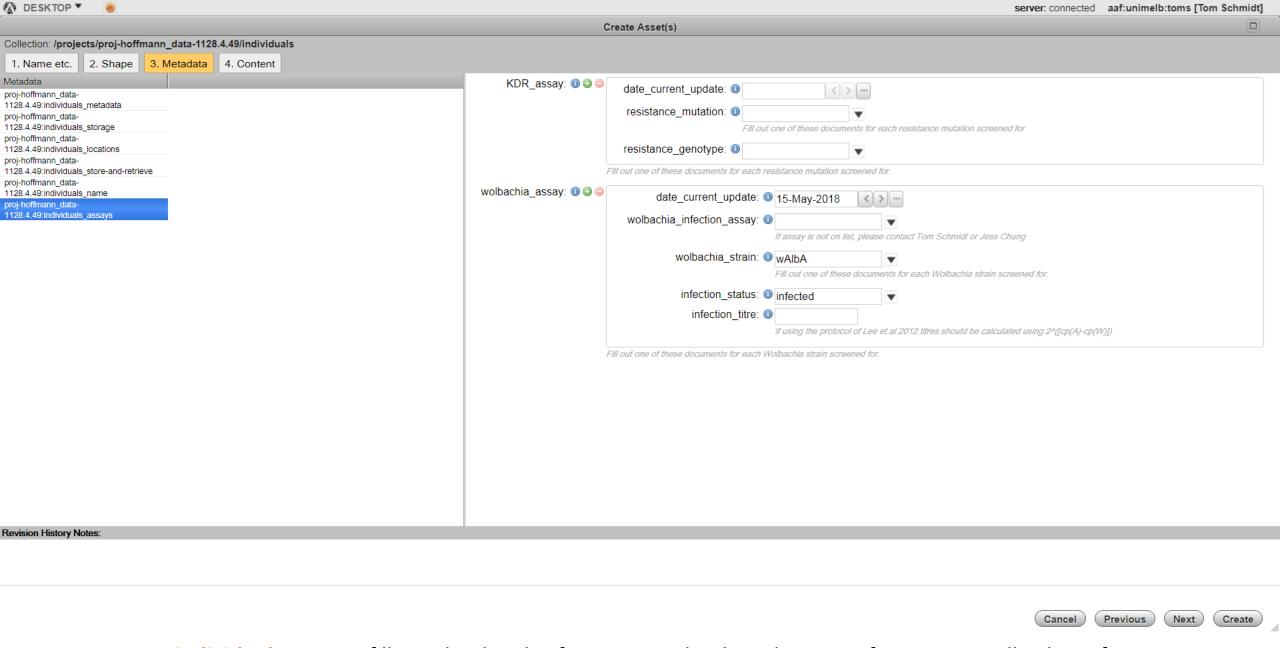
13. The individuals_locations document holds locational metadata. The altitude element can generally be left blank unless this is of significant interest and/or cannot be derived from the georeferenced data provided. The latitude and longitude elements will be the same as entered under the **Shape** tab.



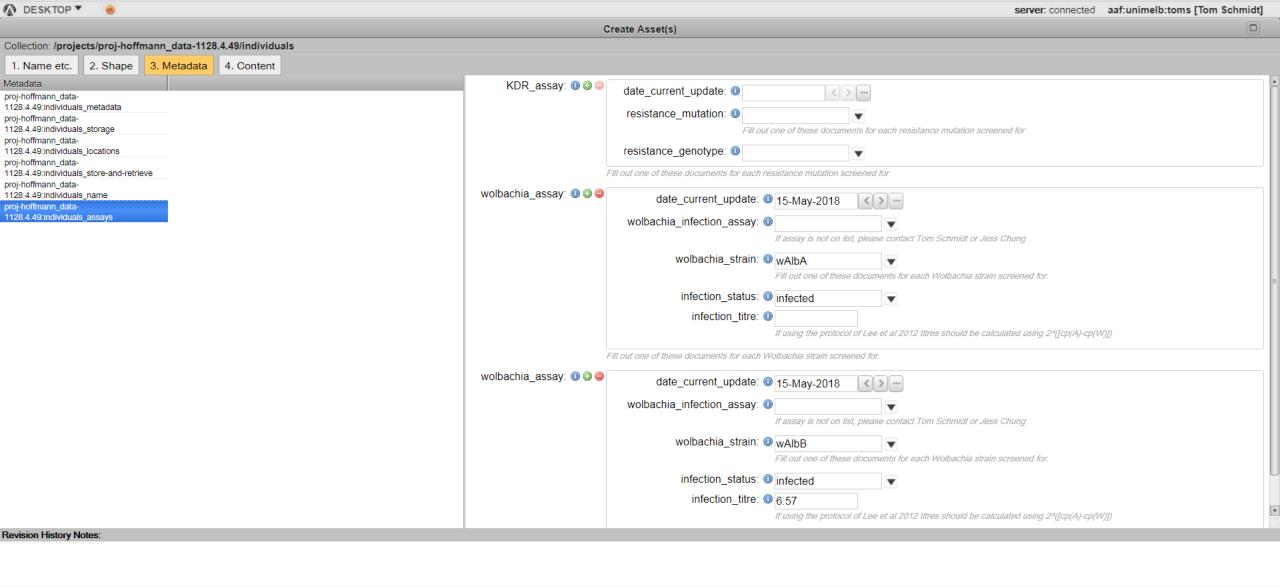
The individuals_store-and-retrieve document specifies which library the individual is part of, and how to retrieve it from the library through demultiplexing. This is clearly of critical importance. The barcode reference list "pearg_bc2017" contains the set of barcodes currently used in the lab, though some libraries were built with an older set of barcodes, and some new barcodes may be added in time.



15. In **individuals_name**, simply give the name (and any aliases) of the individual. An alias could be a previous name of the individual, e.g. as used in a publication or other data set.



16. In individuals_assays, fill out the details of any assays that have been run for KDR or Wolbachia infection.



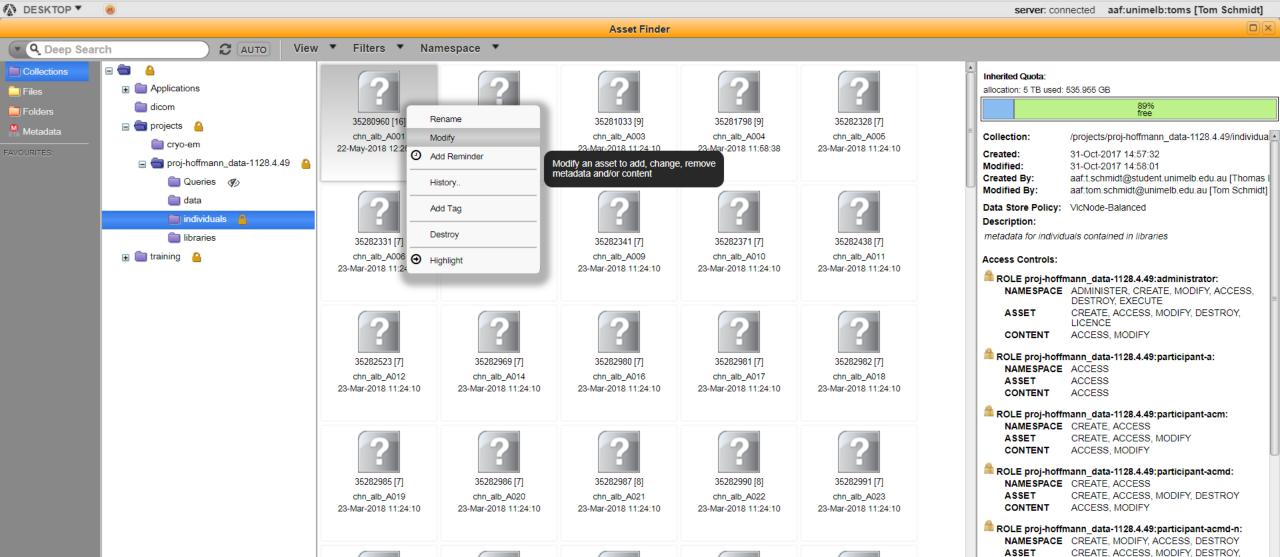
17. If multiple types of assay have been conducted, press the green '+' next to the assay to produce an additional section. Once you have finished, press "Create" in the bottom right hand corner to finish creating the asset.

Previous

Cancel

Next

Create



Sometimes, you will want to modify an asset you created previously. To do this, locate the asset within its namespace, right-click and select "Modify". Now you can make whatever changes you wish. When you are done, select "Modify" in the bottom right hand corner.

35283040 [7]

35283041 [7]

35283037 [7]

35282992 [7]

18.

35282993 [7]

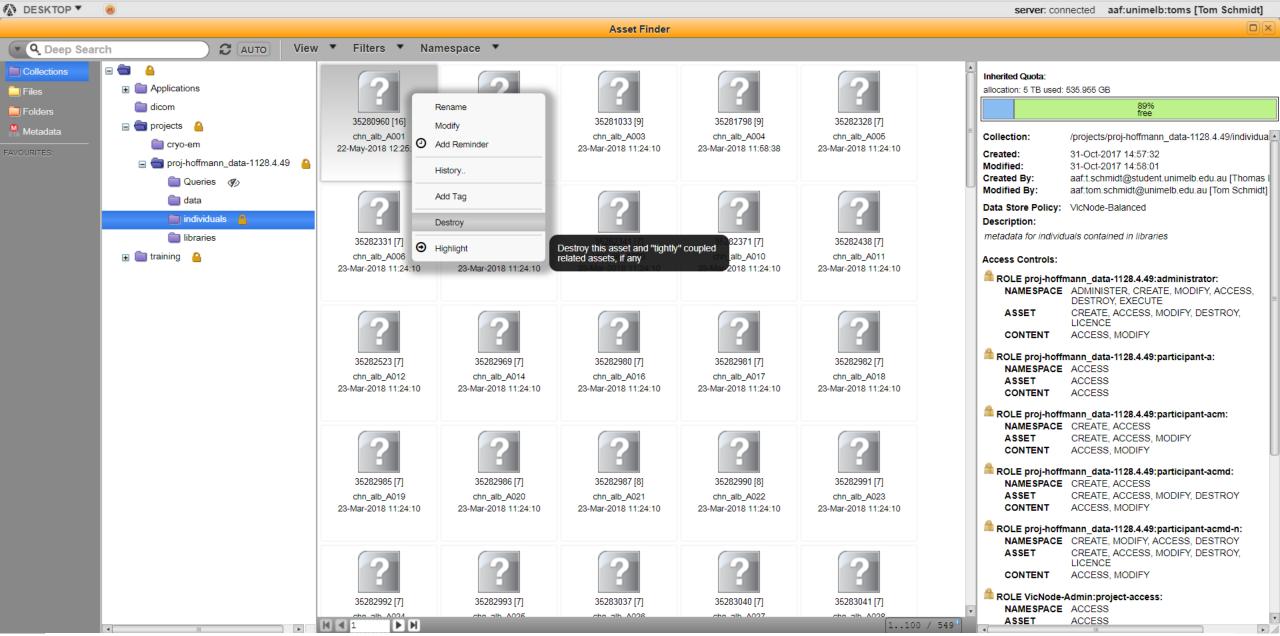
LICENCE

ROLE VicNode-Admin:project-access:

NAMESPACE ACCESS

ACCESS, MODIFY

CONTENT



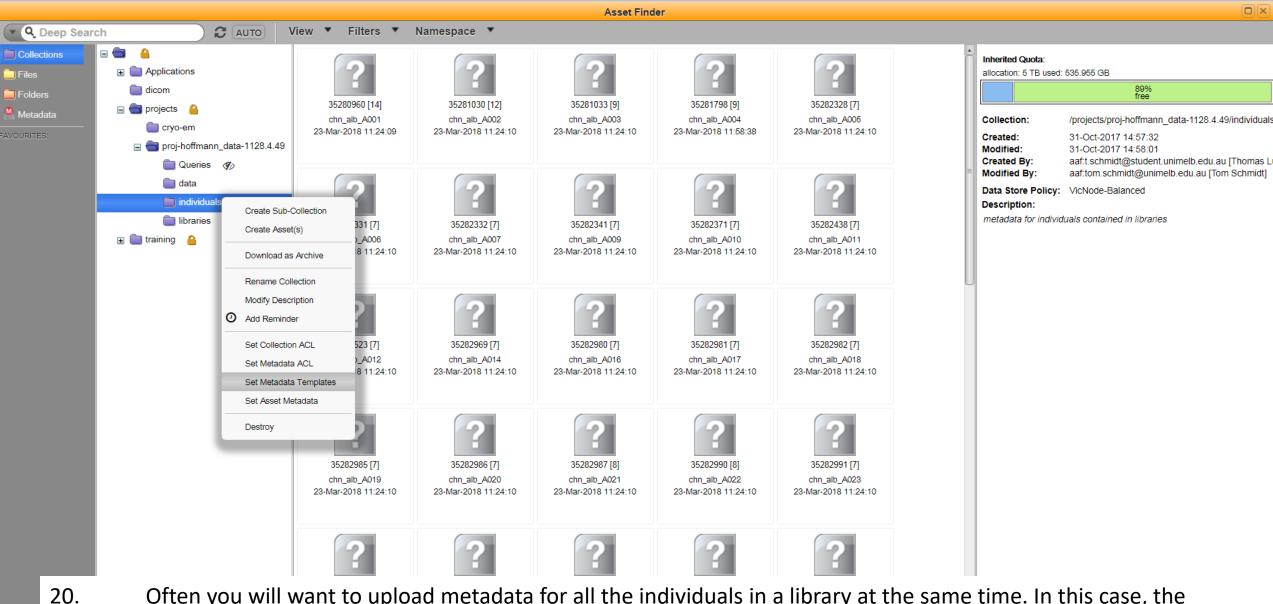
19. To delete an asset, right-click it and select "Destroy". You may only destroy your own assets, not those created by other people.

IMPORTANT NOTICE 1

When an asset is modified or destroyed, the previous version is still saved and recoverable. This prevents malicious or accidental destruction of data and metadata.

Always bear this in mind! If you have accidentally destroyed or modified something you shouldn't have, do not try to hide the mistake or pretend that it did not happen. Contact an admin (e.g. Tom Schmidt or Jess Chung) immediately and they should be able to reset the asset to its previous version.

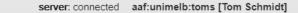
Rectifying these problems immediately is far preferable to being stuck with a database full of missing or incorrect elements.

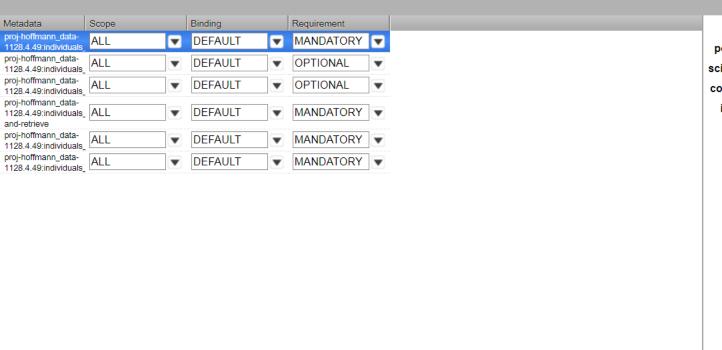


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Often you will want to upload metadata for all the individuals in a library at the same time. In this case, the individuals will frequently have much of the metadata in common. To avoid having to re-enter these values, you can pre-fill these common elements by right-clicking **individuals** and selecting Set Metadata Templates.

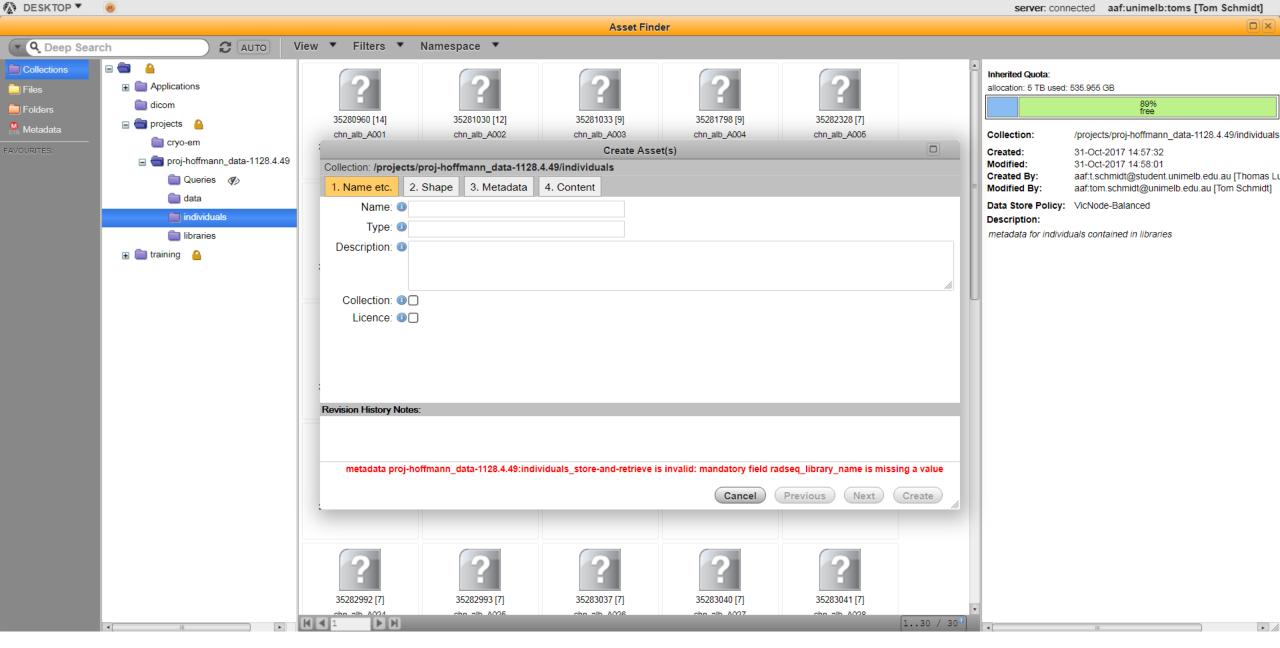




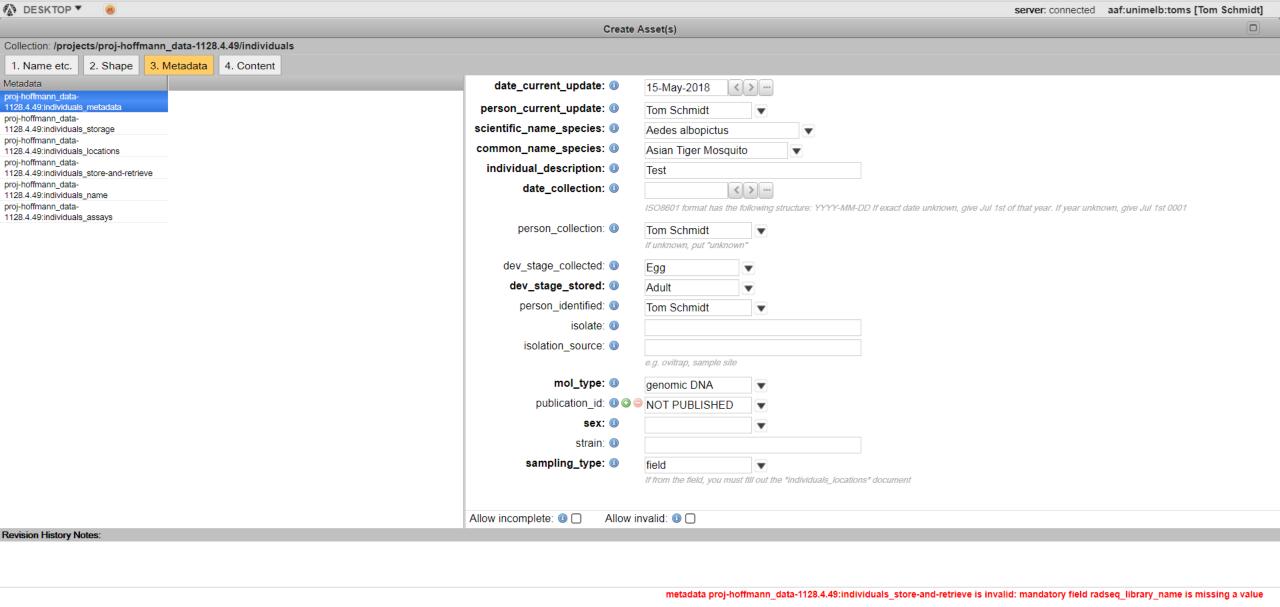
DESKTOP ▼

date_current_update: 0 15-May-2018 < > --person_current_update: 0 Tom Schmidt scientific_name_species: (1) Aedes albopictus common_name_species: 0 Asian Tiger Mosquito individual_description: 0 Test date_collection: 0 < > ... ISO8601 format has the following structure: YYYY-MM-DD If exact date unknown, give Jul 1st of that year. If year unknown, give Jul 1st 0001 person collection: (1) Tom Schmidt If unknown, put "unknown" dev_stage_collected: 0 Egg dev_stage_stored: 0 Adult person_identified: 0 Tom Schmidt isolate: 0 isolation_source: 0 e.g. ovitrap, sample site mol_type: 0 genomic DNA publication id: 000 NOT PUBLISHED sex: 🕕 strain: 0 sampling_type: 0 If from the field, you must fill out the *individuals_locations* document

21. Here we have gone through and pre-filled metadata for the individuals in this library. Note we did not pre-fill date_collection, as not all individuals were collected on the same date. Likewise, they were not all of the same sex, or of the same isolate. These elements will have to be filled out for each individual in turn.



22. Now, we can try creating a new individual asset (right-click **individuals**: Create Asset(s)).



Previous

Cancel

Create

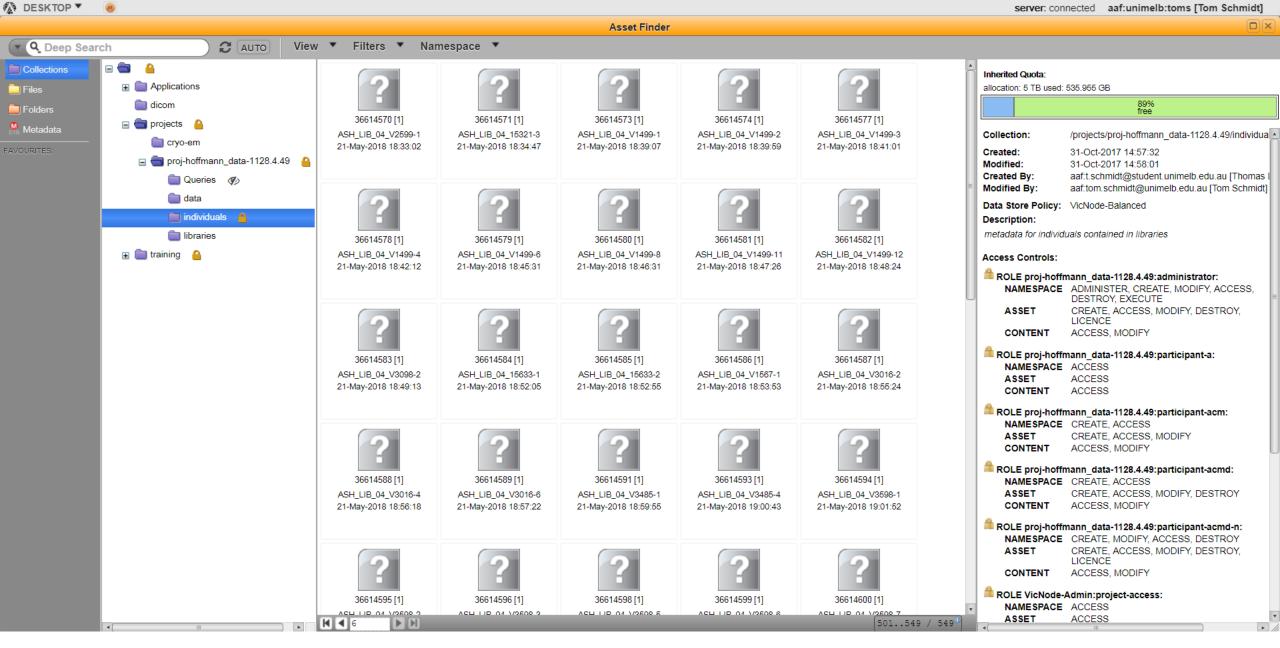
23. And we can see that the elements common to the whole library are now pre-filled.

IMPORTANT NOTICE 2

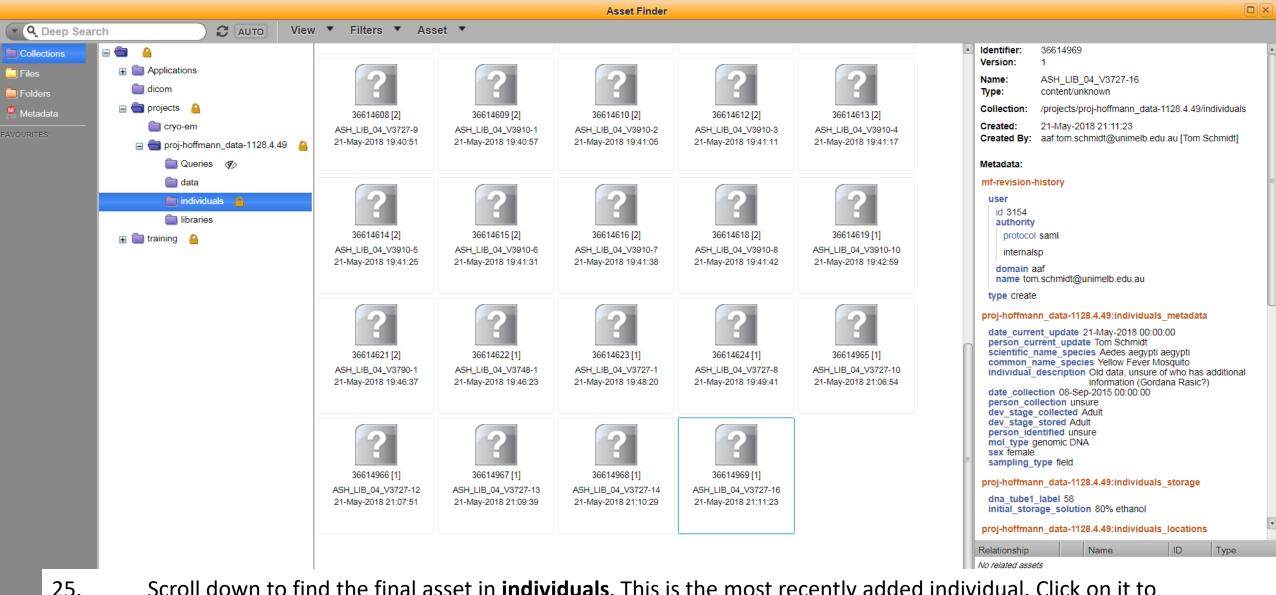
Using the pre-filling option provided through **Set Metadata Templates** can be much faster, but can be troublesome if two or more researchers are attempting to set templates at the same time. You may find yourselves overwriting each other's templates, and entering incorrect metadata.

Because of this, if you wish to use pre-set templates, you should first check if anyone is currently uploading metadata. If they are, you should wait for them to finish before you begin changing their template.

Thankfully, it is very easy to check if someone is currently uploading metadata (see following).



24. First, click on the **individuals** namespace and click the '>|' arrow at the bottom to reach the end of the namespace.



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Scroll down to find the final asset in **individuals**. This is the most recently added individual. Click on it to display when it was created (displayed on the right hand side). If no-one has created an asset recently, you can modify the template. If the asset is newer, however, you should contact the person currently creating assets to negotiate a time for you to upload your metadata.

IMPORTANT NOTICE 3

Once you have finished adding metadata, you should clear the pre-filled information for each element within **Set Metadata Templates**.

This will ensure that the next person to upload metadata does not have to first delete all of your pre-filled metadata before they start.