



What you need before starting:

- an ORCiD account (<u>here</u> to register)
- contact EI.COPO@earlham.ac.uk to be added to the DToL group
- make sure you have the latest version of the DToL manifest (<u>here</u>)
 - if you are submitting as part of the ASG project, please refer to the latest metadata manifest





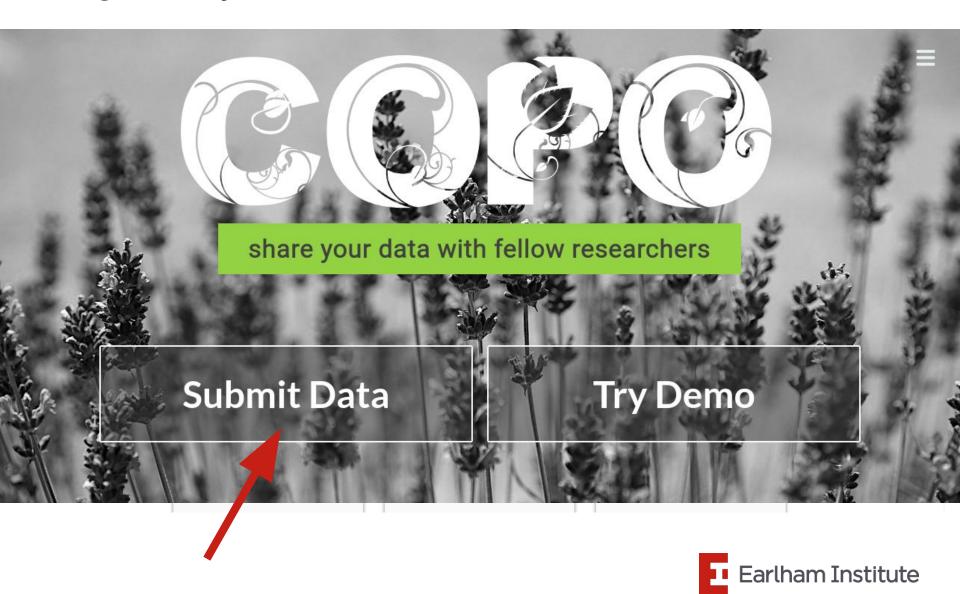
Once you are confident

IMPORTANT - Submissions to ENA through the demo server won't persist, any accessions will be deleted after 24 hours.

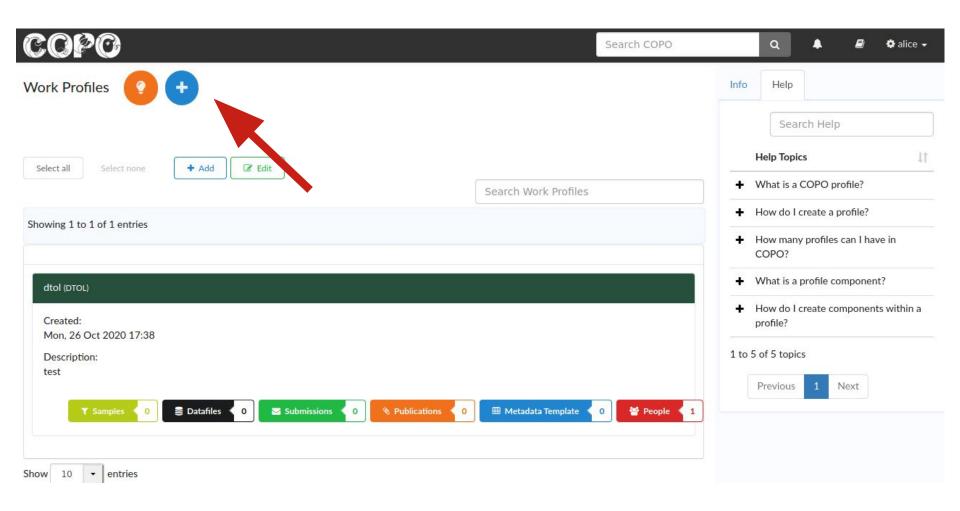
We also update this server quite frequently, so it may occasionally be unreachable and you may find we deleted your past uploads.

Earlham Institute

Log in with your ORCiD credentials:

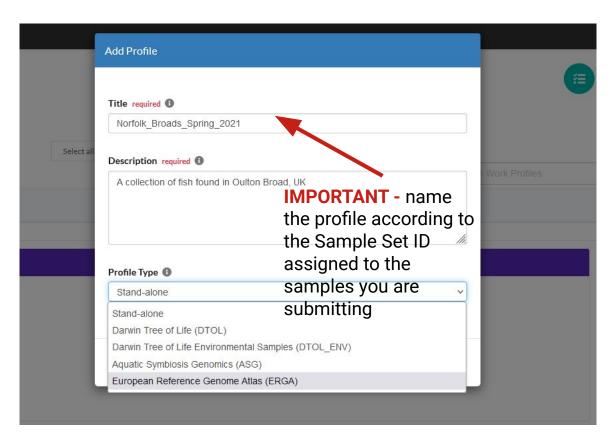


Create a profile:





Create a DTOL profile:

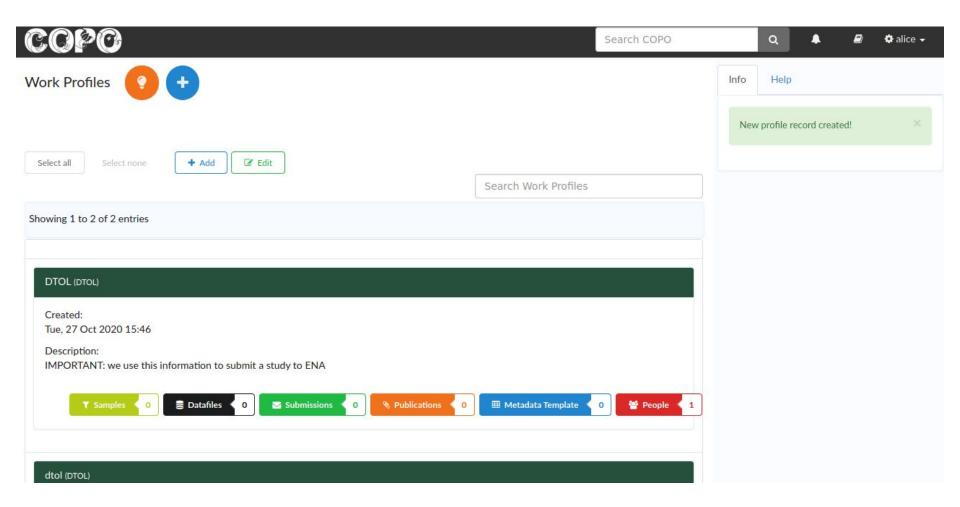


IMPORTANT - If you can't see the project you are associated with in the profile type drop down menu, you need to be added to the relevant group. Please stop here and get in touch with

EI.COPO@earlham.ac.uk

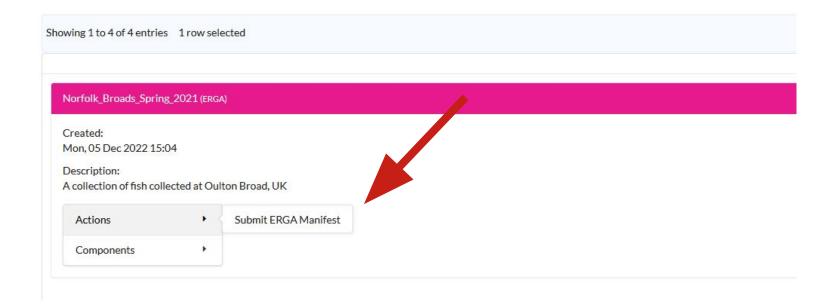


This is your new DToL profile:





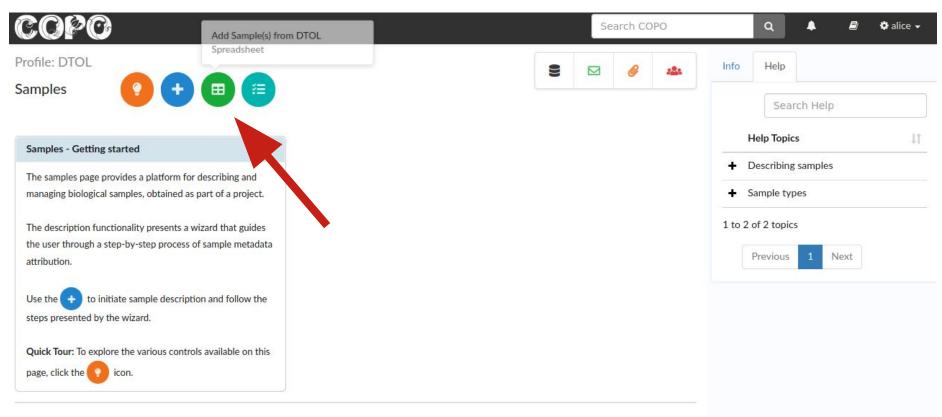
Upload a manifest:



The colour and wording of this panel will differ depending on what project you are submitting for



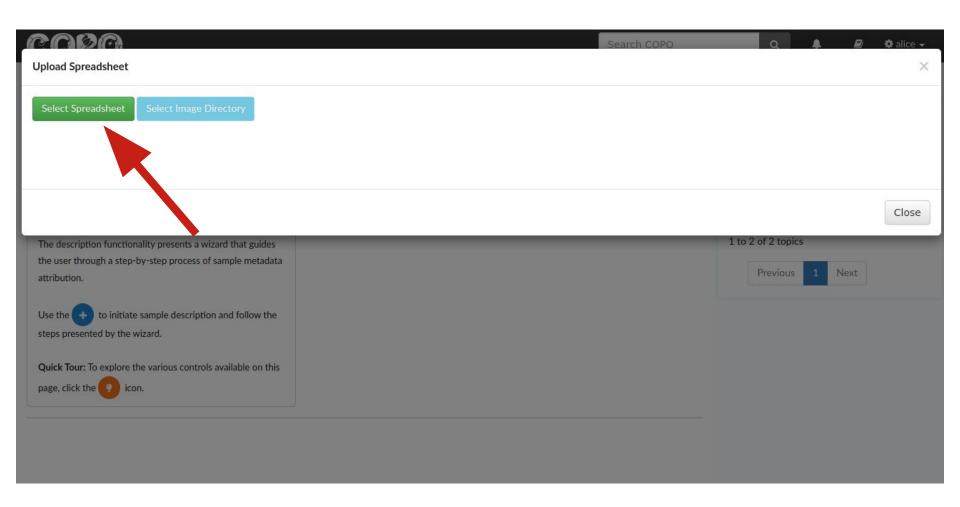
Upload a manifest:



*Only sample managers will see the fourth light blue button next to the green one, if this is not your role don't worry about that, you won't need it

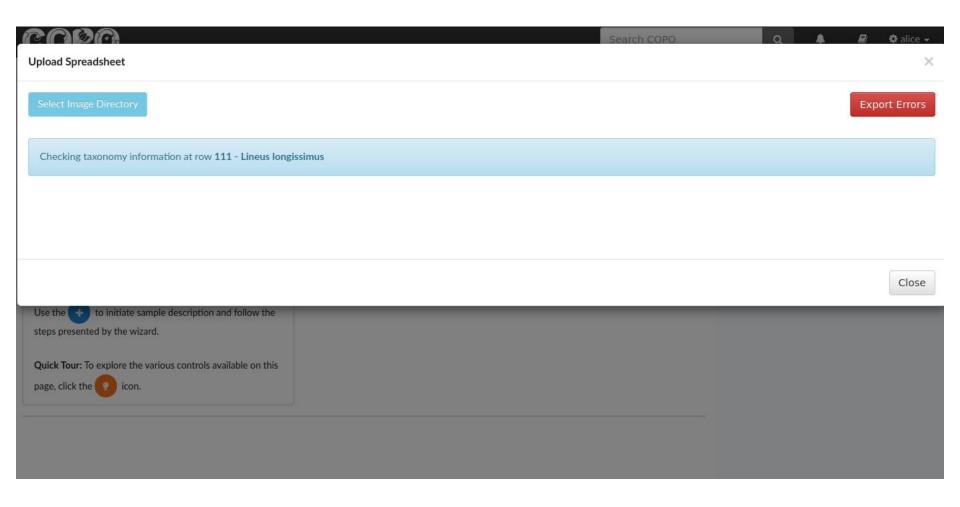


Upload a manifest:





COPO will validate taxonomy information and manifest format:





What's happening (part 1):

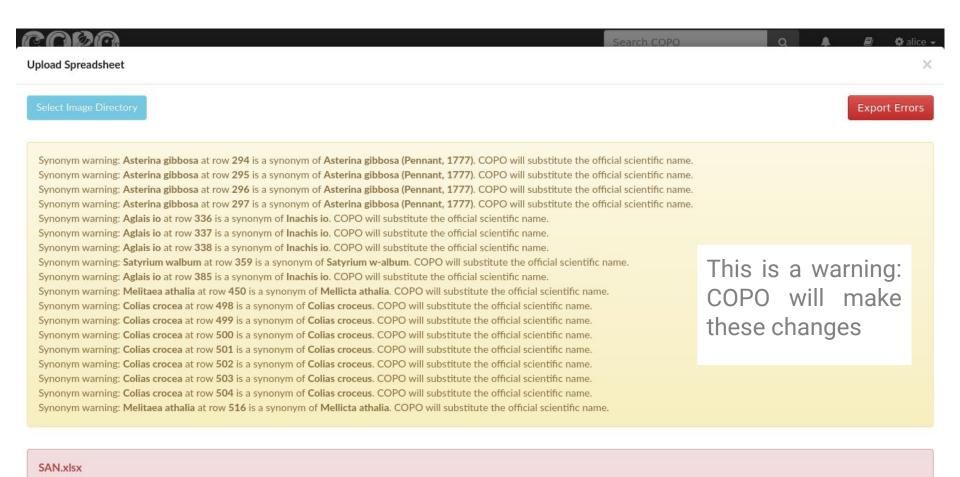
- COPO is retrieving information from NCBI (National Center for Biotechnology Information) to check the taxonomy information provided is correct. We also check the TAXON_ID is submittable to ENA.
- If some of the taxonomy fields are missing (excluding SCIENTIFIC_NAME)
 COPO will make an educated guess about what these fields should be and will display warnings about what is going to be filled in.

The taxonomy checks will be much quicker if you fill in TAXON_ID.

- COPO will substitute scientific name synonyms with the official scientific name. It will display a warning and also record the change in OTHER_INFORMATION
- If any taxonomy field is incorrect COPO will display an error and reject the manifest. You can download the error list with the red "Export Errors" button on the top right.
- If you are unhappy with any of the warning/errors DO NOT press finish.
 Instead contact NCBI to discuss the taxonomy

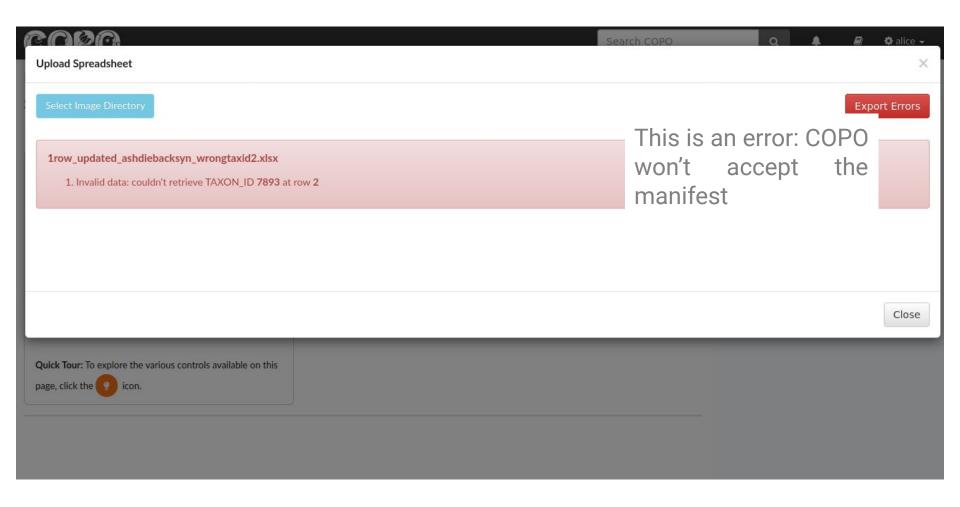


Manifest uploaded -taxonomy warnings-:





Manifest uploaded -taxonomy errors-:

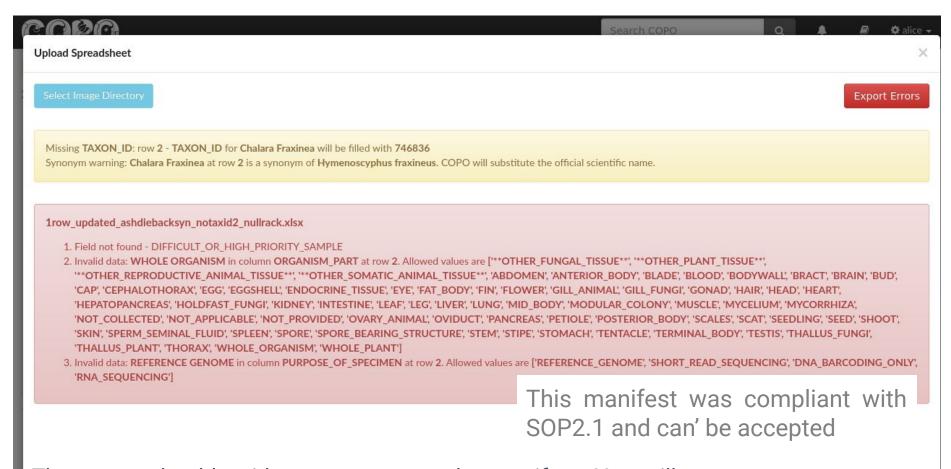




What's happening (part 2):

 ONLY IF the taxonomy validation was successful and produced no errors, will COPO check the manifest against SOP specifications. This includes checks for general format, missing data, cells that have restricted values, etc.

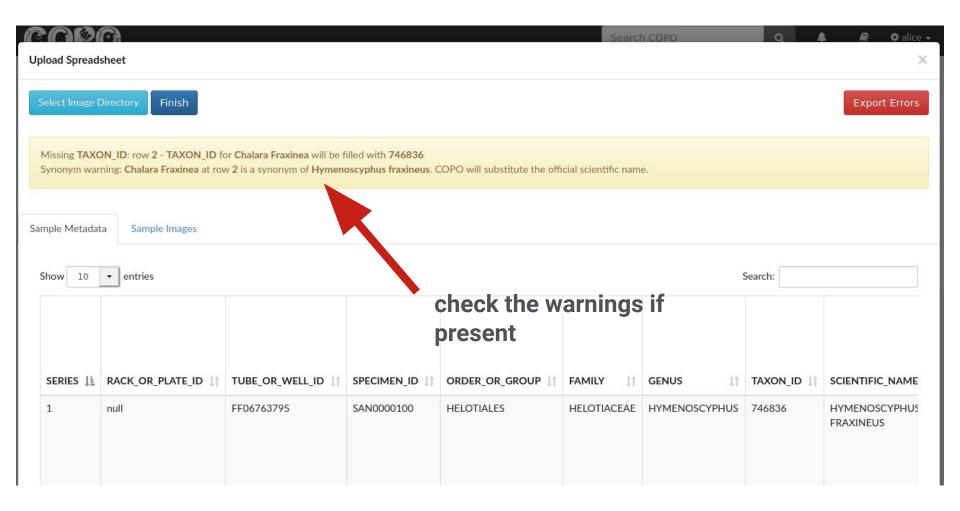
Manifest uploaded -compliance errors-:



The errors should guide you to correct the manifest. You will have to correct and re-upload the updated spreadsheet

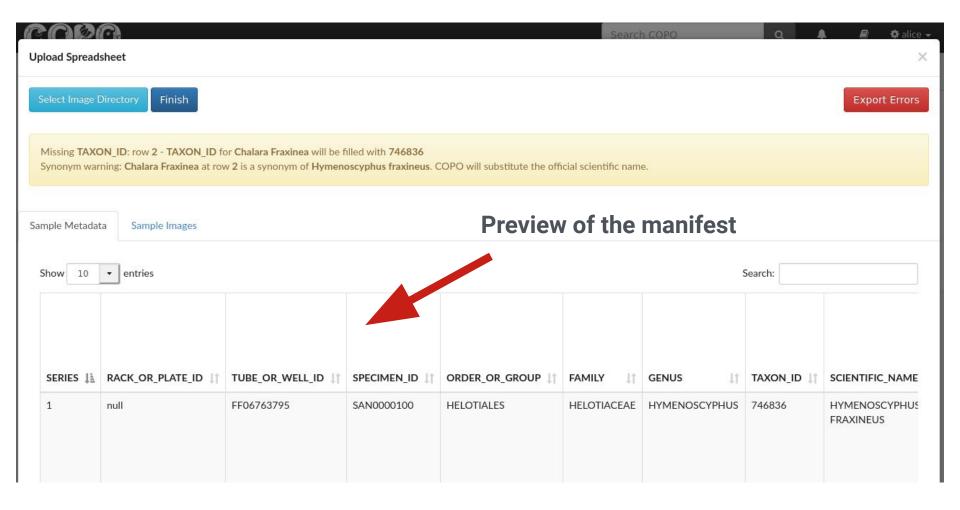


Manifest uploaded -correct manifest-:



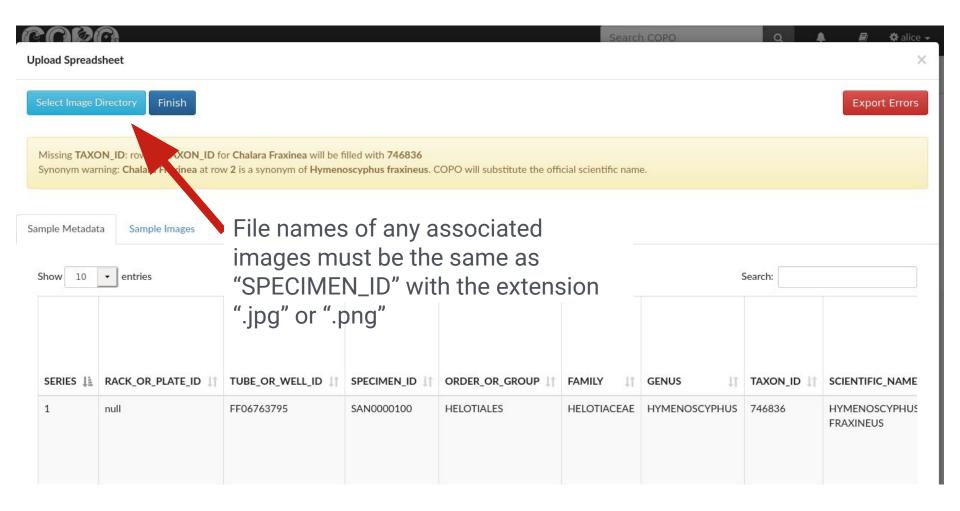


Manifest uploaded -correct manifest-:



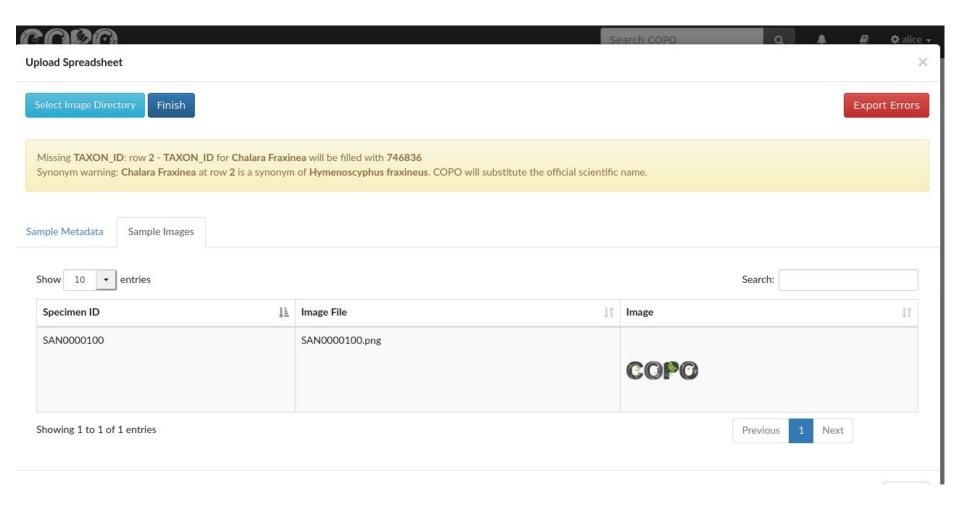


Upload images:



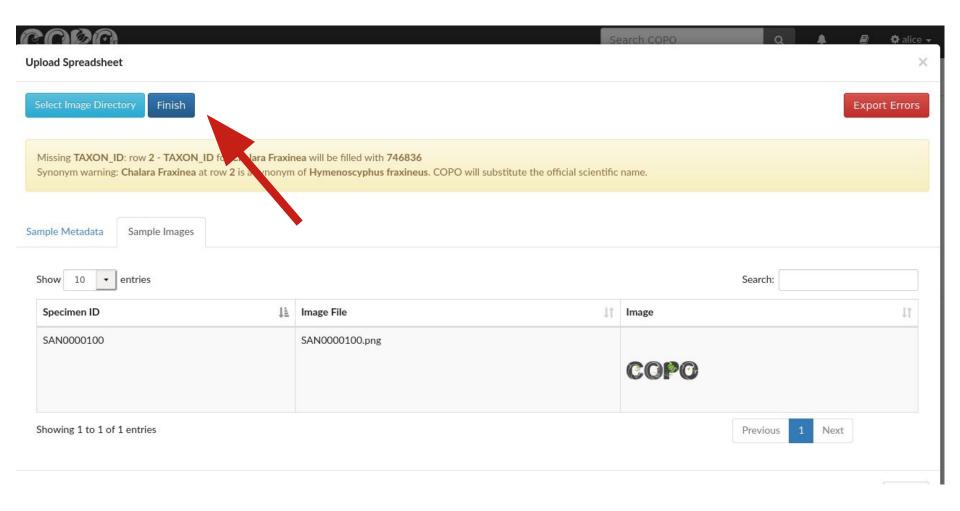


Upload images:



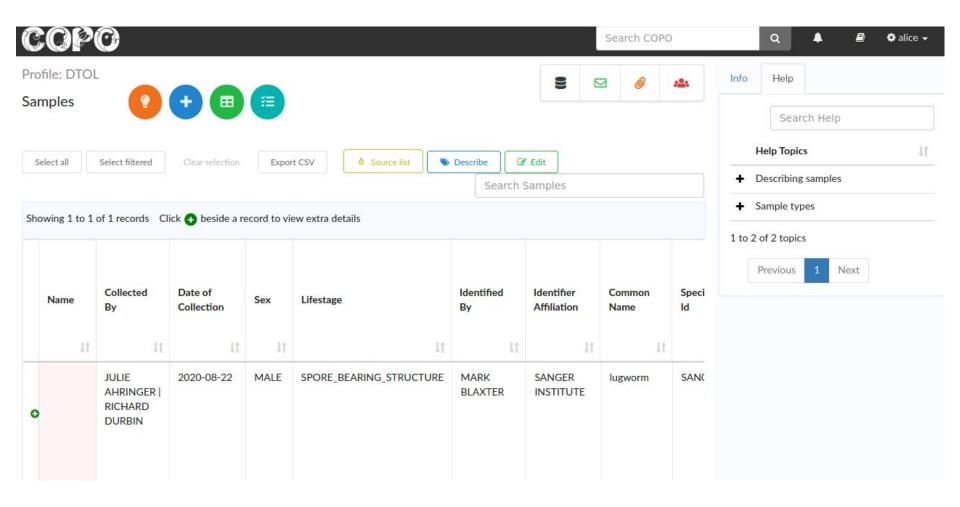


Create the samples in COPO by clicking "Finish":





Uploaded samples:





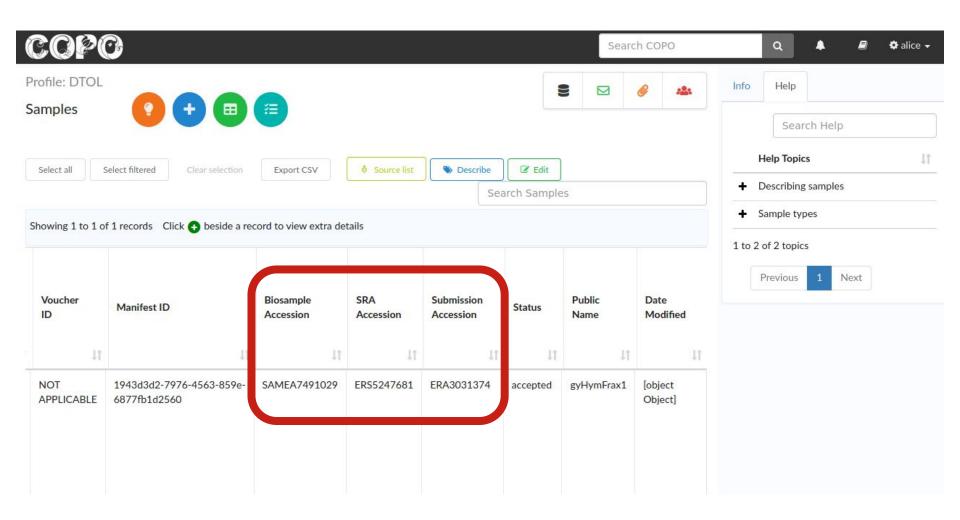
Sample Managers:

 At this point the sample managers will be emailed that a new manifest has been uploaded. They will be able to accept or reject each sample after inspection.

After samples are approved by a sample manager they will be submitted to ENA (European Nucleotide Archive). Accessions can be inspected by scrolling right in the previous view.



Accepted samples:







If you encounter any error or unexpected behaviour please email <u>EI.COPO@earlham.ac.uk</u> or open a github issue in the repository at the bottom of the page.

If you have a feature request for future releases please open an issue in the github repository.

We are currently working on a pipeline to update uploaded samples. For the time being, if you need to update a sample please email us at EI.COPO@earlham.ac.uk specifying the biosample accession, the field to update and the new value. (If you need to update the taxonomy please send biosample accession and new scientific name, we will update all the taxonomy fields accordingly.)

















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