



COPO

VISUAL DOCUMENTATION FOR
MANIFEST SUBMISSION

Collaborative OPen Omics

ei.copo@earlham.ac.uk, @copo-project



E Earlham
Institute

Decoding Living Systems

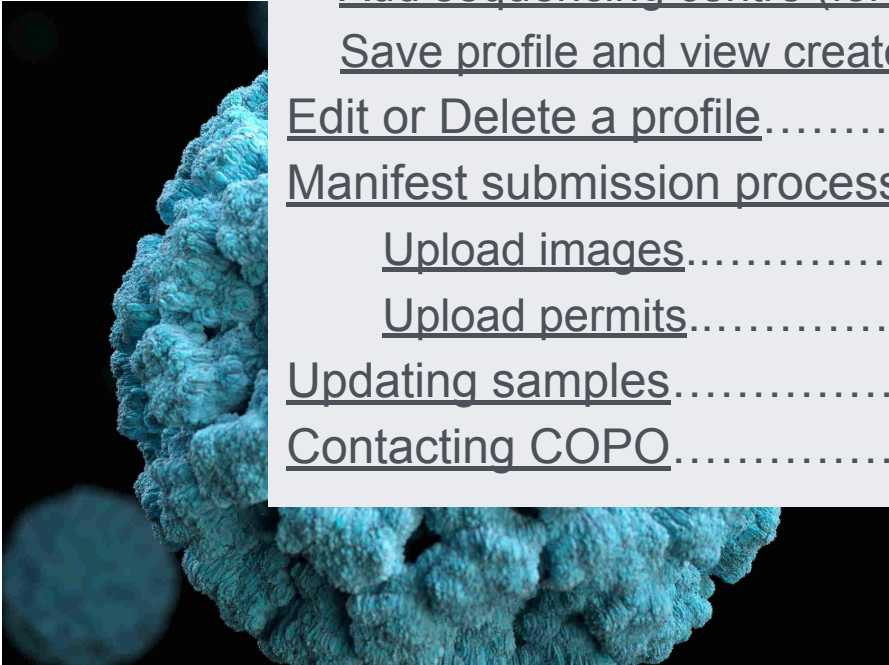


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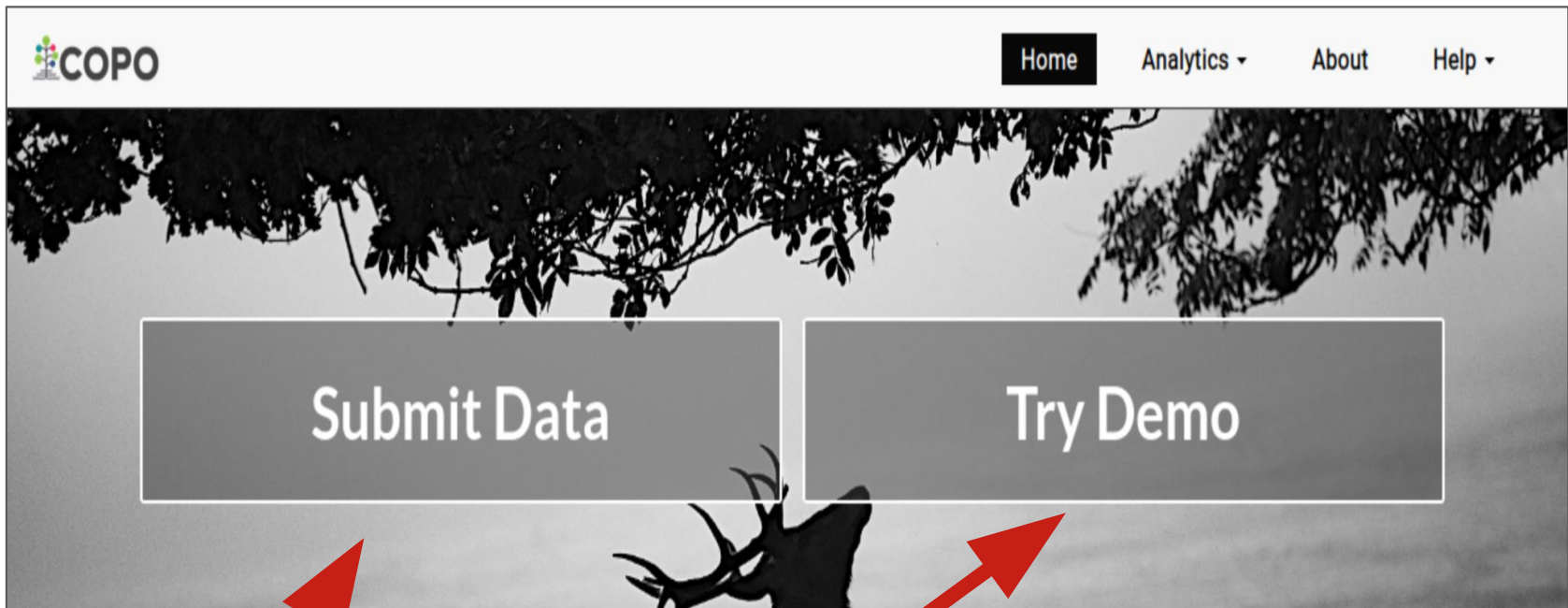
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Prerequisites:

- An [ORCID account](#)
- Contact ei.copo@earlham.ac.uk to be added to a project manifest group
- Ensure that you have the latest version of the manifest if you are submitting samples as part of -
 - Aquatic Symbiosis Genomics (ASG) project, please refer to the latest metadata manifest
 - Darwin Tree of Life (DToL) project, please refer to the latest metadata manifest [here](#)
 - European Reference Genome Atlas (ERGA) project, please refer to the latest metadata manifest [here](#)
- **i** The latest manifest templates can also be found in our [documentation](#).

COPO's home page:



Once you are confident

To familiarise with the platform

IMPORTANT - Submissions to European Nucleotide Archive (ENA) through the demo server will not persist, accessions created will be deleted after 24 hours.

The demo server is frequently updated so it may occasionally be unreachable and you may find that we have deleted your past uploads.

Click “Submit Data” button to log in with your ORCiD credentials:



Home

Analytics ▾

About

Help ▾

Submit Data

Try Demo

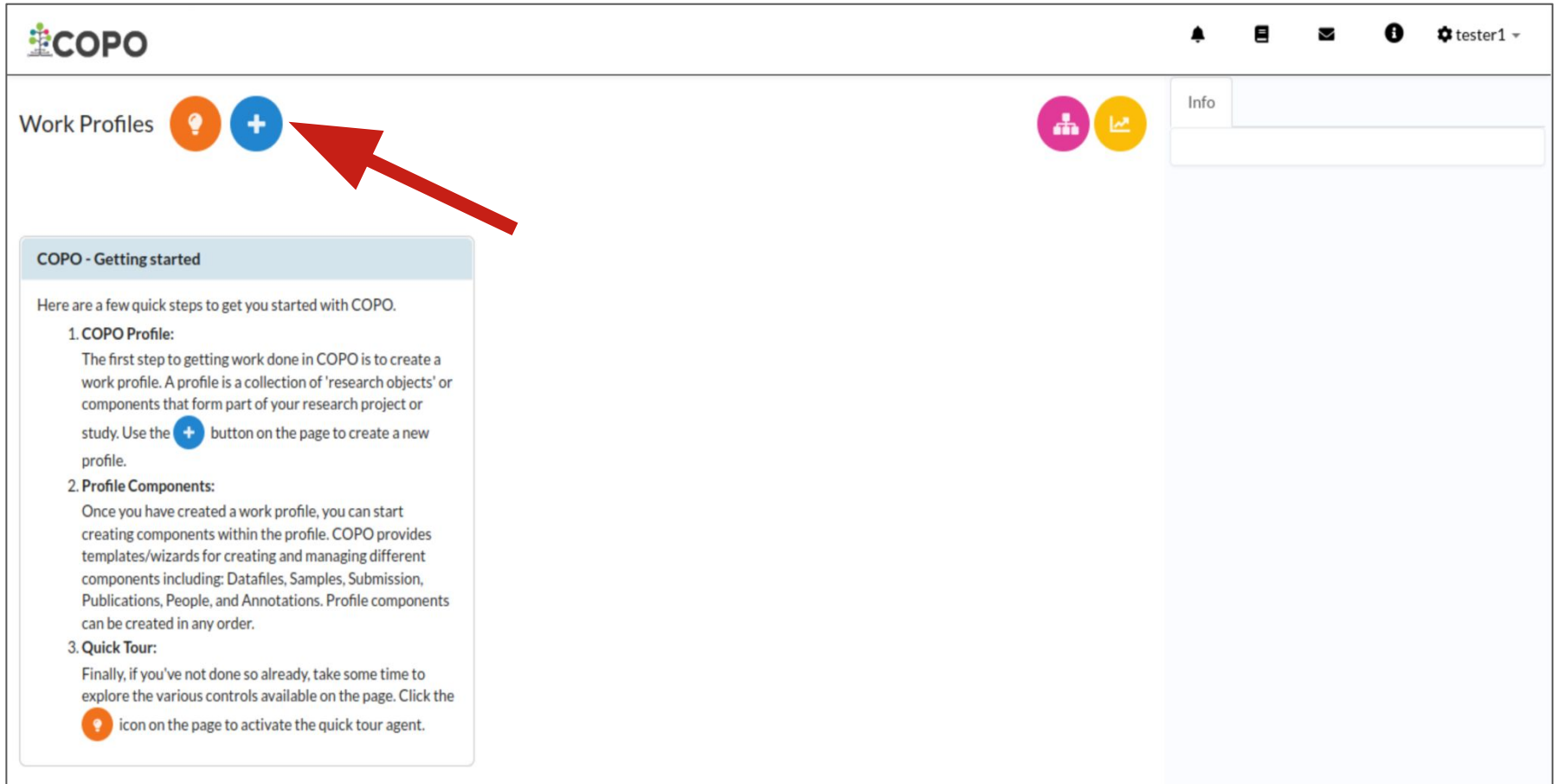


An ORCiD sign-in form will be displayed after you click the **Submit Data** button.

Enter your ORCiD credentials to proceed to the COPO **Work Profiles** web page.





Create a profile:



The screenshot shows the COPO web interface. At the top left is the COPO logo. In the top right corner, there are notification, document, email, and user profile icons, with the user name 'tester1' next to a gear icon. Below the logo, the text 'Work Profiles' is followed by two circular icons: an orange one with a lightbulb and a blue one with a white plus sign. A large red arrow points to the blue plus icon. To the right of these icons are two more circular icons: a pink one with a person icon and a yellow one with a bar chart icon. Below the 'Work Profiles' section is a light blue box titled 'COPO - Getting started' containing a list of instructions for getting started with the platform.

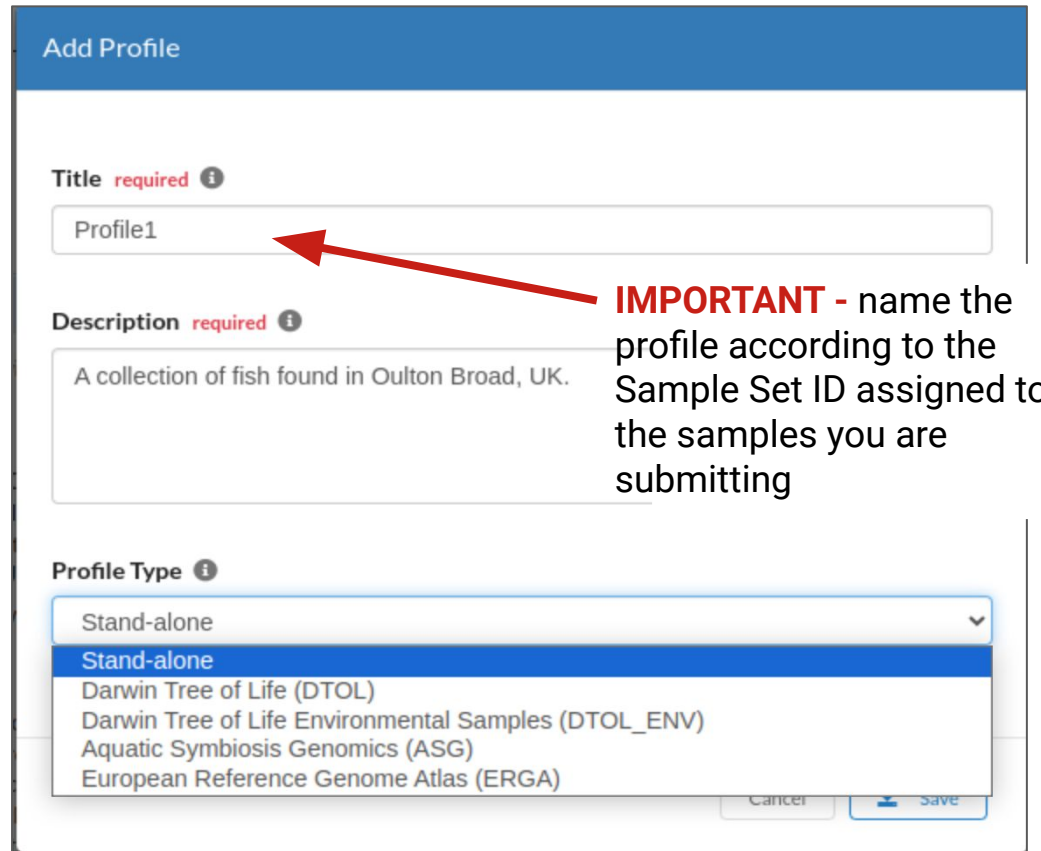
COPO - Getting started

Here are a few quick steps to get you started with COPO.

- 1. COPO Profile:**
The first step to getting work done in COPO is to create a work profile. A profile is a collection of 'research objects' or components that form part of your research project or study. Use the  button on the page to create a new profile.
- 2. Profile Components:**
Once you have created a work profile, you can start creating components within the profile. COPO provides templates/wizards for creating and managing different components including: Datafiles, Samples, Submission, Publications, People, and Annotations. Profile components can be created in any order.
- 3. Quick Tour:**
Finally, if you've not done so already, take some time to explore the various controls available on the page. Click the  icon on the page to activate the quick tour agent.

An **Add Profile** form will be displayed after you click the blue button that has a white plus sign in its centre.

Create a profile:



The screenshot shows the 'Add Profile' form with the following fields:

- Title** required ⓘ: Profile1 (A red arrow points to this field)
- Description** required ⓘ: A collection of fish found in Oulton Broad, UK.
- Profile Type** ⓘ: Stand-alone (The dropdown menu is open, showing options: Stand-alone, Darwin Tree of Life (DTOL), Darwin Tree of Life Environmental Samples (DTOL_ENV), Aquatic Symbiosis Genomics (ASG), and European Reference Genome Atlas (ERGA).)

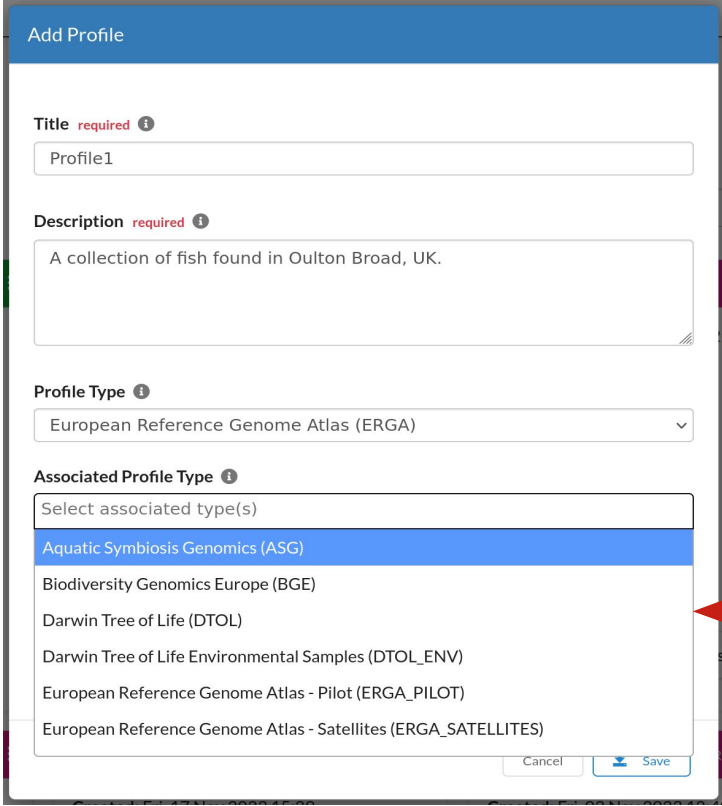
Buttons: Cancel, Save

IMPORTANT - name the profile according to the Sample Set ID assigned to the samples you are submitting

IMPORTANT - If you cannot see the project that you are associated with in the **Profile Type** dropdown menu of the **Add Profile** form, you need to be added to the relevant group.

Please stop here and get in touch with ei.copo@earlham.ac.uk.

Add associated profile type:

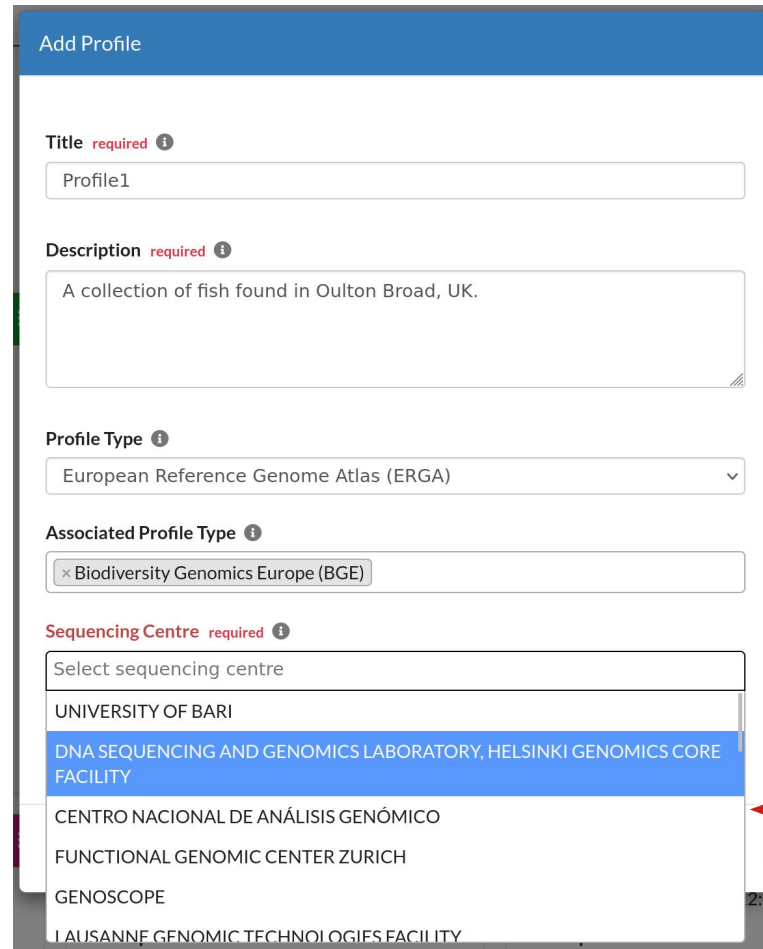


The screenshot shows a web form titled "Add Profile". It contains several fields: "Title" (required) with the value "Profile1"; "Description" (required) with the value "A collection of fish found in Oulton Broad, UK."; "Profile Type" (dropdown) with the value "European Reference Genome Atlas (ERGA)"; and "Associated Profile Type" (dropdown) with a list of options. The "Associated Profile Type" dropdown is open, showing a search bar "Select associated type(s)" and a list of options: "Aquatic Symbiosis Genomics (ASG)", "Biodiversity Genomics Europe (BGE)", "Darwin Tree of Life (DTOL)", "Darwin Tree of Life Environmental Samples (DTOL_ENV)", "European Reference Genome Atlas - Pilot (ERGA_PILOT)", and "European Reference Genome Atlas - Satellites (ERGA_SATELLITES)". The "Aquatic Symbiosis Genomics (ASG)" option is highlighted in blue. A red arrow points to this option from the right. At the bottom right of the form are "Cancel" and "Save" buttons.

NOTE - for ERGA profile types only

- If your desired profile type is a part of a larger project, select the associated type from the **Associated Profile Type** dropdown menu.
- More than one associated type can be selected from the dropdown menu for the profile type.

Add sequencing centre:



The screenshot shows a web form titled "Add Profile" with the following fields:

- Title required**: A text input field containing "Profile1".
- Description required**: A text area containing "A collection of fish found in Oulton Broad, UK."
- Profile Type**: A dropdown menu currently showing "European Reference Genome Atlas (ERGA)".
- Associated Profile Type**: A tag input field containing "x Biodiversity Genomics Europe (BGE)".
- Sequencing Centre required**: A dropdown menu that is open, showing a list of sequencing centres. The option "DNA SEQUENCING AND GENOMICS LABORATORY, HELSINKI GENOMICS CORE FACILITY" is highlighted in blue. A red arrow points to this option from the right side of the image.

Other visible options in the Sequencing Centre dropdown include: UNIVERSITY OF BARI, CENTRO NACIONAL DE ANÁLISIS GENÓMICO, FUNCTIONAL GENOMIC CENTER ZURICH, GENOSCOPE, and LAUSANNE GENOMIC TECHNOLOGIES FACILITY.

NOTE - for ERGA profile types only

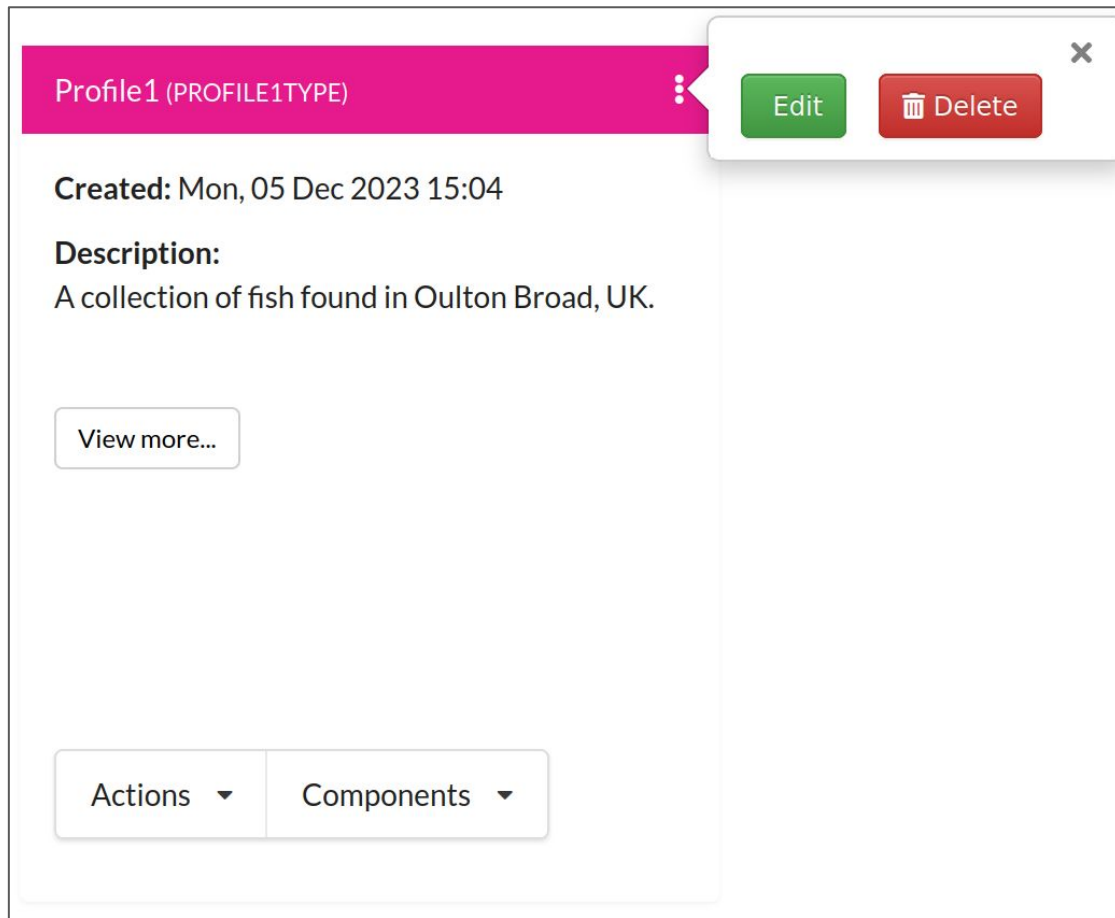
- Select the the centre where your samples will be sequenced at from the **Sequencing Centre** dropdown menu.

New profile created:

The screenshot displays the COPO Work Profiles interface. At the top left is the COPO logo. The main header area includes a 'Work Profiles' section with a lightbulb icon and a plus sign, and a user profile 'tester1' with a gear icon. A navigation bar contains icons for a list, a chart, and an info panel. The main content area shows a list of profiles, with one profile selected and expanded. The selected profile is 'Profile1 (PROFILE1TYPE)', created on Mon, 05 Dec 2023 15:04. Its description is 'A collection of fish found in Oulton Broad, UK.' Below the description is a 'View more...' button. At the bottom of the profile card are 'Actions' and 'Components' dropdown menus. A 'Sort by: Date Created' dropdown is visible above the profile list. On the right side, there is an 'Info' panel and a 'Profile Types Legend' showing 'PROFILE1TYPE' with a pink circle icon. At the bottom left, it says 'Showing: 1 / 1 profiles'.

i After having provided the details in the **Add Profile** form and clicked the **Save** button, your new profile will be displayed on the COPO **Work Profiles** web page

Edit or Delete profile:



The screenshot shows a profile management interface. At the top, there is a pink header bar with the text "Profile1 (PROFILE1TYPE)" and a white vertical ellipsis menu icon on the right. A white dropdown menu is open, containing two buttons: a green "Edit" button and a red "Delete" button with a trash icon. Below the header, the profile details are displayed: "Created: Mon, 05 Dec 2023 15:04" and "Description: A collection of fish found in Oulton Broad, UK." A "View more..." button is located below the description. At the bottom of the profile card, there are two dropdown menus labeled "Actions" and "Components".

- i** If you would like to edit or delete a profile that you have created, click the white vertical ellipsis (:) located at the top right of the desired profile panel to view the profile options to do so

Upload a manifest:

Profile1 (PROFILE1TYPE) ⋮

Created: Mon, 05 Dec 2023 15:04

Description:
A collection of fish found in Oulton Broad, UK.

View more...


Actions ▾ Components ▾

- Submit Annotation
- Submit Assembly
- Submit Barcoding Manifest
- Submit Manifest**
- Submit Reads
- Upload Files

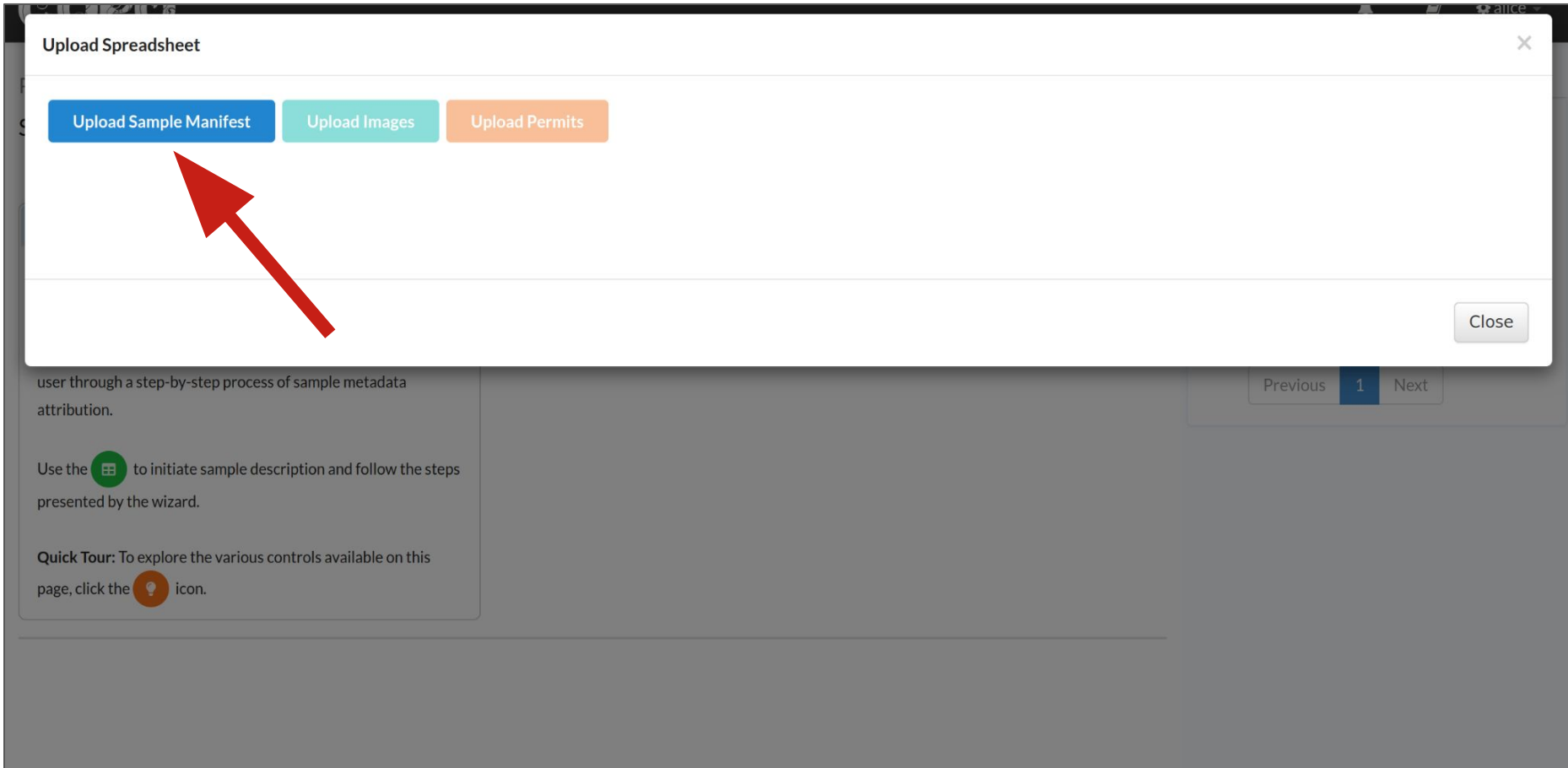
i The colour and wording of this profile panel will differ depending on which project you are submitting a manifest for.

Upload a manifest:

The screenshot shows the COPO web interface. At the top left is the COPO logo. In the top right corner, there are notification, document, mail, and user profile icons, with the user name 'tester1' next to the profile icon. Below the logo, the text 'Profile: Profile1' is displayed. Underneath, the word 'Samples' is followed by four circular icons: a lightbulb (orange), a grid (pink), a download arrow (brown), and another download arrow (yellow). A red arrow points from the grid icon to a 'Samples - Getting started' help box. The help box contains the following text: 'The samples page provides a platform for describing and managing biological samples, obtained as part of a project.', 'The description functionality presents a wizard that guides the user through a step-by-step process of sample metadata attribution.', 'Use the [grid icon] to upload samples.', 'Click the [download icon] to download a blank manifest template.', and 'Quick Tour: To explore the various controls available on this page, click the [lightbulb icon] icon.' To the right of the 'Samples' icons is a toolbar with six icons: a group of people, a puzzle piece, a bar chart, a document, an hourglass, and a shield. Below the toolbar is an 'Info' tab and a large empty white area.

-  The colour and wording of the **Samples** web page will differ depending on which project you are submitting a manifest for.

Upload a manifest:




Upload Spreadsheet


Upload Sample Manifest Upload Images Upload Permits

Close

Previous 1 Next

user through a step-by-step process of sample metadata attribution.

Use the  to initiate sample description and follow the steps presented by the wizard.

Quick Tour: To explore the various controls available on this page, click the  icon.

COPO will validate taxonomy information and manifest format:


Upload Spreadsheet

Upload Images Upload Permits

Checking taxonomy information at row 111 - Lineus longissimus

Close

presented by the wizard.

Quick Tour: To explore the various controls available on this page, click the  icon.

What's happening (part 1):

- COPO is retrieving information from National Centre for Biotechnology Information (NCBI) to check that the taxonomy information provided is correct. We also check that 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 warnings or errors, DO NOT click the finish button instead, contact NCBI to discuss the taxonomy.**

Manifest uploaded -taxonomy warnings-:

Upload Spreadsheet ✕

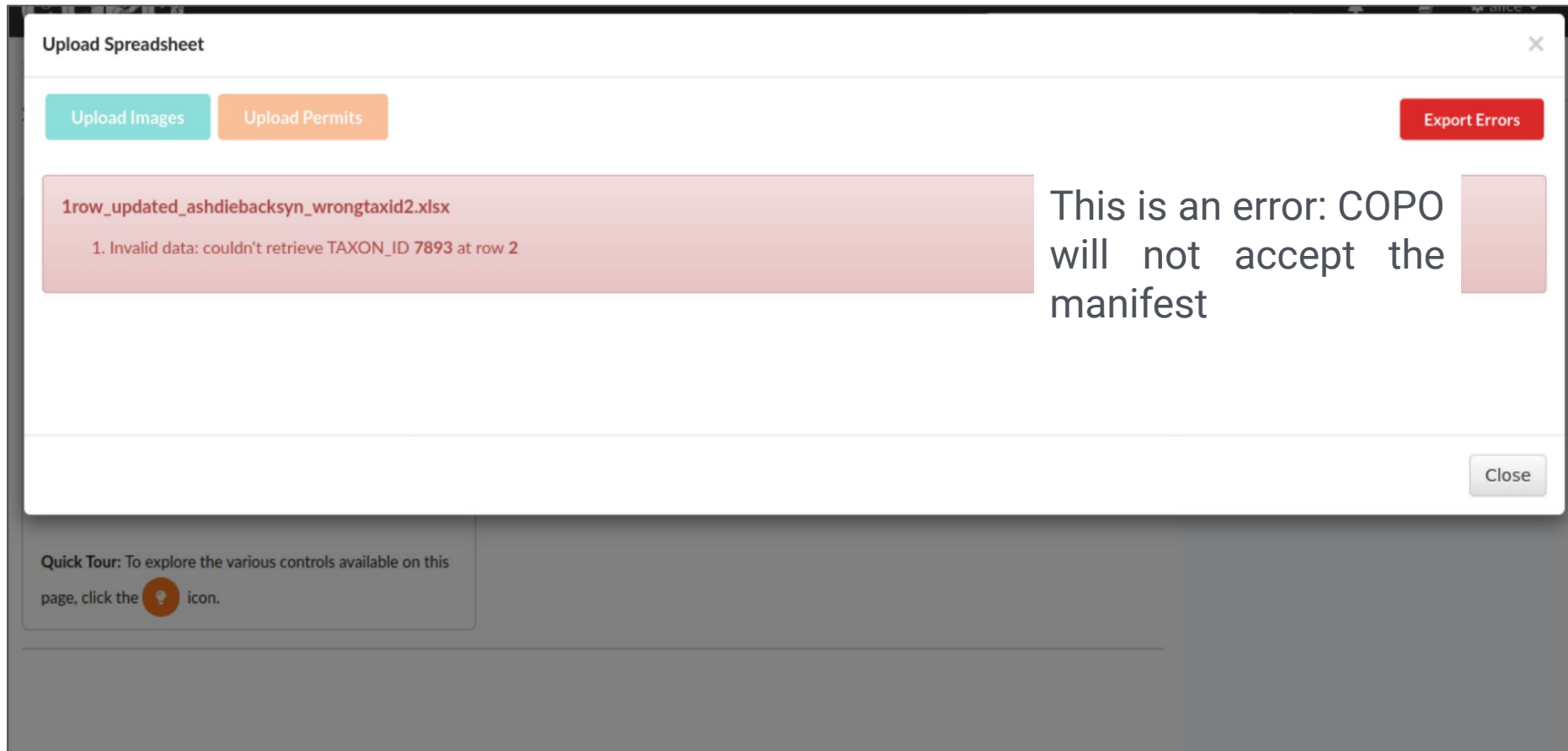
Upload Images Upload Permits Export Errors

Synonym warning: *Asterina gibbosa* at row 294 is a synonym of *Asterina gibbosa* (Pennant, 1777). COPO will substitute the official scientific name.
Synonym warning: *Asterina gibbosa* at row 295 is a synonym of *Asterina gibbosa* (Pennant, 1777). COPO will substitute the official scientific name.
Synonym warning: *Asterina gibbosa* at row 296 is a synonym of *Asterina gibbosa* (Pennant, 1777). COPO will substitute the official scientific name.
Synonym warning: *Asterina gibbosa* at row 297 is a synonym of *Asterina gibbosa* (Pennant, 1777). COPO will substitute the official scientific name.
Synonym warning: *Aglais io* at row 336 is a synonym of *Inachis io*. COPO will substitute the official scientific name.
Synonym warning: *Aglais io* at row 337 is a synonym of *Inachis io*. COPO will substitute the official scientific name.
Synonym warning: *Aglais io* at row 338 is a synonym of *Inachis io*. COPO will substitute the official scientific name.
Synonym warning: *Satyrrium walbum* at row 359 is a synonym of *Satyrrium w-album*. COPO will substitute the official scientific name.
Synonym warning: *Aglais io* at row 385 is a synonym of *Inachis io*. COPO will substitute the official scientific name.
Synonym warning: *Melitaea athalia* at row 450 is a synonym of *Mellicta athalia*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 498 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 499 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 500 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 501 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 502 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 503 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Colias crocea* at row 504 is a synonym of *Colias croceus*. COPO will substitute the official scientific name.
Synonym warning: *Melitaea athalia* at row 516 is a synonym of *Mellicta athalia*. COPO will substitute the official scientific name.

This is a warning:
COPO will make
these changes

SAN.xlsx

Manifest uploaded -taxonomy errors-:



The screenshot shows a web interface for uploading a spreadsheet. At the top, there is a title bar 'Upload Spreadsheet' with a close button (X). Below the title bar, there are two buttons: 'Upload Images' (teal) and 'Upload Permits' (orange). On the right side, there is a red button labeled 'Export Errors'. The main content area features a red error message box with the following text: '1row_updated_ashdiebacksyn_wrongtaxid2.xlsx' and '1. Invalid data: couldn't retrieve TAXON_ID 7893 at row 2'. To the right of this box, there is a larger text area that reads 'This is an error: COPO will not accept the manifest'. At the bottom right of the dialog, there is a 'Close' button. Below the dialog, there is a 'Quick Tour' section with a lightbulb icon and the text: 'Quick Tour: To explore the various controls available on this page, click the icon.'

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 - with compliance errors:-

Upload Spreadsheet

Upload Images Upload Permits Export Errors

Missing TAXON_ID: row 2 - TAXON_ID for *Chalara Fraxinea* will be filled with 746836
Synonym warning: *Chalara Fraxinea* at row 2 is a synonym of *Hymenoscyphus fraxineus*. COPO will substitute the official scientific name.

1row_updated_ashdiebacksyn_notaxid2_nullrack.xlsx

1. Field not found - DIFFICULT_OR_HIGH_PRIORITY_SAMPLE
2. Invalid data: WHOLE ORGANISM in column ORGANISM_PART at row 2. Allowed values are [***OTHER_FUNGAL_TISSUE***, ***OTHER_PLANT_TISSUE***, ***OTHER_REPRODUCTIVE_ANIMAL_TISSUE***, ***OTHER_SOMATIC_ANIMAL_TISSUE***, 'ABDOMEN', 'ANTERIOR_BODY', 'BLADE', 'BLOOD', 'BODYWALL', 'BRACT', 'BRAIN', 'BUD', 'CAP', 'CEPHALOTHORAX', 'EGG', 'EGGSHELL', 'ENDOCRINE_TISSUE', 'EYE', 'FAT_BODY', 'FIN', 'FLOWER', 'GILL_ANIMAL', 'GILL_FUNGI', 'GONAD', 'HAIR', 'HEAD', 'HEART', 'HEPATOPANCREAS', 'HOLDFAST_FUNGI', 'KIDNEY', 'INTESTINE', 'LEAF', 'LEG', 'LIVER', 'LUNG', 'MID_BODY', 'MODULAR_COLONY', 'MUSCLE', 'MYCELIUM', 'MYCORRHIZA', 'NOT_COLLECTED', 'NOT_APPLICABLE', 'NOT_PROVIDED', 'OVARY_ANIMAL', 'OVIDUCT', 'PANCREAS', 'PETIOLE', 'POSTERIOR_BODY', 'SCALES', 'SCAT', 'SEEDLING', 'SEED', 'SHOOT', 'SKIN', 'SPERM_SEMINAL_FLUID', 'SPLEEN', 'SPORE', 'SPORE_BEARING_STRUCTURE', 'STEM', 'STIPE', 'STOMACH', 'TENTACLE', 'TERMINAL_BODY', 'TESTIS', 'THALLUS_FUNGI', 'THALLUS_PLANT', 'THORAX', 'WHOLE_ORGANISM', 'WHOLE_PLANT']
3. Invalid data: REFERENCE GENOME in column PURPOSE_OF_SPECIMEN at row 2. Allowed values are ['REFERENCE_GENOME', 'SHORT_READ_SEQUENCING', 'DNA_BARCODING_ONLY', 'RNA_SEQUENCING']

This manifest was compliant with SOP2.1 and cannot be accepted

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

Manifest uploaded -correct manifest-:

Upload Spreadsheet ✕

[Upload Images](#) [Upload Permits](#)

Missing TAXON_ID: row 2 - TAXON_ID for *Chalara Fraxinea* will be filled with 746836
Synonym warning: *Chalara Fraxinea* at row 2 is a synonym of *Hymenoscyphus fraxineus*. COPO will substitute the official scientific name.

Sample Metadata [Sample Images](#) [Sample Permits](#)

Show entries Search:

SERIES ↓	RACK_OR_PLATE_ID ↓	TUBE_OR_WELL_ID ↓	SPECIMEN_ID ↓	ORDER_OR_GROUP ↓	FAMILY ↓	GENUS ↓	TAXON_ID ↓	SCIENTIFIC_NAME
1	null	FF06763795	SAN0000100	HELOTIALES	HELOTIACEAE	HYMENOSCYPHUS	746836	HYMENOSCYPHUS FRAXINEUS

Check the warnings if present

Manifest uploaded -correct manifest-:

Upload Spreadsheet ✕

[Upload Images](#) [Upload Permits](#)

Missing TAXON_ID: row 2 - TAXON_ID for Chalara Fraxinea will be filled with 746836
Synonym warning: Chalara Fraxinea at row 2 is a synonym of Hymenoscyphus fraxineus. COPO will substitute the official scientific name.

Sample Metadata [Sample Images](#) [Sample Permits](#) **Preview of the manifest**

Show entries Search:

SERIES <small>⌵</small>	RACK_OR_PLATE_ID <small>⌵</small>	TUBE_OR_WELL_ID <small>⌵</small>	SPECIMEN_ID <small>⌵</small>	ORDER_OR_GROUP <small>⌵</small>	FAMILY <small>⌵</small>	GENUS <small>⌵</small>	TAXON_ID <small>⌵</small>	SCIENTIFIC_NAME
1	null	FF06763795	SAN0000100	HELOTIALES	HELOTIACEAE	HYMENOSCYPHUS	746836	HYMENOSCYPHUS FRAXINEUS

Upload images:

Upload Spreadsheet

[Upload Images](#) [Upload Permits](#)

Missing TAXON_ID for row 2 - TAXON_ID for *Chalara Fraxinea* will be filled with 746836
Synonym warning: *Chalara Fraxinea* at row 2 is a synonym of *Hymenoscyphus fraxineus*. COPO will substitute the official scientific name.

Sample Metadata [Sample Images](#) [Sample](#)

Show 10 entries

Search:

SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME
1	null	FF06763795	SAN0000100	HELOTIALES	HELOTIACEAE	HYMENOSCYPHUS	746836	HYMENOSCYPHUS FRAXINEUS

File names of any associated images must be the same as "SPECIMEN_ID"-*"n"* with the extension ".jpg" or ".png"

Uploaded images:


Upload Spreadsheet

[Upload Images](#) [Upload Permits](#)

Missing TAXON_ID: row 2 - TAXON_ID for *Chalara Fraxinea* will be filled with 746836
Synonym warning: *Chalara Fraxinea* at row 2 is a synonym of *Hymenoscyphus fraxineus*. COPO will substitute the official scientific name.

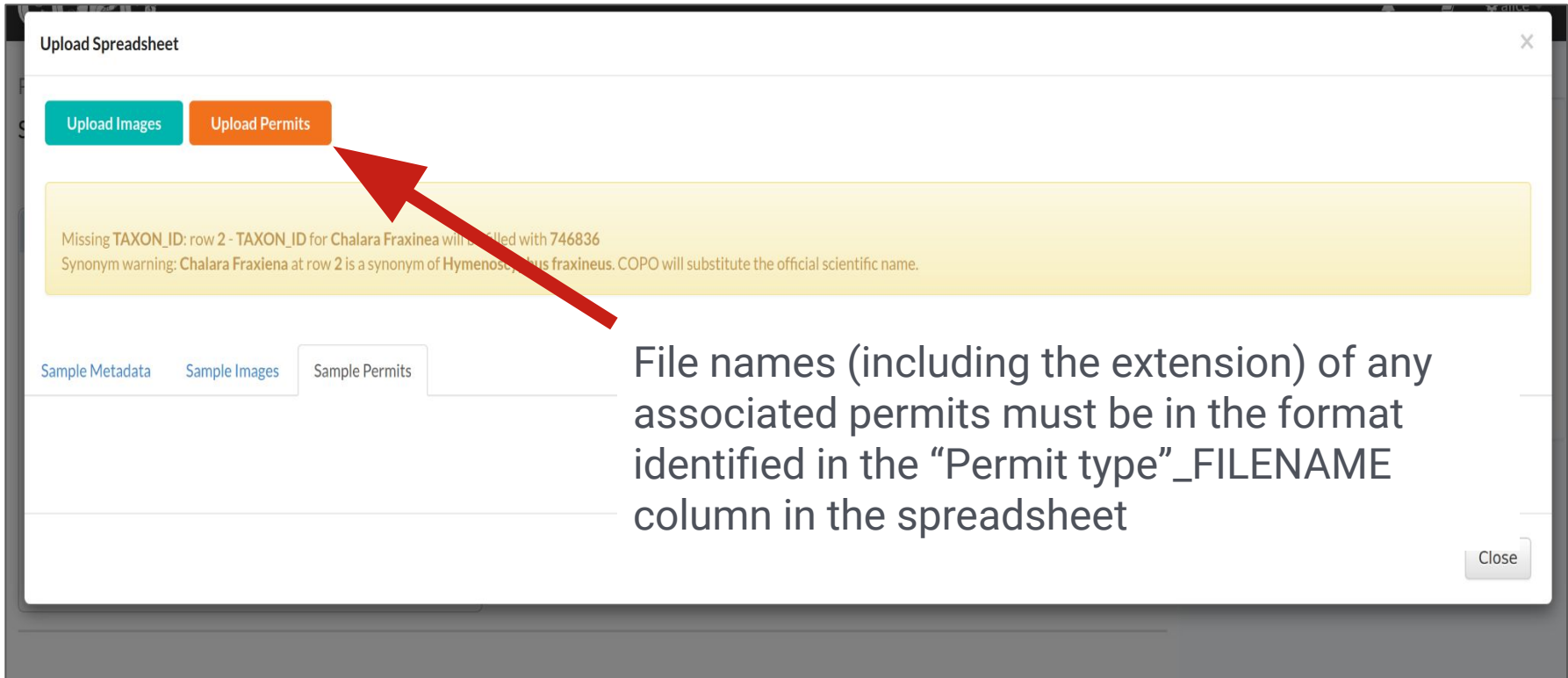
[Sample Metadata](#) [Sample Images](#) [Sample Permits](#)

Show entries Search:

Specimen ID	Image File	Image
SAN0000100	SAN0000100-1.png	

Showing 1 to 1 of 1 entries [Previous](#) [1](#) [Next](#)

Upload permits:



Upload Spreadsheet

Upload Images Upload Permits

Missing TAXON_ID: row 2 - TAXON_ID for *Chalara Fraxinea* will be filled with 746836
Synonym warning: *Chalara Fraxiena* at row 2 is a synonym of *Hymenosyces fraxineus*. COPO will substitute the official scientific name.

Sample Metadata Sample Images Sample Permits

File names (including the extension) of any associated permits must be in the format identified in the "Permit type" _FILENAME column in the spreadsheet

Close

IMPORTANT - If you have more than one permit file to upload, they must be uploaded at the same time i.e. after you have clicked the "Upload Permits" button, navigate to the directory where the permits are stored and **CTRL + click** all of the permits so that all the permits are highlighted and uploaded at the same time.

All permit files have to be selected/opened from the directory and uploaded together not one after the other.

Uploaded permits:

Upload Spreadsheet

[Upload Images](#) [Upload Permits](#) [Finish](#)

Missing TAXON_ID: row 2 - TAXON_ID for Chalara Fraxinea will be filled with 746836
Synonym warning: Chalara Fraxiena at row 2 is a synonym of Hymenoscyphus fraxineus. COPO will substitute the official scientific name.

[Sample Metadata](#) [Sample Images](#) [Sample Permits](#)

Show entries Search:

Specimen ID	Permit Files	Notes
ERGA_DS_382X_01_01	ERGA_DS_382X_01_01_SAMPLING_PERMITS.pdf	
ERGA_TD_5269_01	ERGA_TD_5269_01_SAMPLING_PERMITS.pdf	

Showing 1 to 2 of 2 entries [Previous](#) [1](#) [Next](#)

[Close](#)

i If there are any errors with the permit upload process, they will be displayed in the **Notes** table column of the **Sample Permits** tab

Create the samples in COPO by clicking “Finish”:


Upload Spreadsheet ✕

[Upload Images](#) [Upload Permits](#) [Finish](#)

Missing TAXON_ID: row 2 - TAXON_ID for *Chalara Fraxinea* to be filled with 746836
Synonym warning: *Chalara Fraxinea* at row 2 is a synonym of *Hymenoscyphus fraxineus*. COPO will substitute the official scientific name.


[Sample Metadata](#) [Sample Images](#) [Sample Permits](#)

Show entries Search:





Specimen ID	Image File	Image
SAN0000100	SAN0000100-1.png	







Showing 1 to 1 of 1 entries [Previous](#) [1](#) [Next](#)

Uploaded samples:

 🔔 📄 ✉️ ⓘ ⚙️ tester1 ▾


Profile: Profile1











Samples    

Select all | Select filtered | Clear selection | Export CSV | [Download sample manifest](#) | [Download permits](#) | [View images](#)

Search Samples

Showing 1 to 25 of 417 records | Click  beside a record to view extra details

Tube or Well Identifier	Specimen Identifier	Purpose of Specimen	Sample Coordinator (ERGA Ambassador)	Sample Coordinator (ERGA Ambassador) Affiliation	Sample Coordinator (ERGA Ambassador) ORC
 FF16867824	ERGA_FOS_9317_002	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867825	ERGA_FOS_9317_003	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867826	ERGA_FOS_9317_004	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867827	ERGA_FOS_9317_005	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867828	ERGA_FOS_9317_006	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867829	ERGA_FOS_9317_007	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867830	ERGA_FOS_9317_008	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867831	ERGA_FOS_9317_009	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867832	ERGA_FOS_9317_010	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706
 FF16867833	ERGA_FOS_9317_011	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9688-5706

show records



Previous | **1** | 2 | 3 | 4 | 5 | ... | 17 | Next

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 accepted by a sample manager, they will be submitted to European Nucleotide Archive (ENA).

Accessions can be inspected by:

- Scrolling right in the previous view
- Clicking the  button on the **Samples** web page to access the **Accessions** web page for the desired profile
- Clicking the  component button associated with the desired profile on the **Work Profiles** web page to access the **Accessions** web page

Accepted samples:



Profile: Profile1

Samples    

Info

Search Samples

Showing 1 to 25 of 417 records Click  beside a record to view extra details

Other Information	Associated TOL (Tree of Life) Project	Biosample Accession	Manifest Identifier	Manifest Version	Public Name	SRA Accession	Status	Submission Accession
		SAMEA130812875	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari27	ERS27722072	accepted	ERA27745811
		SAMEA130812877	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari28	ERS27722074	accepted	ERA27745813
		SAMEA130812879	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari29	ERS27722076	accepted	ERA27745815
		SAMEA130812881	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari30	ERS27722078	accepted	ERA27745817
		SAMEA130812883	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari31	ERS27722080	accepted	ERA27745819
		SAMEA130812885	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari32	ERS27722082	accepted	ERA27745821
		SAMEA130812887	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari33	ERS27722084	accepted	ERA27745823
		SAMEA130812889	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari34	ERS27722086	accepted	ERA27745825
		SAMEA130812891	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari35	ERS27722088	accepted	ERA27745828
		SAMEA130812982	6d7f4a0b-989a-429b-aa40-a61bacfaad02	2.5	wuAreMari36	ERS27722179	accepted	ERA27745838

show 25 records

Updating samples:

- To update samples, reupload a manifest with the amended changes. The new value will be detected and updated automatically once the resubmission is successfully completed.

More information regarding sample updates can be found [here](#).

- ❗ Not all field values of existing samples can be updated by resubmitting a manifest with the amendments.

The fields that can be updated are listed [here](#).



If you encounter any errors or unexpected behaviour, please email ei.copo@earlham.ac.uk or open a GitHub issue in the [COPO repository](#).

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

- ❗ For detailed information regarding manifest submission and COPO, please see our [documentation](#).



[collaborative-open-plant-omics/COPO-production](https://github.com/collaborative-open-plant-omics/COPO-production)





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Decoding Living Systems