# Collaborative OPen Omics (COPO) Project Documentation

Release 1.0

The Collaborative OPen Omics (COPO) project team

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Welcome to the guidelines for submission, updates and retrieval for the Collaborative OPen Omics project. Please use the links to find instructions specific to your needs.

# **GETTING STARTED**

Collaborative OPen Omics (COPO) is a website portal where scientists describe their research objects (raw or processed data, reads, samples, images etc.) using community-sanctioned metadata sets and vocabularies<sup>1</sup>.

As a metadata broker, COPO encourages data generators to adhere to FAIR (Findable, Accessible, Interoperable and Reusable)<sup>2</sup> principles when submitting research objects, using semantic terms to add meaning to them and specify relationships between them.

COPO uses public or institutional repositories like European Nucleotide Archive (ENA) and National Center for Biotechnology Information (NCBI) to share the research objects to the wider scientific community.

COPO is developed by a team of Research Software Engineers at the Earlham Institute. Contributions are welcomed in the GitHub repository. All contributors must abide by the code of conduct described in the *Contributor Covenant Code of Conduct* section.

Visit the COPO website to make manifest submissions. An ORCID ID is required to access the application.

The website requires cookies, fonts and the limited processing of your personal data in order to function well. By using the portal you are consenting to this. To find out more about how COPO uses cookies and your personal data, please see our *Privacy Notice* and *Terms of Use*.

Hint: You can register for an ORCID ID on the ORCID website for free.

# 1.1 Accessing COPO Website

There are two ways to access the COPO website: Demo mode and Production mode.

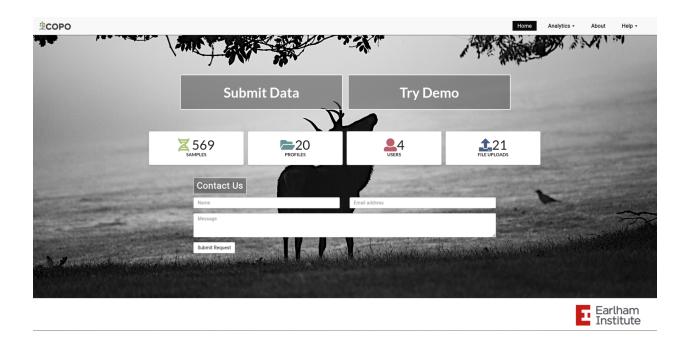
Navigate to COPO live website to access the production mode **or** navigate to the COPO demo website to access the demonstration mode.

### Note:

- **Production mode** is the live version of the COPO application. It is recommended to submit real data to the production mode because the submissions are made to the final repository.
- **Demo mode** is a testing environment for the COPO application. It is not recommended to submit real data to the demo mode because any submissions done are considered test submissions and there will be no submissions to the final repository.

<sup>&</sup>lt;sup>1</sup> SOPs (Standard Operating Procedures) guide the metadata sets and vocabularies for manifests. See: SOP guidelines.

<sup>&</sup>lt;sup>2</sup> See: COPO FAIR data principles.



## COPO homepage: Click Submit Data button to proceed to the ORCID sign-in form (as shown below)

Alternatively, click Try Demo button to access the demo mode.



**COPO** homepage: Click Sign in with Orcid.org button to proceed to the ORCID sign-in form (as shown below)

**Orcid sign-in form: Enter your Orcid login credentials or click** Register now to sign-up for an ORCID account. If the login is successful, a redirection is made to the COPO application.

iD
Sign in to ORCID
۲ Email or 16-digit ORCID iD
example@email.com or 0000-0001-2345-6789
Password
SIGN IN
Forgot your password or ORCID ID?
Don't have an ORCID iD yet? Register now
or
Access through your institution
G Sign in with Google
G   Sign in with Google     Image: Sign in with Facebook



# **PROJECTS BROKERED THROUGH COPO**

### Hint:

- Primary projects are also known as umbrella projects or main projects and are the main focus of the project. In COPO, primary projects are regarded as **Profile type** or ToL (Tree of Life)<sup>1</sup> project.
- Secondary projects are also known as subprojects or child projects and are part of the main project. In COPO, secondary projects are regarded as **Associated profile type** or associated ToL project.

# 2.1 Primary Projects

- Aquatic Symbiosis Genomics (ASG)<sup>2</sup>
- Darwin Tree of Life Samples (DToL)<sup>3</sup>
- Darwin Tree of Life Environmental Samples

### (DToL\_ENV)

- European Reference Genome Atlas (ERGA)<sup>4</sup>
- Stand-alone

## 2.2 Secondary Projects

**Note:** In addition to the secondary projects outlined below, all projects listed under **Primary Projects** except Standalone, can be added as a subproject of a larger project.

- Biodiversity Genomics Europe (BGE)
- European Reference Genome Atlas Pilot (ERGA\_PILOT)
- European Reference Genome Atlas Satellites (ERGA\_SATELLITES)
- Population Genomics (POP\_GENOMICS)

### See also:

- Standard Operating Procedure (SOP) for the various projects
- Manifest template for the various projects
- Using manifest wizard to prefill manifests

<sup>&</sup>lt;sup>1</sup> See term: *Tree of Life (ToL)* 

<sup>&</sup>lt;sup>2</sup> See term: *ASG*.

<sup>&</sup>lt;sup>3</sup> See term: *DToL*.

<sup>&</sup>lt;sup>4</sup> See term: *ERGA*.

## THREE

## **NEW USER**

# 3.1 First time login

If signing in for the first time, a prompt requesting for an email address is displayed.

Enter an email address to proceed. A valid email address and agreement lead to the main web page that comprises all the **work profiles** associated with a user.

The email address supplied will be associated with the user's COPO account and will be used in COPO for tasks such as depositing data to remote repositories involving the user.

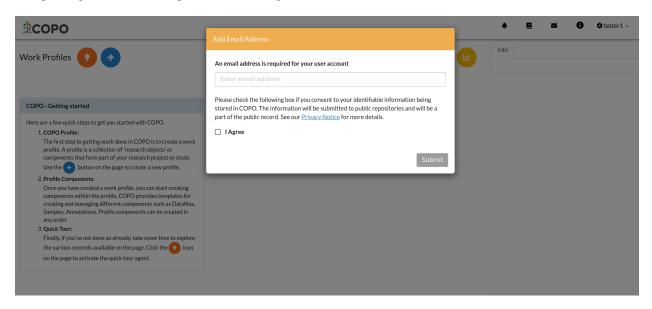


Fig. 1: First time user: Email address prompt shown when a user logs into COPO for the first time

# SAMPLE MANAGERS

This section gives an overview of the COPO features that are delegated to Biodiversity Genomics Europe (BGE) checker or sample managers<sup>1</sup> who are responsible for accepting or rejecting samples produced by sample submitters<sup>2</sup>.

#### Note:

• Make a request to the indicating the type of profile manifest group that you would like to be assigned to as a sample manager BGE (Biodiversity Genomics Europe).

The permission will be granted after the request has been approved.

## See also:

- View images produced by sample submitters
- Download permits produced by sample submitters
- Sample Managers' Frequently Asked Questions

# 4.1 Accessing the Accept or Reject Samples web page

Note: The 📁 button will only appear on the web page if you are granted permission to be a sample manager.

Once the button is clicked, the accept/reject samples web page will be displayed.

If you have been granted permission as a sample manager, you will receive an email notifying you that sample(s) has been submitted after a user uploads a manifest.

Similarly, you will receive an email when samples have been rejected.

Click the <sup>(=)</sup> button to accept or reject samples.

Alternatively, navigate to Accept/Reject Samples' web page.

<sup>&</sup>lt;sup>1</sup> See term: *Sample manager* 

<sup>&</sup>lt;sup>2</sup> See term: *Sample submitter*. Sample submitter may also be referred to as a manifest provider or manifest submitter.

# 4.2 Guidelines for Sample Managers Assigned to More than one Manifest Group

**Note:** The manifest dropdown menu will only be displayed on the **Accept or Reject samples** web page if you as a sample manager, belongs to more than one sample manager manifest group.

**Hint:** If the **dtol** sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics  $(ASG)^3$  profiles and Darwin Tree of Life  $(DToL)^4$  profiles will be displayed in the **All profiles** tab (if any exists).

If you have been granted permission to be a sample manager for more than one manifest group, you can accept or reject samples for more than one manifest group by following the steps below:

1. Click the dropdown menu displayed beside the **Choose to Accept or Reject** web page title on the left side of the **Accept or Reject Samples** web page as shown below:



# Choose to Accept or Reject

## Note clicking accept will immediately send sample info to ENA/Biosamples

# Fig. 1: Accept or Reject Samples web page: Manifest dropdown menu beside 'Choose to Accept or Reject' web page title

2. A list of all the manifest groups that you have been assigned to is then displayed.

Choose the desired manifest group from the dropdown menu as shown below:

3. To accept samples, see the Accepting samples section

OR

To reject samples, see the Rejecting samples section

dtol

<sup>&</sup>lt;sup>3</sup> See term: *ASG*.

<sup>&</sup>lt;sup>4</sup> See term: *DToL*. *DToL* may sometimes be referred to as *DTOL*.





Fig. 2: Accept or Reject Samples web page: Manifest dropdown menu with options displayed

# 4.3 Accepting or Rejecting Samples

**Note:** A **Samples** table record will only be displayed if the desired profile that is clicked/highlighted on the left of the web page has submitted samples.

### Hint:

• See Accept or Reject Samples for more than one manifest group section for guidance if you are assigned to more than one manifest group and would like to accept or reject samples.

## 4.3.1 Accepting samples

The following sections describe how to accept samples depending on the type of manifest group that you have been assigned as a sample manager to:

- Accepting ASG or DTOL samples
- Accepting ERGA samples as a BGE checker
- Accepting ERGA samples as a Sample Manager

## 4.3.2 Accepting ASG or DTOL samples

- 1. Choose desired profile on the left of the Accept or Reject Samples web page
  - From the All Profiles tab if desired profile is an ASG (Aquatic Symbiosis Genomics)<sup>Page 12, 3</sup> or DTOL (Darwin Tree of Life)<sup>Page 12, 4</sup> profile
- 2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the Accept button as shown below.

Choose to Acc	cept or Reject	dtol ~								S	tatus		
											Idle		
ote clicking accept will	immediately send sample	into to ENA/Biosamples											
All profiles				K Reject	Accept Select all vi	sible Select None	Delete Selected D	ownload Permits View Ima	jes				
	Search:		P	ending Sample	Processing Samples A	ccepted Samples Rej	ected Samples						
rofile Title 🕴	Date Created 🖕	Samples link											
TOL Test Profile 4	17/11/2023	Ф.	Sam	ples									
TOL Test Profile 3	01/11/2023	8	Show	v 10 ~	entries							Search:	
OL Test Profile 2	27/10/2023	જ		SERIES 0	RACK OR PLATE ID	TUBE OR WELL ID	SPECIMEN ID	ORDER OR GROUP	FAMILY	GENUS	TAXON ID	SCIENTIFIC NAME	TAXON REMAR
SG Test Profile	10/10/2023	ъ.		1	DtoL_R&D_Protist_cell_sort1		Ox800036	Sphaeropleales	Radiococcaceae			Coenococcus planctonicus	
TOL Test Profile	10/10/2023	B	_										
				2	DtoL_R&D_Protist_cell_sort2	Co_S2_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				3	DtoL_R&D_Protist_cell_sort3	Co_S3_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				4	DtoL_R&D_Protist_cell_sort4	Co_S1_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				5	DtoL_R&D_Protist_cell_sort5	Co_S2_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				6	DtoL_R&D_Protist_cell_sort6	Co_S3_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				7	DtoL_R&D_Protist_cell_sort7	Co_S4_400001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				8	DtoL_R&D_Protist_cell_sort8	Co_S8_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
			_	9	DtoL_R&D_Protist_cell_sort9	Co_S9_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcu	2853155	Coenococcus planctonicus	
				1									

Fig. 3: Accept or Reject Samples web page: Accepting samples within ASG or DTOL profiles

## 4.3.3 Accepting ERGA samples as a BGE checker

### Note:

- In the **Samples** table, sample record(s) will only be displayed in the **Pending BGE Checker Samples** tab, if you are assigned as a **Biodiversity Genomics Europe (BGE) checker** for the desired profile.
- All COPO ERGA (European Reference Genome Atlas)<sup>5</sup> profiles are displayed in the **All Profiles** tab but submitted samples within them cannot be accepted or rejected.
- 1. Choose desired profile on the left of the Accept or Reject Samples web page
  - From the Profiles for My Sequencing Centre tab
- 2. In the **Pending BGE Checker Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the Accept button as shown below.

<sup>5</sup> See term: *ERGA*.

Choose to Acce	ept or Reject	erga v									Status			
Note clicking accept will in	nmediately send sam	ple info to ENA/Biosamples									Idle			
Profiles for My Sequenc	ing Centre All pr Search:	ofiles				lect all visible Select None		Cownload Permits View In						
rofile Title 🕴	Date Created 28/11/2023	Samples link 🕴	Samples	5	entries							c	earch:	
KGA lest Flolle 11	27/11/2023	•		ERIES 0	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN ID	ORDER_OR_GROUP	FAMILY 0	GENUS 🗄	TAXON ID	SCIENTIFIC_NAME	TAXON REMARKS	IN
				ERIEJ	KACICOK FEATEID V	FF06763893	ERGA_FOS_4557_001		Arenicolidae	Arenicola	6344	Arenicola marina	TAXON_REMARKS	
						FF06763894	ERGA_FOS_4557_002		Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763895	ERGA_FOS_4557_003	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763896	ERGA_FOS_4557_004	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763897	ERGA_FOS_4557_005	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763898	ERGA_FOS_4557_006	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763899	ERGA_FOS_4557_007	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763900	ERGA_FOS_4557_008	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
						FF06763901	ERGA_FOS_4557_009	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		

# Fig. 4: Accept or Reject Samples web page: Accepting samples within ERGA profiles as a Biodiversity Genomics Europe (BGE) checker

3. In the **Pending BGE Checker Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the 🗸 🗸	cept	button as sl	nown belo	w.							
<b>≜COPO</b>									▲ ₽	2 0 d	tester4 +
Choose to Accept or Reject erga ~								Status			
Note clicking accept will immediately send sample info to ENA/Biosamples								Idle			
Profiles for My Sequencing Centre All profiles Search: Profile Title  Date Created  Samples link			Select all visible Select Non ing Samples Processin	e Delete Selected	Download Permits View In Samples Rejected Sam						
ERGA Test Profile 2 28/11/2023 %	Samples										
ERGA Test Profile 11 27/11/2023 %	Show 10	~ entries							s	iearch:	
	+ SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY \$	GENUS 🗄	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASE
			FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
			FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
	Showing 1 to 2	of 2 entries							Pr	evious 1 Next	

Fig. 5: Accept or Reject Samples web page: Samples accepted by Biodiversity Genomics Europe (BGE) checker are displayed in 'Pending Samples' tab

## 4.3.4 Accepting ERGA samples as a Sample Manager

### Note:

- In the **Samples** table, sample record(s) will only be displayed in the **Pending Samples** tab for the desired profile **after** they have been accepted by a Biodiversity Genomics Europe (BGE) checker.
- All COPO ERGA<sup>5</sup> profiles are displayed in the **All Profiles** tab but submitted samples within them cannot be accepted or rejected.

Hint: Rejected samples are displayed in the **Rejected Samples** tab.

- 1. Choose desired profile on the left of the Accept or Reject Samples web page
  - From the Profiles for My Sequencing Centre tab
- 2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Then, click the Accept button as shown below.

<b>≜COPO</b>								. ₽	2 0 ¢	tester4 +
Choose to Accept or Reject erga ~							Status			
Note clicking accept will immediately send sample info to ENA/Biosamples							Idle			
Profiles for My Sequencing Centre All profiles	🗶 Reject 🞯 🗸 Accept 🛛 s	elect all visible Select None	Delete Selected	Download Permits	uges					
Search:	Pending BGE Checker Samples Pend	ng Samples Processing	Samples Accepted S	Samples Rejected Sam	ples					
Profile Title 💠 Date Created 🛓 Samples link 🕴										
ERGA Test Profile 2 28/11/2023 %	Samples									
ERGA Test Profile 11 27/11/2023 %	Show 10 v entries							Si	earch:	
	+ SERIES + RACK_OR_PLATE_ID +	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY \$	GENUS 🗄	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRAS
		FF06763893	ERGA_FOS_4557_001	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
		FF06763894	ERGA_FOS_4557_002	Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina		
	Showing 1 to 2 of 2 entries							Pre	vious 1 Next	

### Fig. 6: Accept or Reject Samples web page: Accepting samples within ERGA profiles

A confirmation popup dialogue will be displayed as shown below.

Click the **Ok** button to accept the selected sample record(s) or click the **Cancel** button to cancel the action.

ENA Submission	×
By accepting the samples, these will immediately be submitted to ENA. This action is irreversible.	
Cancel	k

Fig. 7: Accept or Reject Samples web page: Accept samples confirmation dialogue

3. If the **Ok** button is clicked, the accepted samples will proceed to the processing stage and will be displayed in the **Processing Samples** tab as shown below:

OR

4. After the samples have been processed, the samples will proceed to the accepted stage and will be displayed in the **Accepted Samples** tab as shown below:

<b>COPO</b>												<b>≜ 8 ⊠</b>	0 ¢tester3
Choose to Acce	ept or Reject	dtol v								s	itatus		
Note clicking accept will in	mediately send sample in	fo to ENA/Biosamples									Adding to Sampl	e 65578db801a736763afde3	Ic8 Batch: Ox800036
All profiles			×	Reject 🧿	Accept Select all	visible Select None	Delete Selected	Download Permits View Im	ages				
	Search:		Pe	nding Sample	s Processing Samples	Accepted Samples Re	elected Samples						
Profile Title	Date Created 🖕	Samples link		namb compre	r occosing samples	accepted outpies in the	jeeted ouripies						
DTOL Test Profile 4	17/11/2023	90	Samp	oles									
DTOL Test Profile 3	01/11/2023	æ	Show	10 ~	entries							Search:	
DTOL Test Profile 2	27/10/2023	96							FAMILY :		TAMONIA		TAXON REMARKS
ASG Test Profile	10/10/2023	96		SERIES 🕴	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS 🕴	TAXON_ID 🕴	SCIENTIFIC_NAME	TAXON_REMARKS
DTOL Test Profile	10/10/2023	96		1	DtoL_R&D_Protist_cell_sort1	Co_S1_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
				2	DtoL_R&D_Protist_cell_sort2	Co_S2_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
			Show	ing 1 to 2 of 2	entries							Previous	Next

Fig. 8: Accept or Reject Samples web page: Accepted ASG or DTOL samples at the processing stage

<b>≜COPO</b>			▲ ₽	2 0 d	tester4 +
Choose to Accept or Reject erga ~		Status			
Note clicking accept will immediately send sample info to ENA/Biosamples		Nothing mor	e to submit		0
Profiles for My Sequencing Centre All profiles Search: Profile Title  Date Created Samples link	X         Reject         Image: Constraint of the second state of				
ERGA Test Profile 2         28/11/2023         %           ERGA Test Profile 11         27/11/2023         %	Samples Show 10 v entries			earch:	
				TAXON_REMARKS	INFRASE
			Arenicola marina		
	Showing 1 to 1 of 1 entries		Pri	evious 1 Next	

Fig. 9: Accept or Reject Samples web page: Accepted ERGA samples at the processing stage

<b>COPO</b>												•	8	•	0 ¢teste
Choose to Acce	pt or Reject	dtol ~								s	tatus				
Note clicking accept will im	nediately send sample info	to ENA/Biosamples									Bioimage not sul	omitted			
All profiles			×	Reject d	r 🗸 Accept Select all	visible Select None	Delete Selected	Download Permits View Im	lages						
	Search:		Pe	nding Sample	s Processing Samples	Accepted Samples Re	ejected Samples								
Profile Title 🕴	Date Created 🖕	Samples link													
DTOL Test Profile 4	17/11/2023	9	Sam	ples											
DTOL Test Profile 3	01/11/2023	æ	Show	/ 10 v	entries								Search		
DTOL Test Profile 2	27/10/2023	æ		-						051110					
ASG Test Profile	10/10/2023	æ	-	SERIES 🕴	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY 🕴	GENUS 🕴	TAXON_ID 🗄	SCIENTIF			XON_REMAR
DTOL Test Profile	10/10/2023	æ		1	DtoL_R&D_Protist_cell_sort1	Co_S1_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococ	cus planctor	icus	
				2	DtoL_R&D_Protist_cell_sort2	Co_S2_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococ	cus planctor	iicus	
			Show	ving 1 to 2 of 2	2 entries								Previous	1	Next

Fig. 10: Accept or Reject Samples web page: Accepted ASG or DTOL samples at the accepted stage

±соро				2 0 ·	<b>¢</b> tester4 ≁
Choose to Accept or Reject erga ~		Status			
Note clicking accept will immediately send sample into to ENA/Biosamples		Idle			
Profiles for My Sequencing Centre All profiles Search:	X Reject 🚱 🖌 Accept Select al viable Select None Dielet Select Deveload Promits View Images				
Profile Title 💠 Date Created 🍦 Samples link ≑	Pending BGE Checker Samples Pending Samples Processing Samples Accepted Samples Rejected Samples				
ERGA Test Profile 2         28/11/2023         %           ERGA Test Profile 11         27/11/2023         %	Samples Show 10 ventries		s	iearch:	
	* SERIES © RACK_OR_PLATE_ID © TUBE_OR_WELL_ID © SPECIMEN_ID © ORDER_OR_GROUP © FAMILY © GENUS ©	TAXON_ID ‡	SCIENTIFIC_NAME	TAXON_REMARKS	+ INFRASE
	FF06763893 ERGA_FOS_4557_001 Capitellida Arenicolidae Arenicol	6344	Arenicola marina		
	Showing 1 to 1 of 1 entries		Pr	evious 1 Next	

OR

Fig. 11: Accept or Reject Samples web page: Accepted ERGA samples at the accepted stage

## 4.3.5 Rejecting samples

- 1. Choose desired profile on the left of the Accept or Reject Samples web page
  - From the Profiles for My Sequencing Centre tab if desired profile is an ERGA<sup>Page 14, 5</sup> profile

OR

- From the All Profiles tab if desired profile is not an ERGA<sup>Page 14, 5</sup> profile
- 2. In the **Pending Samples** tab, select desired sample record(s) by clicking the checkbox(es) associated with the sample record(s).

Similarly, if you are a Biodiversity Genomics Europe (BGE) checker, select desired sample record(s) from the **Pending BGE Checker Samples** tab.

Then, click the **Reject** button as shown below:

Choose to Acce	pt or Reject	dtol v								St	atus		
lote clicking accept will im	mediately send sample in	fo to ENA/Biosamples	5								idle		
All profiles			>	Reject	Accept Select all	visible Select None	Delete Selected D	ownload Permits View Ima	ges				
	Search:		Pe	ending Sample	es Processing Samples	Accepted Samples Rej	ected Samples						
Profile Title	Date Created 🖕	Samples link											
DTOL Test Profile 4	17/11/2023	%	Sam	ples									
OTOL Test Profile 3	01/11/2023	96	Shov	v 10 ~	entries							Search:	
TOL Test Profile 2	27/10/2023	90	÷	SERIES 0	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS 🔅	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMAR
ASG Test Profile	10/10/2023	%		3	DtoL R&D Protist cell sort3	Co S3 150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
DTOL Test Profile	10/10/2023	ø			DtoL R&D Protist cell sort4	Co S1 150000 sc1	Ox800036	Sphaeropleales	Radiococcaceae			Coenococcus planctonicus	
				5	DtoL_R&D_Protist_cell_sort5	Co_S2_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
				6	DtoL_R&D_Protist_cell_sort6	Co_S3_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
					DtoL_R&D_Protist_cell_sort7		Ox800036						
				8	DtoL_R&D_Protist_cell_sort8		Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
						Co_S8_10ml1		Sphaeropleales Sphaeropleales	Radiococcaceae Radiococcaceae			Coenococcus planctonicus Coenococcus planctonicus	
				8	DtoL_R&D_Protist_cell_sort8	Co_S8_10ml1 Co_S9_10ml1	Ox800036				2853155		
				8	DtoL_R&D_Protist_cell_sort8 DtoL_R&D_Protist_cell_sort9	Co_S8_10ml1 Co_S9_10ml1 Co_S9_10ml1 Co_S10_10ml1	Ox800036 Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	

Fig. 12: Accept or Reject Samples web page: Rejecting samples

3. The samples will proceed to the rejected stage and will be displayed in the **Rejected Samples** tab as shown below:

Choose to Acc	ept or Reject	dtol v								s	tatus		
lote clicking accept will i	mmediately send sample in	to ENA/Biosamples									Idle		
All profiles			×	Reject (	Accept Select all	visible Select None	Delete Selected	Download Permits View In	nages				
	Search:		Pe	nding Sampl	es Processing Samples	Accepted Samples Re	jected Samples						
	Date Created	Samples link											
rofile Title	Date created y	Jampies link											
	17/11/2023	Samples link 💡	Sam	les									
TOL Test Profile 4			Sam; Show		entries							Search:	
ITOL Test Profile 4 ITOL Test Profile 3	17/11/2023	8	Show	10 ~						650.05			
ITOL Test Profile 4 ITOL Test Profile 3 ITOL Test Profile 2	17/11/2023 01/11/2023	ъ ъ			entries RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY +	GENUS 🕴	TAXON_ID ‡	Search: SCIENTIFIC_NAME	TAXON_REMARKS
rofile Title TOL Test Profile 3 TOL Test Profile 3 TOL Test Profile 2 SG Test Profile TOL Test Profile	17/11/2023 01/11/2023 27/10/2023	90 90 90	Show	10 ~	RACK_OR_PLATE_ID		SPECIMEN_ID	ORDER_OR_GROUP Sphaeropleales	FAMILY \$	GENUS 🔅 Coenococcus	<b>TAXON_ID</b> 2853155		TAXON_REMARKS

Fig. 13: Accept or Reject Samples web page: Rejected samples at the rejected stage

# 4.4 Download Submitted Permits

If you have been assigned as a **sample manager**, you can view the permits submitted for submitted sample(s) on the Accept/Reject Samples' web page by following the steps below:

#### Note:

- Permits can only be downloaded for submitted samples that are **pending** action by a sample manager or have been **accepted** by a sample manager.
- Permits exist for ERGA<sup>Page 14, 5</sup> profiles only.

Hint:	To download	submitted	permits for	samples	within the	Accepted	Samples tab	, CTRL	+ C1	lick the	e desired
sample	record(s) then	, click the	Download Permit	s butto	on to down	load permi	t(s) submitted	l for the	selec	ted reco	ord(s).

1. Navigate to the Accept or Reject Samples web page.

See *How to access Accept or Reject Samples web page* section for guidance on how to access the **Accept or Reject Samples** web page.

2. Select the sample record(s) that you would like to download the permits for.

Then, click the **Download Permits** button to download permit(s) submitted for the selected sample record(s).

3. If any permit submission(s) exist for the selected sample record(s), the permits will be automatically downloaded for the selected sample record(s) as shown below:

Hint: Permits are downloaded as a .zip file

If no permits were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

	and an Defect	dhal				Download per	lints			Status			
noose to Acc	cept or Reject	dtol v					for the selected sample						
te clicking accept will						record(s)							
All profiles				Reject or	🗸 Accept 🛛 Se	lect all vi	0		Images				
	Search:		Pe	nding Samples	Processing Samples	Accepted Samples	Rejected Samples						
ofile Title 🕴	Date Created 👙	Samples link											
TOL Test Profile 4	17/11/2023	æ	Sam	oles									
OL Test Profile 3	01/11/2023	9	Show	10 ~	entries							Search:	
t Profile 1	27/10/2023	<i>в</i>	Å	SERIES 👙	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TA
G Test Profile	10/10/2023	<b>€</b>		5	FK00526544	FF03454485	MBA-190930-003E	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS	
IOL Test Profile	10/10/2023	~			FK00526545	FF03454486	MBA-190930-003F		CHORDEUMATIDAE	Melogona	2979188	Melogona scutellaris	
					FK00526546	FF03454487	MBA-190930-003G		Lvonetiidae	Lyonetia	753195	Lyonetia clerkella	
					FK00526547	FF03454488	MBA-190930-003H		Momphidae	Mompha	1594371	Mompha subbistrigella	
					FK00526548	FF03454489	MBA-190930-003I		Lyonetiidae	Leucoptera	1101014	Leucoptera laburnella	
				10	FK00526549	FF03454490	MBA-190930-003J	Opiliones	Phalangiidae	Oligolophus	2979189	Oligolophus hansenii	
				11	FK00526550	FF03454491	MBA-190930-003K	Coleoptera	Chrysomelidae	Longitarsus	1845050	Longitarsus pellucidus	
				12	FK00526551	FF03454492	MBA-190930-003L	Diptera	Tipulidae	Tipula	2881124	Tipula confusa	
				13	FK00526552	FF03454493	MBA-190930-003M	Stylommatophora	Oxychilidae	Oxychilus	145642	Oxychilus cellarius	
										PROPOLYDESMUS		PROPOLYDESMUS TESTACEUS	

Fig. 14: Accept or Reject Samples web page: Popup dialogue displaying message, 'No permits exist for selected sample record(s)'

## 4.5 View Submitted Images

If you have been assigned as a **sample manager**, you can view the images submitted for submitted sample(s) on the Accept/Reject Samples' web page by following the steps below:

Hint: To view submitte	ed images fo	or samples within the Accepted Samples tab, CTRL + Click the desired samples	ple
record(s) then, click the	View Images	button to view image(s) submitted for the selected record(s).	

1. Navigate to the Accept or Reject Samples web page.

See How to access Accept or Reject Samples web page section for guidance on how to access the Accept or Reject Samples web page.

2. Select the sample record(s) that you would like to view the images for.

Then, click the

View Images button to view image(s) submitted for the selected sample record(s).

3. If any image submission(s) exist for the selected sample record(s), a popup dialogue will be displayed with the image(s) submitted for the selected sample record(s) as shown below:

Hint: Click the image to view a larger version.

OR

If no images were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

<b>COPO</b>												A # 2 0	🎝 tester3 🔻
Choose to Acce	pt or Reject	dtol ~								Stat	us		
Note clicking accept will imr	mediately send sample in	fo to ENA/Biosamples								Id	e		
All profiles			>	Reject	Accept Se	elect all visible Select None	Delete Selected	Download Permits View	rimages				
	Search:		Pe	ending Sample	Processing Samples	Accepted Samples	Rejected Samples		R				
Profile Title	Date Created 🍦	Samples link											
DTOL Test Profile 4	17/11/2023	۰	Sam	ples									
DTOL Test Profile 3	01/11/2023	96	Shov	v 10 ~	entries							Search:	
Test Profile 1	27/10/2023	જ		SERIES 0	RACK OR PLATE ID	TUBE OR WELL ID	SPECIMEN ID	ORDER OR GROUP	FAMILY 0	GENUS	TAXON ID	SCIENTIFIC NAME	TAXON REM/
ASG Test Profile	10/10/2023	8										-	INVION_REM/
DTOL Test Profile	10/10/2023	8		1	FK00526580	FF03454481	MBA-190930-003A	Hymenoptera	Ichneumonidae	Itoplectis	2776046	Itoplectis maculator	
				2	FK00526581	FF03454482	MBA-190930-003B	Diptera	Tipulidae	Tipula	2881124	Tipula confusa	
				3	FK00526582	FF03454483	MBA-190930-003C	Isopoda	Porcellionidae	Porcellio	172005	Porcellio spinicornis	
				4	FK00526583	FF03454484	MBA-190930-003D	Opiliones	Phalangiidae	Oligolophus	2979189	Oligolophus hansenii	
				5	FK00526584	FF03454485	MBA-190930-003E	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS	
			Shov	ving 1 to 5 of !	5 entries 1 row selected							Previous 1 Nex	t

Fig. 15: Accept or Reject Samples web page: Pointer to 'View images' button

#COPO					1	Sample Images							<b>4 # ≅ 0</b>	🗘 tester3 👻
Choose to Acce	pt or Reject	dtol ~				Sample mages			×		Statu	ıs		
Note clicking accept will im									2					
All profiles	Search:			Reject (						ges				
Profile Title	Date Created 👙	Samples link	Pe	nding Samp	les Proc			00	2					
DTOL Test Profile 4	17/11/2023	%	Samj	ples										
DTOL Test Profile 3	01/11/2023	90	Show	10 \	entries								Search:	
		<del>в</del>	A	SERIES	RACK_O				1	AMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REM
ASG Test Profile	10/10/2023	Ф						la la	<b>K</b>				-	TAXON_REM
DTOL Test Profile	10/10/2023	Ъ.		1	FK00526		Image: MBA	-190930-003A-1.jpe;	g;	hneumonidae	Itoplectis	2776046	Itoplectis maculator	
				2	FK00526		SPECIMEN_I	D: MBA-190930-003	A	ïpulidae	Tipula	2881124	Tipula confusa	
				3	FK005265	82 FF03	454483	M	Isopoda	Porcellionidae	Porcellio	172005	Porcellio spinicornis	
				4	FK005265	83 FF03	454484	MBA-190930-003D	Opiliones	Phalangiidae	Oligolophus	2979189	Oligolophus hansenii	
				5	FK005265	84 FF03	454485	MBA-190930-003E	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS	
			Show	ring 1 to 5 of	5 entries 1 r	row selected							Previous 1 Next	

Fig. 16: Accept or Reject Samples web page: Popup dialogue displaying submitted image(s) for selected sample record(s)

COPO						View images					•		ster3 +
Choose to Acce	pt or Reject	dtol ~								Status			
						No images exist f record(s)	or the selected sample						
All profiles			×	Reject 🕢	🕈 🖌 Accept 🛛 Se	lect all vi	0		/Images				
	Search:		Pe	nding Sample	s Processing Samples	Accepted Samples	Rejected Samples						
rofile Title 🔅	Date Created 👙	Samples link 👙											
OTOL Test Profile 4	17/11/2023	Ф	Samj	oles									
TOL Test Profile 3	01/11/2023	°€	Show	10 ~	entries							Search:	
st Profile 1	27/10/2023	%	Å	SERIES	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY	GENUS	TAXON ID	SCIENTIFIC_NAME	TAX
SG Test Profile	10/10/2023	8		5	FK00526544	FF03454485	MBA-190930-003E		Polydesmidae	PROPOLYDESMUS	1560407	PROPOLYDESMUS TESTACEUS	
TOL Test Profile	10/10/2023	9			FK00526545	FF03454486	MBA-190930-003F		CHORDEUMATIDAE		2979188	Melogona scutellaris	
				7	FK00526546	FF03454487	MBA-190930-003G	Lepidoptera	Lyonetiidae	Lyonetia	753195	Lyonetia clerkella	
				8	FK00526547	FF03454488	MBA-190930-003H	Lepidoptera	Momphidae	Mompha	1594371	Mompha subbistrigella	
				9	FK00526548	FF03454489	MBA-190930-003I	Lepidoptera	Lyonetiidae	Leucoptera	1101014	Leucoptera laburnella	
				10	FK00526549	FF03454490	MBA-190930-003J	Opiliones	Phalangiidae	Oligolophus	2979189	Oligolophus hansenii	
				11	FK00526550	FF03454491	MBA-190930-003K	Coleoptera	Chrysomelidae	Longitarsus	1845050	Longitarsus pellucidus	
				12	FK00526551	FF03454492	MBA-190930-003L	Diptera	Tipulidae	Tipula	2881124	Tipula confusa	
				13	FK00526552	FF03454493	MBA-190930-003M	Stylommatophora	Oxychilidae	Oxychilus	145642	Oxychilus cellarius	
				14	FK00526553	FF03454494	MBA-190930-003N	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS	
			Show	ring 1 to 10 o	47 entries					Previous 1 2	3 4 5		

Fig. 17: Accept or Reject Samples web page: Popup dialogue displaying message, 'No images exist for selected sample record(s)'

# 4.6 Upload Manifest or Update Submitted Manifest on behalf of Manifest Submitters

#### Note:

- The manifest dropdown menu will only be displayed on the Accept or Reject samples web page if you as a sample manager, belongs to more than one sample manager manifest group.
- If the **dtol** sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics (ASG) profiles and Darwin Tree of Life (DToL) profiles will be displayed in the **All profiles** tab (if any exists).
- The Samples table will only be displayed if the selected/highlighted profile has submitted samples.

#### Hint:

• See the *Updating Samples* section for information about which field values can be updated. Samples can be updated by resubmitting the manifest with the updated metadata.

The following steps can be followed to upload a manifest or update a submitted manifest on behalf of a manifest submitter Page 11, 2:

1. Navigate to the Accept or Reject Samples web page.

See How to access Accept or Reject Samples web page section for guidance.

2. On the left of the Accept or Reject Samples web page, click the  $\infty$  icon in the Samples link table column of the table row for the profile that you would like upload a manifest for or update a submitted manifest for as shown below:

If the desired profile is an ASG profile or DTOL profile, navigate to the **Samples** web page by clicking the  $\infty$  icon in the **Samples link** table column of the table row for the desired profile in the **All Profiles** tab as shown

#### below:

Choose to Acc	cept or Reject	dtol 🗸								S	tatus		
lote clicking accept will	immediately send sample in	fo to ENA/Biosamples									Idle		
			_										
All profiles			3	Reject 🤆	Accept Select all v	isible Select None	Delete Selected D	Iownload Permits View Ima	ges				
	Search:		Pe	nding BGE C	hecker Samples Pending Sam	ples Processing Sam	oles Accepted S	amples Rejected Samp	les				
rofile Title	Date Created 🖕	Samples link											
TOL Test Profile 4	17/11/2023	°° <mark>∧</mark>	Sam	ples									
TOL Test Profile 3	01/11/2023	8	Show	10 ~	entries							Search:	
OL Test Profile 2	27/10/2023	8	÷	SERIES 🔅	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY 0	GENUS 🕴	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMAR
G Test Profile	10/10/2023	<u></u>		3	DtoL_R&D_Protist_cell_sort3	Co_S3_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
TOE lest Profile	10/10/2023	0		4	DtoL_R&D_Protist_cell_sort4	Co_S1_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
				5	DtoL_R&D_Protist_cell_sort5	Co S2 150000 sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenococcus planctonicus	
				8	DtoL R&D Protist cell sort8	Co 58 10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Cooperativ	2853155	Coenococcus planctonicus	
				9	DtoL_R&D_Protist_cell_sort9	Co_S9_10ml1	Ox800036	Sphaeropleales	Radiococcaceae			Coenococcus planctonicus	
				10	DtoL_R&D_Protist_cell_sort10		Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus		Coenococcus planctonicus	
				11	DtoL_R&D_Protist_cell_sort11	Pt_S1_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
				12	DtoL_R&D_Protist_cell_sort12	Pt_S2_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
				13	DtoL_R&D_Protist_cell_sort13	Pt_\$3_150001	Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	
				14	DtoL R&D Protist cell sort14		Ox800057	Chlamydomonadales	Phacotaceae	Pteromonas	77548	Pteromonas angulosa	

# Fig. 18: Accept or Reject Samples web page: Navigate to 'Samples' web page by clicking the link associated with a DTOL profile

Similarly, if the desired profile is an ASG profile, the same action occurs.

OR

If the desired profile is an ERGA profile, navigate to the **Samples** web page by clicking the  $\Im$  icon in the **Samples link** table column of the table row for the desired profile in the **Profiles for My Sequencing Centre** tab as shown below:

3. The **Samples** web page will be displayed as shown below:

Similarly, if the desired profile is an ASG profile, the **Samples** web page will be displayed.

#### OR

4. If you do not have the submitted manifest for the profile, see the *How to Download Submitted Sample Manifest* section for guidance on how to download the submitted sample manifest. Then, refer to the *Updating Samples* section for guidance on how to submit the modified manifest.

#### OR

If you have the submitted manifest for the profile, see the *Updating Samples* section for guidance on how to update the submitted manifest.

#### OR

If you would like to upload a newer version of a manifest that has already been submitted on behalf of the manifest provider, please follow the steps below:

- 1. Download the submitted manifest by following the guidelines described in the *How to Download Submitted Sample Manifest* section if you do not have the newer version of the manifest with the sample metadata information.
- 2. Transfer the sample metadata from the submitted manifest into the newer version of the manifest.
- 3. Send an email to the COPO team at , indicating the profile type as well as the profile title and requesting that the samples be **removed** from the profile.

DOPO										. ₽	<b>Z</b> 0 (	tester4 +
Choose to Accept or Reject erga ~									Status			
ote clicking accept will immediately send sample info to ENA/Biosamples									Idle			
Profiles for My Sequencing Centre All profiles Search:				lect all visible Select None		Download Permits View In						
Profile Title Date Created Samples link	Pen	nding BGE C	hecker Samples Pendir	ng Samples Processin	s Samples Accepted	Samples Rejected Sam	nples					
ERGA Test Profile 2         28/11/2023         %	Sampl	les										
RGA Test Profile 11 27/11/2023 %	Show	10 v	entries							S	earch:	
	÷	SERIES \$	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID	SPECIMEN_ID	ORDER_OR_GROUP	FAMILY \$	GENUS 🗄	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRA
	÷	SERIES 🔅	RACK_OR_PLATE_ID	TUBE_OR_WELL_ID FF06763893	SPECIMEN_ID ERGA_FOS_4557_001		FAMILY ‡	GENUS ‡	<b>TAXON_ID</b> 6344	SCIENTIFIC_NAME	TAXON_REMARKS	INFRA
		SERIES 🔅	RACK_OR_PLATE_ID +			Capitellida					TAXON_REMARKS	INFR/
		SERIES 🝦	RACK_OR_PLATE_ID	FF06763893	ERGA_FOS_4557_001	Capitellida Capitellida	Arenicolidae	Arenicola	6344	Arenicola marina	TAXON_REMARKS	INFR
		SERIES 🗍	RACK_OR_PLATE_ID ÷	FF06763893 FF06763894	ERGA_FOS_4557_001 ERGA_FOS_4557_002	Capitellida Capitellida Capitellida	Arenicolidae Arenicolidae	Arenicola Arenicola	6344 6344	Arenicola marina Arenicola marina	TAXON_REMARKS	INFR
		SERIES \$	RACK_OR_PLATE_ID ‡	FF06763893 FF06763894 FF06763895	ERGA_FOS_4557_001 ERGA_FOS_4557_002 ERGA_FOS_4557_003	Capitellida Capitellida Capitellida Capitellida	Arenicolidae Arenicolidae Arenicolidae	Arenicola Arenicola Arenicola	6344 6344 6344	Arenicola marina Arenicola marina Arenicola marina	TAXON_REMARKS	INFR.
		SERIES \$	RACK_OR_PLATE_ID ;	FF06763893 FF06763894 FF06763895 FF06763896	ERGA_FOS_4557_001 ERGA_FOS_4557_002 ERGA_FOS_4557_003 ERGA_FOS_4557_004	Capitellida Capitellida Capitellida Capitellida Capitellida	Arenicolidae Arenicolidae Arenicolidae Arenicolidae	Arenicola Arenicola Arenicola Arenicola	6344 6344 6344 6344	Arenicola marina Arenicola marina Arenicola marina Arenicola marina	TAXON_REMARKS	INFR
		SERIES 🕆	RACK_OR_PLATE_ID ;	FF06763893 FF06763894 FF06763895 FF06763896 FF06763897	ERGA_FOS_4557_001 ERGA_FOS_4557_002 ERGA_FOS_4557_003 ERGA_FOS_4557_003 ERGA_FOS_4557_004 ERGA_FOS_4557_005	Capitellida Capitellida Capitellida Capitellida Capitellida Capitellida	Arenicolidae Arenicolidae Arenicolidae Arenicolidae Arenicolidae	Arenicola Arenicola Arenicola Arenicola	6344 6344 6344 6344 6344	Arenicola marina Arenicola marina Arenicola marina Arenicola marina Arenicola marina	TAXON_REMARKS	INFR.
		SERIES \$	RACK_OR_PLATE_ID ÷	FF06763893           FF06763894           FF06763895           FF06763896           FF06763897           FF06763898	ERGA_FOS_4557_001 ERGA_FOS_4557_002 ERGA_FOS_4557_003 ERGA_FOS_4557_004 ERGA_FOS_4557_005 ERGA_FOS_4557_006	Capitellida Capitellida Capitellida Capitellida Capitellida Capitellida Capitellida	Arenicolidae Arenicolidae Arenicolidae Arenicolidae Arenicolidae	Arenicola Arenicola Arenicola Arenicola Arenicola	6344 6344 6344 6344 6344 6344 6344	Arenicola marina Arenicola marina Arenicola marina Arenicola marina Arenicola marina Arenicola marina	TAXON_REMARKS	INFR

Fig. 19: Accept or Reject Samples web page: Navigate to 'Samples' web page by clicking the link associated with an ERGA profile

Profile: D	TOL Test Profile 4										_	_		Info		
amples								4				X	•			
Select all	Select filtered Clear selection	Export CSV	Download sample manifest	A Download permit	s View images											
Showing 1 t	to 10 of 39 records Click 🚯 besi	de a record to view extra d	lotails													
Series	Rack or Plate Identifier	Tube or Well Identifier	Specimen Identifier	Order or Group	Family 🔅	Genus 🔆	Taxon Identifier	Scientifi	c Name		Taxon Rei	narks	Infraspec			
<b>o</b> 1	DtoL_R&D_Protist_cell_sort1	Co_S1_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plane	tonicus						
0 2	DtoL_R&D_Protist_cell_sort2	Co_S2_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plano	tonicus						
<b>o</b> 3	DtoL_R&D_Protist_cell_sort3	Co_S3_150001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plane	tonicus						
<b>o</b> 4	DtoL_R&D_Protist_cell_sort4	Co_S1_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plano	tonicus						
o 5	DtoL_R&D_Protist_cell_sort5	Co_S2_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plane	tonicus						
0 6	DtoL_R&D_Protist_cell_sort6	Co_S3_150000_sc1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plane	tonicus						
0 7	DtoL_R&D_Protist_cell_sort7	Co_S4_400001	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plane	tonicus						
<b>o</b> 8	DtoL_R&D_Protist_cell_sort8	Co_S8_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plano	tonicus						
<b>o</b> 9	DtoL_R&D_Protist_cell_sort9	Co_S9_10ml1	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco	occus plano	tonicus						
	DtoL_R&D_Protist_cell_sort10	C= 510 10-11	Ox800036	Sphaeropleales	Radiococcaceae	Coenococcus	2853155	Coenoco								

Fig. 20: Samples web page for a DTOL profile

rofile: ERGA Test Pro amples				4	· · · · · · · · · · · · · · · · · · ·	Info
Select all Select filtered	Clear selection Expo	ort CSV	nple manifest A Download permits S Vie	wimages		
howing 1 to 9 of 9 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	
FF06763893	ERGA_FOS_4557_001	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
FF06763894	ERGA_FOS_4557_002	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
FF06763895	ERGA_FOS_4557_003	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
FF06763896	ERGA_FOS_4557_004	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
	ERGA_FOS_4557_005	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
FF06763897	ERGA_FOS_4557_006	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
FF06763897	EKGA_F03_4337_000					
FF06763898	ERGA_FOS_4557_007	REFERENCE_GENOME	JANE DOE	EARLHAM_INSTITUTE	0000-0001-9649-5906	
				EARLHAM_INSTITUTE	0000-0001-9649-5906	

Fig. 21: Samples web page for an ERGA profile

The samples has to be removed from the profile so that the sample metadata in the newer version of the manifest can be registered in the profile.

**Important:** Please request that the samples be removed from the profile **only** if you are certain and have the newer version of the manifest with the sample metadata information.

The samples **cannot** be restored after they have been removed from the profile.

- 4. Upload the newer version of the manifest by referring to the guidelines described in the desired link below to learn more about each type of manifest submission:
  - Aquatic Symbiosis Genomics (ASG) manifest submission
  - Darwin Tree of Life (DToL) manifest submission
  - Darwin Tree of Life Environmental (DToL\_ENV) manifest submission
  - European Reference Genome Atlas (ERGA) manifest submission

Hint: See *Downloading Manifest Templates* section for information about downloading manifest templates.

# **STAND-ALONE PROFILE**

In COPO, a Stand-alone work profile<sup>1</sup> is required to submit files, reads, assemblies and sequence annotations. **See also:** 

• See Steps to create Tree of Life (ToL) profile if you would like to make ToL manifest submissions

# 5.1 Steps to Create a Stand-alone Profile

1. Click the • Add new record icon to view the Add Profile form

ork Profiles 😲 🕂		Info	
COPO - Gettling 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 <i>Q</i> = <b>D</b> utonon on the page to create a new profile.			
<ol> <li>Profile Components:</li> <li>Once you have created a work profile, you can start creating components within the profile. COPO provides templates/wixards for creating and managing different components including: patients, samples, Submission Publications, Poppia, and Annotations. Profile components can be created in any or vole.</li> </ol>			
<ol> <li>Quick Tour: Finally, if you've not done so already, take some time to explore the various controls available on the page. Click the</li></ol>			

Fig. 1: Stand-alone Profile: Add new profile record icon

2. **Contact COPO via email** dialogue is displayed indicating that the user is not a member of any manifest group and that the user must make a request to be added to a manifest group to make ToL manifest submissions if the user would like to do so.

Click **Okay** to close the dialogue.

**Note:** Submissions such as files, reads, assemblies, files and sequence annotations can only be made using a Stand-alone profile type.

<sup>&</sup>lt;sup>1</sup> Also known as COPO profile. See: *COPO profile or work profile*.

Contact COPO via email
If you would like to make manifest submissions to an ASG, ERGA or DToL manifest group
Please contact <u>ei.copo@earlham.ac.uk</u> in order to be added to the manifest group. We will grant you the permission to select the desired group, create a profile for the group and subsequently upload a manifest to the group.
Okay
Profile Type 🚯
Stand-alone 🗸
Cancel 👱 Save

Fig. 2: Stand-alone Profile: Contact COPO dialogue is displayed regarding getting access to make ToL manifest submissions

3. Provide details for the new profile then, click Save

Add Profile	
Title required 1	
Description required	
	lis
Profile Type 🕕	
Stand-alone	~
	Cancel Save

Fig. 3: Stand-alone Profile: Add profile form dialogue

Hint: Both profile Title and profile Description are mandatory form fields.

Meaningful field values are recommended in the form boxes because the information will appear in submissions of the research objects<sup>2</sup> associated with the profile, in public remote repositories.

4. The new profile will be displayed in the Profile list

Hint: The Work Profiles' list can be sorted by date created, profile title or profile type.

Choose the desired sort type from the Sort by dropdown menu (at the top-right of the profile record).

<sup>&</sup>lt;sup>2</sup> Research objects refer to files, reads, assemblies, files and sequence annotations. A Stand-alone profile is considered as a *project* research object. See: *Profile component*.

±COPO		🖡 😹 🗿 💠 tester 1 👻
Work Profiles 😲 🛨		Info
	Sort by: Date Created 🗸 🗸	
El Standalone Profile (standalone)		Profile Types Legend
Created: Fr. 2.1 Jul 2023 21:37		6 Standalone
Description: This Start-alone profile will be used to make submissions for various research objects.		
Actions • Components •		
Showing: 1 / 1 profiles		

Fig. 4: Stand-alone Profile: Work profiles' web page displaying the created profile

# 5.2 Stand-alone Profile Components

A COPO profile defines a set of component types from which instances of research objects can be created.

The following component types are currently defined:

- 1. Accessions
- 2. Assembly
- 3. Files
- 4. Reads
- 5. Sequence Annotations
- Component instances defined within a profile will only be visible within that profile<sup>Page 27, 1</sup>.
- To access a component within a profile, click the component button displayed within the popup after the

Components 💌

button was clicked (see the screenshot above).



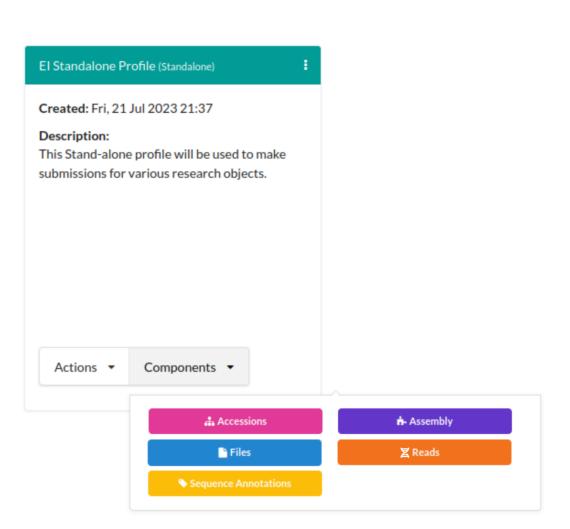


Fig. 5: Stand-alone Profile Components

## **TREE OF LIFE PROFILE**

In COPO, a Tree of Life  $(ToL)^1$  work profile<sup>2</sup> is required to submit research objects<sup>3</sup> such as samples, barcoding manifests, sequence annotations, reads, assemblies and files.

A ToL profile can be used to create one of the following biodiversity projects:

- Aquatic Symbiosis Genomics (ASG)
- European Reference Genome Atlas (ERGA)
- Darwin Tree of Life Environmental (DTOL\_ENV)
- Darwin Tree of Life (DTOL)

#### See also:

- How to Update Profiles
- How to Delete Profiles
- Sharing Profiles
- Sorting Profiles
- Profile Types Legend

# 6.1 Steps to Create a Tree of Life Profile

1. Click the • Add new record icon to view the Add Profile form

2. Contact COPO via email dialogue is displayed indicating that the user is not a member of any manifest group and that the user must make a request to be added to a manifest group to make ToL manifest submissions if the user would like to do so.

Click **Okay** to close the dialogue.

<sup>&</sup>lt;sup>1</sup> See term: *Tree of Life (ToL)*.

<sup>&</sup>lt;sup>2</sup> Also known as COPO profile. See term: *COPO profile*.

<sup>&</sup>lt;sup>3</sup> Research objects refer to files, reads, assemblies, files and sequence annotations. A Stand-alone profile is considered as a *project* research object. See term: *Profile component*.

<sup>≜</sup> COPO				0	¢tester1
Work Profiles 😲 🕈	Info				
COPO - Getting started					
Here are a few quick singes logs hyou started with COPO. 1.COP Induce The office of the start of getting work down in COPO to be created a work profile. A profile is a collection of the start of getting work down in COPO to be created a new profile. 2. Profile Components: Draces you have created a work profile, you can start creating components within the profile. COPO provide templates with and the grant of managing different components including. Datafiles: Supples, Submission Fulliatious, People, and 2. Advit Tour: Testyly, if you're not down as a stark plate some time to congive the variants controls wallable on the page. Click the for on on the page to activate the quick tour agent.					

Fig. 1: ToL Profile: Add new profile record icon

Contact COPO via email
If you would like to make manifest submissions to an ASG, ERGA or DToL manifest group
Please contact <u>ei.copo@earlham.ac.uk</u> in order to be added to the manifest group. We will grant you the permission to select the desired group, create a profile for the group and subsequently upload a manifest to the group.
Okay
Profile Type 🚯
Stand-alone v
Cancel <b>±</b> Save

Fig. 2: ToL Profile: Contact COPO dialogue is displayed regarding getting access to make ToL manifest submissions

## 6.1.1 Provide Profile Title & Description

3. In the Add Profile form dialogue, provide details for the new profile then, click Save

Note: The Profile Type dropdown menu by default will only display the Stand-alone option.

If your desired profile type is not displayed in the **Profile Type** dropdown menu, indicating the type of profile group that you would like to be granted access to. Thereafter, the desired profile type option will be displayed in the dropdown menu.

Add Profile	
Title required <b>()</b>	
Description required <b>1</b>	
//	
Stand-alone ~	
Stand-alone	
Darwin Tree of Life (DTOL)	
Darwin Tree of Life Environmental Samples (DTOL_ENV)	
Aquatic Symbiosis Genomics (ASG)	
European Reference Genome Atlas (ERGA)	

Fig. 3: ToL Profile: Add profile form dialogue

Hint: Both profile Title and profile Description are mandatory form fields.

Meaningful field values are recommended in the form boxes because the information will appear in submissions of the research objects associated with the profile, in public remote repositories.

## 6.1.2 Choose Profile Type

Add Profile	
Title required ()	
Description required 1	
	Ĩ.
Profile Type  Stand-alone	~
	Cancel Save

Fig. 4: ToL Profile form: Choose profile type

If you request to be added to any of the profile types displayed (excluding the default **Stand-alone** profile type), only that profile type will be listed in the **Profile type** dropdown menu.

## 6.1.3 Choose Associated Profile Type(s) (if required)

Note: The Associated Profile Type dropdown menu will only display if the European Reference Genome Atlas (ERGA) profile type is selected.

• More than one associated type also known as subproject or child project can be chosen.

OR

OR

<sup>&</sup>lt;sup>4</sup> See term: *ASG*.

<sup>&</sup>lt;sup>5</sup> See term: *DToL*.

<sup>&</sup>lt;sup>6</sup> See term: *ERGA*.

Add Profile
Title required 3
Description required
Profile Type
Aquatic Symbiosis Genomics (ASG)
Associated Profile Type 🚯
Select associated type(s)
Darwin Tree of Life (DTOL)
Darwin Tree of Life Environmental Samples (DTOL_ENV)
European Reference Genome Atlas (ERGA)

Fig. 5: ASG Profile Type: Choose associated profile type or a subproject Page 36, 4

Add Profile
Title required ①
Description required
Profile Type 🚯
Darwin Tree of Life (DTOL) ~
Associated Profile Type 🚯
Select associated type(s)
Aquatic Symbiosis Genomics (ASG)
Darwin Tree of Life Environmental Samples (DTOL_ENV)
European Reference Genome Atlas (ERGA)

Fig. 6: DTOL Profile Type: Choose associated profile type or a subproject Page 36, 5

Add Profile
Title required
Description required
Profile Type 1 European Reference Genome Atlas (ERGA)
Associated Profile Type 🚯
Select associated type(s)
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)
Population Genomics (POP_GENOMICS)

Fig. 7: ERGA Profile Type: Choose associated profile type or a subproject Page 36, 6

## 6.1.4 Choose Sequencing Centre (if required)

Note: The Sequencing Centre dropdown menu will only display if the European Reference Genome Atlas (ERGA) profile type is selected.

Add Profile
Title required 1
Description required
Profile Type 🚯
European Reference Genome Atlas (ERGA)
Select associated type(s)
Sequencing Centre required 1
Select sequencing centre
SANGER INSTITUTE
EARLHAM INSTITUTE
CENTRO NACIONAL DE ANÁLISIS GENÓMICO
SCILIFELAB
WEST GERMAN GENOME CENTRE
NGS COMPETENCE CENTER TÜBINGEN

Fig. 8: ERGA Profile Type: Choose sequencing centre

### 6.1.5 Profile created

4. The new profile will be displayed in the **Profile** list

**Hint:** The list of profiles or profile records on the **Work Profiles** web page can be sorted by date created, profile title or profile type.

Choose the desired sort type from the Sort by dropdown menu (at the top-right of the profile record).

See more information in the *Sorting Profiles* section.

±соро		🌲 🖻 🗷 🛈 🗘 tester 1 🗸
Work Profiles 😢 🛨	<b>() (2)</b>	Info
	Sort by: Date Created V	
First ERGA Profile(ERGA)		Profile Types Legend
Created: Mon, 17 Apr 2023 09:39		O ERGA
Description: This is the first ERGA profile to be created.		
View more		
Actions - Components -		
Actions - Components -		
Showing: 1 / 1 profiles		

Fig. 9: ToL Profile: 'Work Profiles' web page displaying the created profile

#### See also:

• See Steps to create Stand-alone profile if you would like to make other submissions

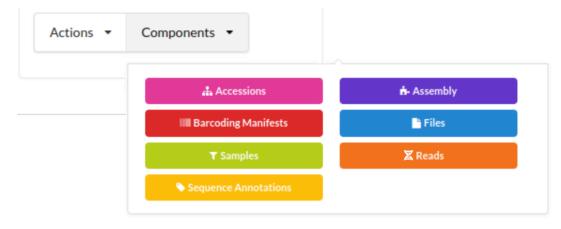
# 6.2 Tree of Life Profile Components

A COPO profile<sup>Page 33, 2</sup> defines a set of component types from which instances of research objects can be created.

The following component types are currently defined:

- 1. Accessions
- 2. Assembly
- 3. Barcoding manifests
- 4. Files
- 5. Reads
- 6. Samples
- 7. Sequence Annotations
- Component instances defined within a profile will only be visible within that profile.
- To access a component within a profile, click the component button displayed within the popup after the Components •

button was clicked (see the screenshot above).





## SEVEN

# **SHARING PROFILES**

Sharing profiles or creating a group enable other COPO users to upload or submit research objects such as samples, experiment, runs, reads, assemblies and sequence annotations etc. to a profile owned or created by another COPO user.

#### Hint:

- Profile owner or Sharer refers to the person who created the profile.
- **Shared user** or **Sharee** refers to the person who has been granted permission by the profile owner to upload or submit research objects to the profile created by the profile owner.

In general, the **sharer** shall create a profile, create a group, add the profile to be shared to the created group then, add the COPO user(s) to the created group.

Thereafter, the shared profile shall appear on the Work Profiles web page of the sharee.

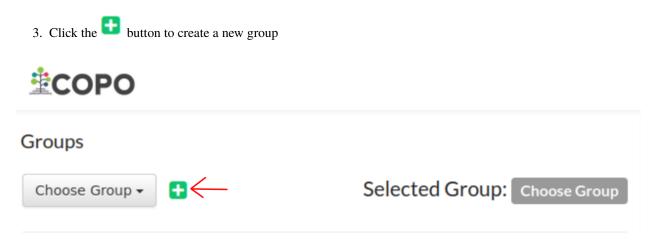
The following describes how to share a profile or create a group on COPO:

# 7.1 Sharer

- 1. Click your name in the top right hand corner of the web page (after you have logged in) to access settings
- 2. Click the **View Groups** option from the settings dropdown menu as shown below to navigate to the **Groups** web page

Info View	Groups
@ User I	nfo
🕞 Logou	t

Fig. 1: Groups: Navigating to Groups web page via the 'View Groups' settings dropdown menu option





4. Provide details for the new group as shown below then, click Submit

Create New Group	
Group Name	
COPO Test Shared Group	
Description	
This is a group created to share a profile with another user so that the user can upload/submit research objects.	
Submit	

Fig. 3: Groups: Add new group form dialogue

Hint: Both group Name and profile Description are required form fields.

Meaningful field values are recommended in the form boxes.

5. In the **Your Profiles** section under the **Profiles in Group** header, choose a profile from the list of profiles that you would like to share with another user (so that the user can upload/submit research objects to) by **double-clicking** the profile title.

The profile is then, transferred to the **Added to Group** section after the profile title was double-clicked as shown below.

6. Search for the user who you would like to share the profile with in the **Users in Group** section located at the right of the web page. Then, click the name of the user to add the user to the group.

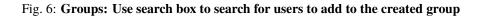
<b>≜COPO</b>		•	<i>8</i> 2	tester1
Groups	Selected Group: COPO Test Shared Group	Info Group created!		
Profiles in Group	Users in Group	Group created:		
Your Profiles Added to Group DTOL Test Profile	If you would like to share an ASG, DTOL, DTOL, ENV or ERGA profile with users, please confirm with X the users that they have already been added to the particular manifest group. Please ask the users to contact <u>el.copp@eartham.ac.uk</u> in order to be added to the manifest group if they			
ção	do not belong to it. Search for User Printane, Latrane or Username)			
	4			

#### Fig. 4: Groups: Group created successfully

COPO					•	2	0	O teste
COPO Test Shared Gro	up≁	8 🕫 🖨	Selected Group: COPO Test Shared Group	Info				
Profiles in Group			Users in Group					
Your Profiles	ţ,	Added to Group DTOL Test Profile	If you would like to share an ASG, DTOL, DTOL, ENV or ERGA profile with users, please confirm with the users that they have already been added to the particular manifest group. Please ask the users to contact <u>eiccopo@eartham.ac.uk</u> in order to be added to the manifest group if they do not belong to it.					
			Search for User (Finsteame, Lastrame or Username)					

Fig. 5: Groups: Profile appears in 'Added to Group' section after having been double-clicked in the 'Your Profiles' section

				•	<b>▲</b> <i>₽</i>	<b>↓</b>	<b>↓ ₽ ≥ 0</b>
		Info	Info	Info	Info	Info	Info
Selected Group: COPO Test Shared Group	р						
in Group							
•							
would like to share an ASG, DTOL, DTOL_ENV or ERGA profile with users, please confirm with ers that they have already been added to the particular manifest group.							
ask the users to contact <u>ei.copo@earlham.ac.uk</u> in order to be added to the manifest group if they belong to it.							
					•		
or User (Firstname, Lastname or Username)			1	1	1		



# 7.2 Sharee

- 1. Login to COPO.
- 2. Request to be added to a profile group associated with that the profile type that you would like to be added if you would like to submit or upload research objects to a Tree of Life (ToL) project.

If you have not been added to the profile group, make a request to the indicating the type of profile group that you would like to be assigned to.

See the *Projects Brokered through COPO* section for information about types of ToL projects.

3. After the sharer has added you to the group, you will see the shared profile on the **Work Profiles** web page as shown below:

#### Note:

- If the profile owner has shared the profile with you and you do not see the shared profile on the **Work Profiles** then, please perform step 2.
- Shared profiles are indicated by an orange label as shown below.

See *Profile Types Legend* section for more information about profile types' colour labels.

		Info
Profiles 🤨 🛨		
	Sort by: Date Created 🗸 🔻	
DL Test Profile(Shared With Me)		
DL Test Profile(Shared With Me)		Profile Types Legend
ated: Wed, 25 Oct 2023 16:09		Shared
<pre>icription: s profile is created to submit various research objects.</pre>		
ew more		
Actions  Components		

Showing: 1 / 1 profiles

Fig. 7: Groups: Shared profile appears on the sharee's 'Work Profiles' web page

# SORTING PROFILES

On the Work Profiles web page, profiles<sup>1</sup> can be sorted by date created, profile title or profile type.

Choose the desired sort option from the **Sort by** dropdown menu, Sort by: Date Created , (at the top-right of the profile record section) as shown below.

Then, click the  $\checkmark$  arrow to sort in descending order or the  $\blacktriangle$  arrow to sort in ascending according to the chosen sort option.

Sort by:	Date Created	~	•
	Date Created		
	Profile Title		
	Profile Type		

Fig. 1: Profile Sort Menu: Sort options displayed

<sup>&</sup>lt;sup>1</sup> Also known as COPO profile. See term: *COPO profile*.

NINE

# **PROFILE TYPES LEGEND**

The **Profile Types legend**<sup>1</sup> is displayed at the right of the **Work Profiles** web page.

It displays the acronym as well as the corresponding profile type colour for each profile that has been created.

**Hint:** Hover over the **1** icon located beside the profile type acronym in the **Profile Types Legend**, the backronym for the profile type will be displayed.

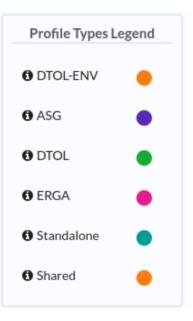


Fig. 1: Profile Types Legend: Various profiles types that can be created in COPO and their corresponding label colours

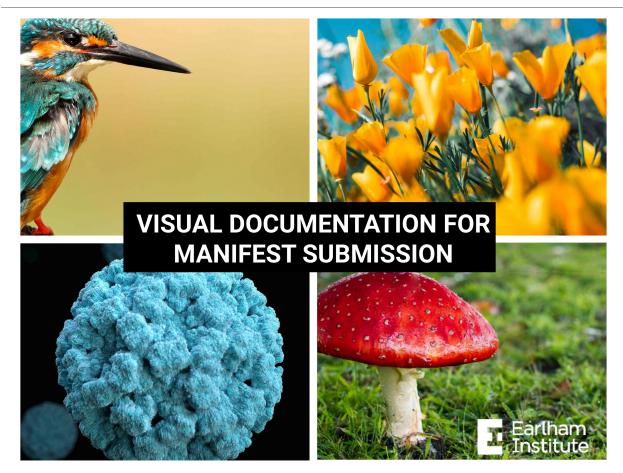
<sup>1</sup> See term: *Profile Types legend*.

Colour	Acronym	Backronym
Orange 🔴	DTOL-ENV or Shared	Darwin Tree of Life Environmental or Shared
Purple	ASG	Aquatic Symbiosis Genomics
Green	DTOL	Darwin Tree of Life
Pink	ERGA	European Reference Genome Atlas
Teal 🔵	Standalone	Stand-alone

Table 1: Explanation of Profile Types Legend

TEN

# GENERAL TREE OF LIFE VISUAL SUBMISSION DOCUMENTATION



Download visual documentation

### **ELEVEN**

## **ASSEMBLY SUBMISSION**

Note:

• Once assemblies have been submitted, they cannot be updated.

#### See also:

• How to Delete Assemblies

## **11.1 How to Submit Assemblies**

### 11.1.1 Accessing the Assembly Web Page

The Assembly<sup>1</sup> web page can be accessed from the **Components** button or **Actions** button associated with a profile<sup>2</sup>.

#### Use Components' Button to Navigate to Assembly Web Page

Click the components button associated with a profile. Then, click the from the popup menu displayed as shown below:

### Use Actions' Button to Navigate to Assembly Web Page

Click the Actions • button associated with a profile. Then, click the action, **Submit Assembly** action from the popup menu displayed as shown below:

<sup>1</sup> See: Assembly.

<sup>&</sup>lt;sup>2</sup> Also known as COPO profile. See: *COPO profile or work profile*.



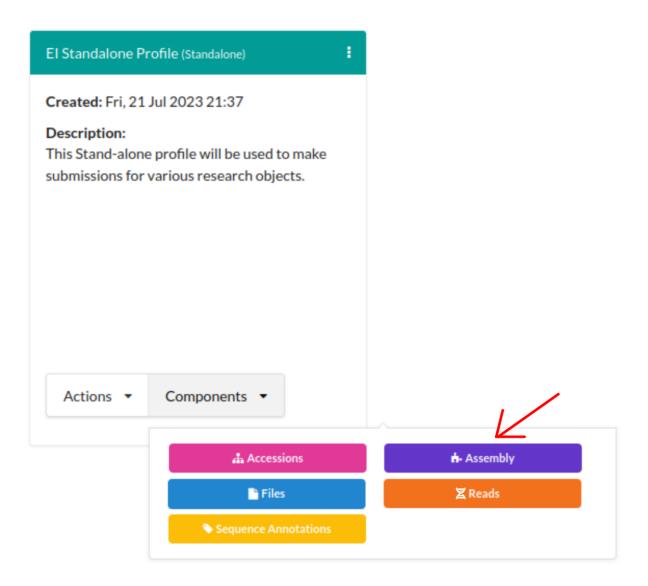


Fig. 1: Stand-alone Profile Components: Assembly component button

E	l Standalone Profi	le (Standalone)	÷					
D TI		Aug 2023 10:30 rofile will be used to make rious research objects.						
	Actions •	Components 🔻						
	Upload Files							
ho	Submit Reads							
	Submit Assembl	у <						
Submit Annotation								

Fig. 2: Stand-alone Profile Actions: 'Submit Assembly action

## 11.1.2 Submit Assembly

1. Click • button to add an **assembly** as shown below:

СОРО
ofile: El Standalone Profile sembly
Assembly - Getting started
The assembly' page provides a platform for aligning and merging ragments of a Deoxyribonucleic acid (DNA) sequence to reconstruct he original structure of the DNA.

Fig. 3: Assembly submission: Click 'Add record' button

- 2. An Add Assembly dialogue is displayed. Provide the details then, click the Submit Assembly button.
- 3. The new assembly will be displayed on the Assembly web page after a successful submission.

# **11.2 How to Delete Assemblies**

Click the desired assembly from the list of assemblies displayed on the **Assembly** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

STUDY* PRJEB66432	
SAMPLE*	
ERS16431676	~
ASSEMBLYNAME*	
Unique assembly name, user-provided ASSEMBLY_TYPE*	
clone COVERAGE*	~
The estimated depth of sequencing coverage PROGRAM*	
The assembly program	
PLATFORM*	
The sequencing platform, or comma-separated list	
MINGAPLENGTH	
MOLECULETYPE	
genomic DNA	~
DESCRIPTION	
RUN, REF	
RUN_REF	
RUN, REF Comma separated bit of run accession(d)	~
RUN, REF Commensemented bit of non-second and a FASTA	~
RUN, REF ("remains separated fait of ran accession) FASTA None	•
RUN REF Comes appared for of run screekingd FASTA None FLATFILE	~
RUN, REF Commo spanned for of our accession/of FASTA None FLATFILE None	2
RUN REF Fasta None FLATELE None AGP	
RUN_REF Comes separated lat of run accessived FASTA None ELITFILE None AGP None	
RUN_REF Consequented for or on accelerated FASTA None FLATFILE None AGP None CACHMOSOME_LIST	2 2 2
RUN BEF Counter reported his of two sockeeledd FASTA None ACP None CHROMOSOMELLST None	

Fig. 4: Assembly submission: 'Add Assembly' dialogue

±́СОРО				🖡 🖉 🗷 🛈 🗢 tester 1 👻
Profile: Standalone Test Profile Assembly	Select all Select filtered Clear velocitio		Celete	Info Assembly submission has been scheduled!
Showing 1 to 1 of 1 records Click 💽 beside a record to view extra details		Search Asser		
STUDY    SAMPLE  ASSEMBLYNAME  ASSEMBLY_TYPE	COVERAGE  PROGRAM  PLATFORM	MINGAPLENGTH 🕴 MOLECULETYPE 🕴		
PRJEB66432 ERS16431676 Test_Assembly1 clone	123456 Test Test platform programme	genomic DNA		
show 10 v records				

Fig. 5: Assembly submission: Assembly web page displaying the uploaded assemblies

±COPO				•	🖻 🗷 🛈 🜣 tester 1
Profile: Standalone Test Profile Assembly			III T S D	Info	
	Select all Select filtered Clear selection	Export CSV + Add 2 Edit Search Asser	Delete     i Submit		
Showing 1 to 1 of 1 records 1 record selected					
STUDY  \$\$ SAMPLE  \$\$ ASSEMBLYNAME  \$\$ ASSEMBLY_TYPE  \$\$	COVERAGE  PROGRAM  PLATFORM	MINGAPLENGTH   MOLECULETYPE			
PRJEB66432 ERS16431676 Test_Assembly1 clone	123456 Test Test platform programme	genomic DNA			
show 10 v records					

Fig. 6: Assembly deletion: Click the "Delete" button to remove the highlighted assembly from the profile

LOPO				
Profile: Standalone Test Profile		r	8	
Assembly +				
Assembly - Getting started				
The assembly' page provides a platform for aligning and merging fragments of a Deoxyribonucleic acid (DNA) sequence to reconstruct the original structure of the DNA.				
To add assemblies, click the + icon.				

Fig. 7: Assembly deletion: Assembly record has been deleted

## TWELVE

# **BARCODING MANIFEST SUBMISSION**

#### Note:

- **Barcoding manifest** submission can only be done via a ToL<sup>1</sup> profile<sup>2</sup>. Please see: *Steps to Create a Tree of Life Profile* for guidance.
- Samples must be submitted before barcoding manifests can be submitted. Once the samples have been approved their biosample accessions, specimen ID (identification) and taxon ID are needed to fill in the barcoding manifest prior submission.

#### See also:

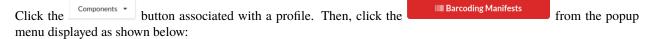
- How to Delete Barcoding Manifests
- How to Submit Aquatic Symbiosis Genomics (ASG) samples
- How to Submit Darwin Tree of Life (DToL) samples
- How to Submit Darwin Tree of Life Environmental (DToL\_ENV) samples
- How to Submit European Reference Genome Atlas (ERGA) samples

# 12.1 How to Submit Barcoding Manifests

### 12.1.1 Accessing the Barcoding Manifest Web Page

The **Barcoding Manifest** web page can be accessed from the **Components** button or **Actions** button associated with a profile.

### Use Components' Button to Navigate to Barcoding Manifest Web Page



<sup>1</sup> See term: *Tree of Life (ToL)*.

<sup>&</sup>lt;sup>2</sup> Also known as COPO profile. See: *COPO profile or work profile*.

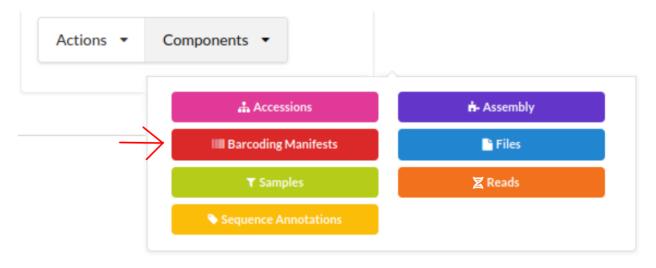


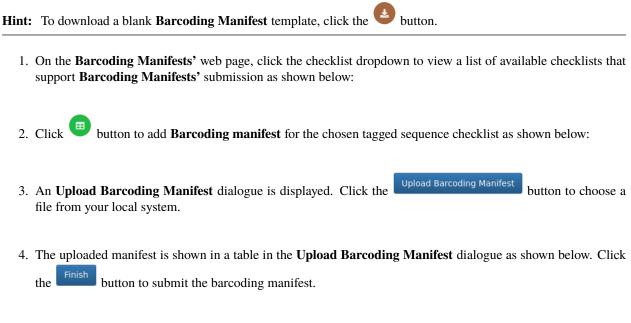
Fig. 1: Tree of Life Profile Components: Barcoding Manifest component button

#### Use Actions' Button to Navigate to Barcoding Manifest Web Page

Click the <u>Actions</u> button associated with a profile. Then, click the action, **Submit Barcoding Manifest** action from the popup menu displayed as shown below:

Note: The action will be available for all of the Tree of Life profile types.

## 12.1.2 Upload Barcoding Manifest



5. The new barcoding manifest(s) will be displayed on the **Barcoding Manifests** web page after a successful submission.

ASG Test Profile (ASG)	÷
<b>Created:</b> Fri, 15 Sep 2023 16:08 <b>Description:</b> This ASG profile will be used to make submissions for various research objects.	
Actions  Components	
Submit Annotation	
Submit Assembly	
Submit Barcoding Manifest	
Submit DTOL/ASG manifest	
Submit Reads	
Upload Files	

Fig. 2: Tree of Life Profile Actions: 'Submit Barcoding Manifest action

业 COPO							8	M	0	🌣 tester
e: DTOL Test Profile oding Manifests (ERT000020 : COI gene ) E ERT000020 : COI gene ERT000002 : rRNA gene	*	ė.	T	X	•	Info				
ERT000020 : COI gene										
The Barcode Manifest component of a profile										
Select the correct checklist and then click the 🛃 button to download the blank manifest. Once complete the manifest, you can click 💷 button to upload the manifest.										

Fig. 3: Barcoding Manifests' web page: Checklist dropdown menu with checklist options displayed

DL Test Profile	А	÷.	T	X	•	Info
oding Manifests (ERT000002 : rRNA gene 🗸) 🖽 🛃						
ling Manifest - Getting started						
arcode Manifest component of a profile						
the correct checklist and then click the 🛃 button to download the						
anfiest. Once complete the manifest, you can click 🖽 button to upload						
nifest.						

Fig. 4: Barcoding Manifest upload: Click 'Add Tagged Sequence (s) from Tagged Sequence Spreadsheet' from Spreadsheet' button

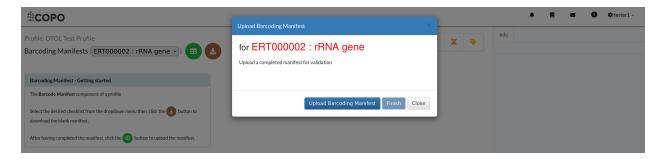


Fig. 5: Barcoding Manifest upload: 'Upload Barcoding Manifest' dialogue

всоро	Upload Barcoding Manifest			×		4	8 2	0 Otester1 -
Profile: DTOL Test Profile Barcoding Manifests (ERT000002 : rRNA gene •)	for ERT000002 : Upload a completed manifest for variables	-			<b>T</b> III	Info		
Barcoding Manifest - Getting started The Barcode Manifest component of a profile	Spreadsheet is Valid							
Select the correct checklist and then click the 🕑 button to download the blank manfiest. Once complete the manifest, you can click 🖽 button to	Show 10 v entries	Search:						
upload the manifest.	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	∳	† TAXON_ID	SPECIMEN				
	yes	SAMEA130748926	172005	MBA-1909				
	Showing 1 to 1 of 1 entries	Previous	1 Next					
	Uş	bload Barcoding Mar	ifest Finish	Close				

Fig. 6: Barcoding Manifest upload: 'Upload Barcoding Manifest' dialogue with uploaded manifest

**Hint:** Barcoding manifest records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

<b>≜COPO</b>							🌲 🖉 💆 🗘 tester1 -
Profile: DTOL Test Profile Barcoding Manifests (ERT000002 : rRNA ge	ene 🗸 ) 🖽 🛃		a i	•	T Z	•	Info Biocoding manifest submission has been scheduled!
	Select all Se	Clear selects		Delete is	ubmit hifests		
Showing 1 to 1 of 1 records Click 💿 beside a record to view of	extra details						
Organism Organism		Clone Isolate identifier name	Isolation source	Variety (varietas)	Ecotype 🗄	Breed	
SAMEA130748926 yes	5.85						
show 10 v records				Previous 1	Next		

Fig. 7: Barcoding manifest upload: Barcoding Manifests' web page displaying the uploaded barcoding manifests(s)

## 12.1.3 Submit Barcoding Manifests

Hint: The submitted barcoding manifest record will be highlighted green.

Click the desired barcoding manifests records from the list of barcoding manifests displayed on the **Barcoding manifests** web page. Then, click the **Submit** button (located in the top-right corner of the table) as shown below:

COPO												•	<i>.</i> .	0
Profile: DTOL Test Pr Barcoding Manifes	rofile ts (ERT000002 : rRNA g	ene 🗸 ) 🖽					# #	•	T Z	•	Info			
			Select all	Select filtered	Clear select	ion Export		<b>Delete</b>	Submit C	_				
Showing 1 to 1 of 1 record	ls 1 record selected													
Organism 🕴	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle 🗍	Sedimentation	Clone	Isolate name	Isolation source	Cultivar 🍦	Variety (varietas)	Ecotype 🕴	Breed				

Fig. 8: Barcoding manifest submission: Click the "Submit" button to submit the highlighted barcoding manifest from the profile

rofile: DTOL Test Pro	ofile	_	-				<b>#</b> 1	6- B	T	Z	•	
arcoding Manifest	s (ERT000002 : rRNA ge	ene 🗸 ) 🖽					m	<b>-</b>		<b>A</b>		Barcoding sequence has been submitted with accession ERZ21826949
			Select all	Select filtered	Clear select	ion Export		Delete Barcoding I	<b>i Submit</b> Manifest			Info
nowing 1 to 1 of 1 records	Click 🕑 beside a record to view	extra details										Biocoding manifest submission has been scheduled!
Organism 🗍	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle 🗍	Sedimentation	Clone	Isolate name	Isolation source	Cultivar 🗧	Variety (varietas)	÷ Eco	type 🍦	Breed	
SAMEA130748926	yes		5.85									
ow 10 v records												
								Previous	1 Nex	+		

Fig. 9: Barcoding manifest submission: The barcoding manifest has been submitted

# 12.2 How to Delete Barcoding Manifests

Note: Barcoding manifests can only be deleted **before** they have been submitted.

Click the desired barcoding manifest from the list of barcoding manifests displayed on the **Barcoding Manifests** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

<u>*</u>	СОРО														0
	ofile: DTOL Test Pro	ofile ts (ERT000002 : rRNA ge	ene v)				[	# #	•	T	z	•	Info		
				Select all	Select filtered	Clear select	ion Export			Submit					
Sho	owing 1 to 1 of 1 records	s 1 record selected							Barcod ng M	anifests					
	Organism 🛓	Is your organism from an environmental/metagenomic /uncultured sample? (yes/no)	Organelle 🝦	$ \begin{array}{c} \text{Sedimentation} \\ \text{coefficient} \end{array} \\ \end{array} \\ \label{eq:sedimentation}$	Clone	Isolate name	Isolation source	Cultivar 🍦	Variety (varietas)	Ecoty	pe 🕴 E	Breed			

Fig. 10: Barcoding manifest deletion: Click the "Delete" button to remove the highlighted barcoding manifest from the profile



Fig. 11: Barcoding manifest deletion: Barcoding manifest record has been deleted

## THIRTEEN

# **FILES SUBMISSION**

# 13.1 How to Submit Files

### 13.1.1 Accessing the Files' Web Page

The Files' web page can be accessed from the **Components** button or **Actions** button associated with a profile<sup>1</sup>.

### Use Components' Button to Navigate to Files' Web Page

Click the components • button associated with a profile. Then, click the from the popup menu displayed as shown below:

### Use Actions' Button to Navigate to Files' Web Page

Click the <u>Actions</u> button associated with a profile. Then, click the action, **Upload Files** action from the popup menu displayed as shown below:

## 13.1.2 Submit Files from your Local (Computer) System

- 1. Click the 🙂 button on the Files web page to add a new file by browsing your local file system
- 2. An Upload File dialogue is displayed. Click the Upload button to choose a file from your local system.
- 3. The new file(s) will be displayed on the **Files** web page after a successful submission.

Hint:	To add more files from your local system, click the	🖵 Add	button (once f	files have been
submit	ted to the profile) as an alternative to clicking the 모	button.		

<sup>&</sup>lt;sup>1</sup> Also known as COPO profile. See: COPO profile or work profile.



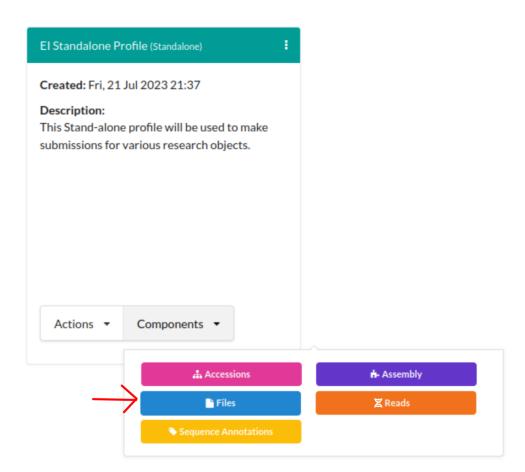


Fig. 1: Stand-alone Profile Components: Files component button

E	l Standalone Pr	ofile (Sta	ndalone)	:
D T	reated: Wed, 2 escription: his Stand-alone ubmissions for v	profile	will be used	
	Actions 🔹	Comp	onents 🔻	
	Upload Files	<		
יסו	Submit Reads			
	Submit Assem	nbly		
	Submit Annot	ation		

Fig. 2: Stand-alone Profile Actions: 'Upload Files' action

	4	X	٠	ġ.	Info	>
- Getting started						
e files' page provides a platform for uploading files from a cluster or from e's local (computer) system.						
o add files from your local system, click the 🖵 icon.						
To add files via the terminal, click the 🔎 icon.						

Fig. 3: Files web page: 'Add new file by browsing local file system' button

Upload File		×
Upload files by browsing your local system		
	Upload	Close

Fig. 4: Files submission: Upload File dialogue

<b>≜</b> CO	PO				🌲 🖉 🗃 Ö Ötester1 🗸
Files			# X	• *	Info
		Select all Select filtered Clear selection	n Export CSV 📿 Add >_ Add 🔒 Delete Search Files	]	Flet(share been uplaadod!
Showing 1	to 5 of 5 records Click	ails			
	FILE NAME	FILE MD5	LAST UPLOADED	SIZE 👙	
	Cafeteria_transcriptome_1.fasta.gz	8443773d4cf4053d51e343252f899e87	2023-09-28 09:01:39.138000+00:00	5773	
	small1_r1.fastq.gz	8443773d4cf4053d51e343252f899e87	2023-09-28 09:02:23.242000+00:00	5773	
	small2_r2.fastq.gz	8443773d4cf4053d51e343252f899e87	2023-09-28 09:01:49.399000+00:00	5773	
	small3_r3.fastq.gz	8443773d4cf4053d51e343252f899e87	2023-09-28 09:02:00.983000+00:00	5773	
	small4_r4.fastq.gz	8443773d4cf4053d51e343252f899e87	2023-09-28 09:02:12.762000+00:00	5773	

Fig. 5: Files submission: Files' web page displaying the uploaded file(s)

### 13.1.3 Submit Files via the Terminal

**Hint:** If you encounter the server certificate error, curl: (60) Peer's Certificate issuer is not recognized., please perform one of the the following resolutions:

• Resolution #1: Run the command below in the terminal (if you have sudo rights on your device)

\$ sudo apt-get install ca-certificates

OR

- **Resolution #2**: Replace https with http in the generated command indicated *here* then, run the command in the terminal again.
- 1. Click the button on the Files web page to add a new file from a cluster via the terminal.

illes       Image: Comparison of the strated         Files - Getting started       Image: Compare? system.         To add files from your local system, click the (Image) icon.       Image: Compare? system.
The files' page provides a platform for uploading files from a cluster or from one's local (computer) system.
one's local (computer) system.
To add files from your local system, click the 🤤 icon.
To add files via the terminal, click the 😕 icon.

Fig. 6: Files web page: 'Add new file via terminal' button

- 2. A **Move Data** dialogue is displayed. Follow the instructions displayed then, click the **Process** button to submit the file(s) to the profile.
  - •

  - -
- 3. The new file(s) will be displayed on the **Files** web page after a successful file submission via the terminal i.e. after the command has been executed successfully in the terminal.

Hint:	To add more files via the terminal, click the $2$ -Add	button (once files have been submitted
to the	profile) as an alternative to clicking the 😕 button.	

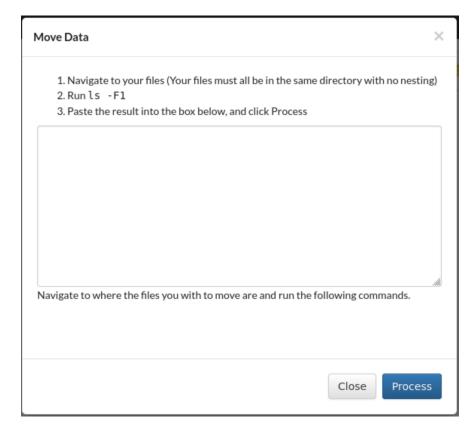
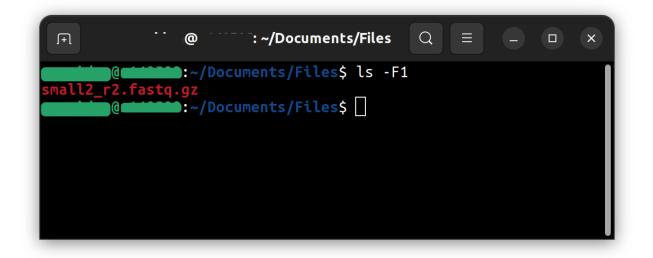
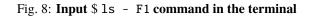


Fig. 7: Files submission: Move Data dialogue





Move Data	×
<ol> <li>Navigate to your files (Your files must all be in the same directory with no ne</li> <li>Run ls -F1</li> <li>Paste the result into the box below, and click Process</li> </ol>	esting)
small2_r2.fastq.gz	
Navigate to where the files you with to move are and run the following commands.	/k
Close Prod	cess

Fig. 9: Move Data dialogue: Input the filename(s) returned after having ran the 1s - F1 command in the terminal. Then, click the Process button.

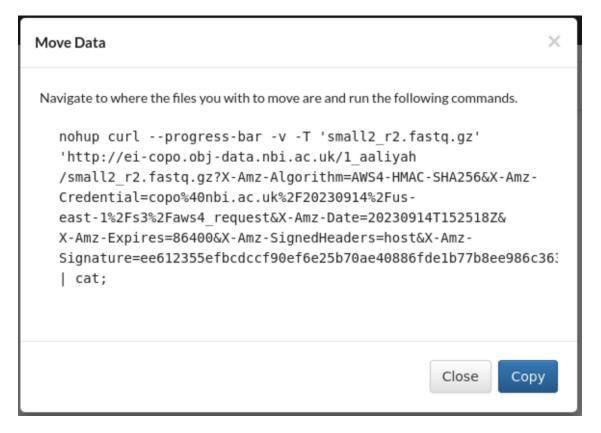
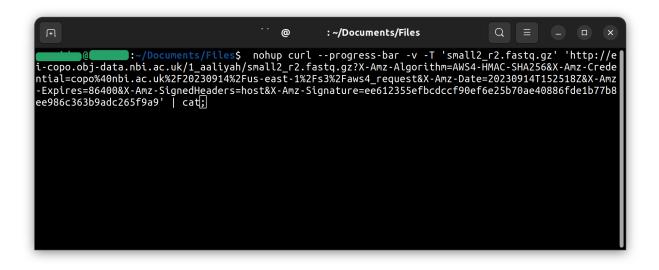
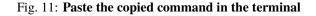


Fig. 10: Move Data dialogue: Command outputted after having clicked command in the Process button. Copy the command displayed.

If you encounter the server certificate error, curl: (60) Peer's Certificate issuer is not recognized., please see the *hint* at the beginning of this section.





			4	X • #	✿ tester1
wing 1 to 1 of 1 records Click 😜 be	eside a rec	Select all Select filtered	Clear selection Export CSV Q Add A Gold	•	
FILE NAME		FILE MD5	LAST UPLOADED	SIZE \$	
small2_r2.fastq.gz		3181f0f98825ca11a47185e9d534a2b7	2023-09-14 15:38:09.184000+00:00	9639565	

Fig. 12: Files submission: Files' web page displaying the uploaded file(s)

# **13.2 How to Delete Files**

Click the desired file from the list of files displayed on the Files' web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

⊉cc	PO								•	2	M	0	🌣 tester 1 👻
Files	9 2		Select all Select filtered C	ter selection Eport CSV 📿 Add 5. Add Search Fi	Delete rec		<b>Å</b> -	Info					
Showing :	to 1 of 1 records 1 record selected												
	FILE NAME	FILE MD5		LAST UPLOADED		SIZE							
	small1_r1.fastq.gz	4853e4ee19d123f2397556679a5979ba-2		2023-09-14 13:31:10.567000+00:00		9639565							

Fig. 13: File deletion: Click the "Delete" button to remove the highlighted file from the profile

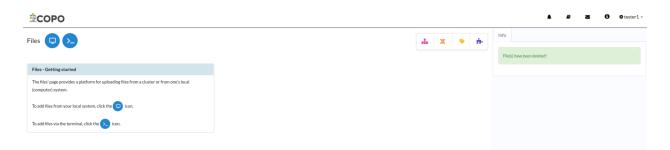


Fig. 14: File deletion: File has been deleted

# FOURTEEN

# **IMAGES SUBMISSION**

# 14.1 How to Submit Images

#### Note:

- Images can only be submitted after samples have been uploaded in the Upload Spreadsheet dialogue.
- Images can only be submitted via a ToL<sup>1</sup> profile. Please see: Steps to Create a Tree of Life Profile for guidance.
- The filename of sample images must be named as {Specimen\_ID}-{n}.[jpg|png] where {n} is the image number, {Specimen\_ID} is the specimen ID of the sample in the manifest and jpg or png is the extension of the file.

#### See also:

- Viewing Submitted Images
- Permits Submission
- How to Submit ASG Manifests
- How to Submit DTOL Manifests
- How to Submit ERGA Manifests
- How to Submit Barcoding Manifests
- 1. The images table is empty under the Sample Images tab in the Upload Spreadsheet dialogue.

Upload Spreadsheet	×
Upload Images Upload Permits Finish	
Sample Metadata Sample Images Sample Permits	
	Close

### Fig. 1: Manifest submission: 'Upload Spreadsheet' dialogue with no images uploaded

<sup>&</sup>lt;sup>1</sup> See term: *Tree of Life (ToL)*.

2. The images table is populated with the images uploaded under the **Sample Images** tab in the **Upload Spreadsheet** dialogue.

Upload Spreadsheet		×						
Upload Images     Upload Permits     Finish       Sample Metadata     Sample Images     Sample Permits								
Show 10 v entries		Search:						
Specimen ID	Image File	Image						
ERGA_BCE_9858_104	ERGA_BCE_9858_104-2.jpeg	*						
Showing 1 to 1 of 1 entries		Previous 1 Next						
		Close						

Fig. 2: Manifest submission: 'Upload Spreadsheet' dialogue with image(s) uploaded

3. Click the Finish button to submit the images and samples.

A **Submit Samples** confirmation dialogue is displayed. If you decide to confirm the samples submission, click the **Confirm** button.

# 14.2 View Submitted Images

#### Note:

- Images can only be viewed after they have been submitted.
- Images **cannot** be deleted or modified after they have been submitted.

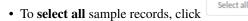
• The <sup>[]</sup> button will only appear on the web page if you are assigned as a sample manager.

Select filtered

Clear selection

#### Hint:

- To **select multiple** sample records, hold down the Ctrl key on your keyboard and click on the sample records that you would like to select.
- To select a range of sample records, hold down the Shift key on your keyboard and click on the first and last sample records that you would like to select.



- To select filtered sample records, click
- To clear selection of sample records, click

Chapter 14. Images Submission

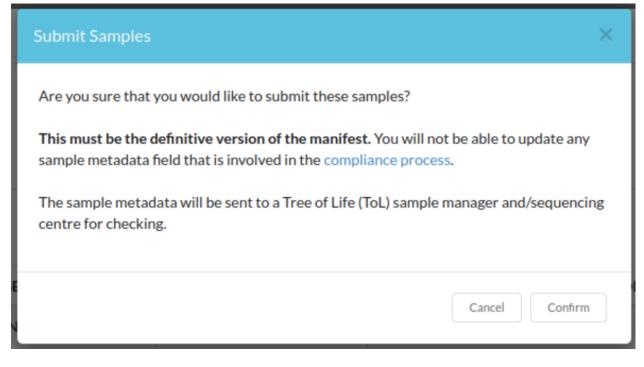


Fig. 3: Manifest submission: 'Submit Samples' confirmation dialogue

### 14.2.1 On Samples web page

1. Navigate to the **Samples** web page.

See How to access Samples web page section for guidance.

2. Select the sample record(s) that you would like to view images for.

Then, click the view image(s) submitted for the selected sample record(s).

<b>СОРО</b>						🜲 🖻 🗷 🛈 Otester1 -
Profile: Test Profi Samples		<b>(</b>			4 + = 1 × >	Info
Select all Select fo	Search Samples					
Showing 1 to 3 of 3 re	ecords 1 record selected					
Tube or Well Id	Specimen Id	Purpose Of Specimen	Sample Coordinator (ERGA Ambassador)	Sample Coordinator (ERGA Ambassador) Affiliation	Sample Coordinator (ERGA Ambassador) ORCID ID	
O F50000001	ERGA_BCE_0000_101	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002	
o FS0000002	ERGA_BCE_0000_102	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002	
• FS0000003	ERGA_BCE_0000_103	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002	
show 10 v reco	ords				Previous 1 Next	

Fig. 4: Samples web page: Pointer to 'View images' button

3. If any image submission(s) exist for the selected sample record(s), a popup dialogue will be displayed with the image(s) submitted for the selected sample record(s) as shown below:

Hint: Click the image to view a larger version.



Fig. 5: Samples web page: Popup dialogue displaying submitted image(s) for selected sample record(s)

OR

If no images were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

<b>±</b> СОРО				View images			<b>*</b>	•	s (	• •	tester1 -
Profile: Test Profile Samples 🚺 🖽 🍐 (言		No images exist for the selected sample record(s)	· · · · · · · · · · · · ·	Info							
Select al Select formed Clear whechin Export CSV A Developt sample matchet A Developt permits View Ox					Search Samples						
Showing 1 to 3 of 3 m	cords 1 record selected										
Tube or Well Id	Specimen Id 🕴	Purpose Of Specimen	Sample Coordinator (ERGA Ambassador)	Sample Coordinator (ERGA Ambassador) Affiliation	Sample Coordinator (ERGA Ambassador) ORCID ID						
o FS0000001	ERGA_BCE_0000_101	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002						
O FS0000002	ERGA_BCE_0000_102	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002						
O FS0000003	ERGA_BCE_0000_103	REFERENCE_GENOME	Jane Doe   John Doe	EARLHAM_INSTITUTE   EARLHAM_INSTITUTE	0000-0001-0867-0001 0000-0002-4719-0002						
show 10 v rec	ords				Previous 1 Next						

Fig. 6: Samples web page: Popup dialogue displaying message, 'No images exist for selected sample record(s)'

## 14.2.2 On Accept or Reject Samples web page

If you have been assigned as a **sample manager**, see *View submitted images section for sample managers <images-submission-view-images-sample-managers>* for more information.

## **FIFTEEN**

# PERMITS SUBMISSION

# **15.1 How to Submit Permits**

#### Note:

- Permits can only be submitted after ERGA<sup>1</sup> samples have been uploaded in the Upload Spreadsheet dialogue.
- Permits can only be submitted via a ToL<sup>2</sup> profile<sup>3</sup>. Please see: Steps to Create a Tree of Life Profile for guidance.

#### Warning:

• 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.

### See also:

- Downloading Submitted Permits
- Images Submission
- How to Submit ERGA Manifests
- How to Submit Barcoding Manifests
- 1. The uploaded samples are shown in a table in the **Upload Spreadsheet** dialogue as shown below. Click the Upload Permits button to browse your local (computer) system for .pdf permits for the samples.
- 2. The permits table is empty under the Sample Permits tab in the Upload Spreadsheet dialogue.
- 3. The permits table is populated with the permits uploaded under the **Sample Permits** tab in the **Upload Spread**-**sheet** dialogue

<sup>&</sup>lt;sup>1</sup> See term: *ERGA*.

<sup>&</sup>lt;sup>2</sup> See term: *Tree of Life (ToL)*.

<sup>&</sup>lt;sup>3</sup> Also known as COPO profile. See: COPO profile or work profile.

now 10 v entries					Search:	
TUBE_OR_WELL_ID	SPECIMEN_ID	PURPOSE_OF_SPECIMEN		SAMPLE_COORDINATOR_AFFILIATION	SAMPLE_COORDINATOR_ORCID_ID	o
F542596104	ERGA_BCE_9858_104	REFERENCE_GENOME	Tester1   Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY I INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-00001 0000-0000-0000-0002	M
F\$42596105	ERGA_BCE_9858_105	REFERENCE_GENOME	Tester1   Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY I INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-00001 0000-0000-0000-0002	Μ
FS42596106	ERGA_BCE_9858_106	REFERENCE_GENOME	Tester1   Tester2	INSTITUTE_OF_EVOLUTIONARY_BIOLOGY   INSTITUTE_OF_EVOLUTIONARY_BIOLOGY	0000-0000-0000-00001 0000-0000-0000-000	M
nowing 1 to 3 of 3 entrie:	5				Previous 1 Next	

Fig. 1: ERGA manifest submission: 'Upload Spreadsheet' dialogue with uploaded samples

Upload Spreadsheet		×
Upload Images Upload Permit		
Sample Metadata Sample Images	Sample Permits	
		Close

Fig. 2: ERGA manifest submission: 'Upload Spreadsheet' dialogue with no permits uploaded

Upload Images Upload Permits Finish			
ple Metadata Sample Images Sample Permits			
how 10 v entries		Se	arch:
Specimen ID	Permit Type	Permit Files	<sup>≜</sup> Notes
ERGA_BCE_9858_104	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_104	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_104	Nagoya Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_105	Nagoya Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Ethics Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Sampling Permit	SAMPLING_PERMITS.pdf	
ERGA_BCE_9858_106	Nagoya Permit	SAMPLING_PERMITS.pdf	
howing 1 to 9 of 9 entries		Pre	vious 1 Next



4. Click the **Finish** button to submit the permits and samples.

A **Submit Samples** confirmation dialogue is displayed. If you decide to confirm the samples submission, click the **Confirm** button.

# **15.2 Download Submitted Permits**

### Note:

- Permits can only be downloaded after they have been submitted.
- Permits cannot be deleted or modified after they have been submitted.
- The <sup>(=)</sup> button will only appear on the web page if you are assigned as a sample manager.

Select all

#### Hint:

- To **select multiple** sample records, hold down the Ctrl key on your keyboard and click on the sample records that you would like to select.
- To select a range of sample records, hold down the Shift key on your keyboard and click on the first and last sample records that you would like to select.

• To select all sample records, click

Submit Samples ×	
Are you sure that you would like to submit these samples?	
This must be the definitive version of the manifest. You will not be able to update any sample metadata field that is involved in the compliance process.	
The sample metadata will be sent to a Tree of Life (ToL) sample manager and/sequencing centre for checking.	
Cancel Confirm	

Fig. 4: ERGA manifest submission: 'Submit Samples' confirmation dialogue

• To <b>select filtered</b> sample records, click	tfiltered
· ,	Clear selection

### 15.2.1 On Samples web page

1. Navigate to the **Samples** web page.

See How to access Samples web page section for guidance.

2. Select the sample record(s) that you would like to download permits for.



Fig. 5: Samples web page: Pointer to 'Download permits' button

3. If any permit submission(s) exist for the selected sample record(s), the permits will be automatically downloaded for the selected sample record(s) as shown below:

Hint: Permits will be downloaded as a .zip file

If no permits were submitted for the selected sample record(s), a message is displayed in the popup dialogue indicating such as shown below:

≜СОРО	Download permits			<i>B</i> 2	s 0	Otester1 +
Profile: Test Profile 2 Samples 🚺 🖽 📥 🔚	No permits exist for the selected sample record(s)	h ń- III B X 🎙	Info			
Select all Select Married Clar selection Export CSV & Developing in marries & Developing motion ( • Vere Showing 1 to 1 of 1 means 1 means selected	ОК	, Search Samples				
Tube or Well Id Specimen Id Purpose Of Specimen Sample Coordinator (ERGA Ambassador) Sample	Coordinator (ERGA Ambassador) Affiliation	Sample Coordinator (ERGA Ambassador) ORCID ID				
F542595097 ERGA_BCE_9858_097 REFERENCE_GENOME Jane Doe John Doe EARLH	IAM_INSTITUTE	0000-0000-0000-0000 0000-0000-0000-00001				
show 10 v records		Previous 1 Next				

Fig. 6: Samples web page: Popup dialogue displaying message, 'No permits exist for selected sample record(s)'

### 15.2.2 On Accept or Reject Samples web page

If you have been assigned as a **sample manager**, see *Download submitted permits section for sample managers* <*permits-submission-download-permits-sample-managers>* for more information.

## SIXTEEN

# **READS SUBMISSION**

# 16.1 How to Submit Reads

#### Note:

- Once **Reads** have been submitted, they cannot be deleted.
- Files must be uploaded before a **Reads** manifest can be submitted.

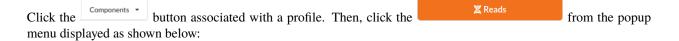
#### See also:

- How to Update Reads
- Explore Various Types of Reads Checklist
- How to Submit Files

### 16.1.1 Accessing the Reads' Web Page

The **Reads**<sup>1</sup> web page can be accessed from the **Components** button or **Actions** button associated with a profile<sup>2</sup>.

### Use Components' Button to Navigate to Reads' Web Page



### Use Actions' Button to Navigate to Reads' Web Page

Click the Actions button associated with a profile. Then, click the action, **Submit Reads** action from the popup menu displayed as shown below:

<sup>&</sup>lt;sup>1</sup> See: *Reads*.

<sup>&</sup>lt;sup>2</sup> Also known as COPO profile. See: *COPO profile or work profile*.



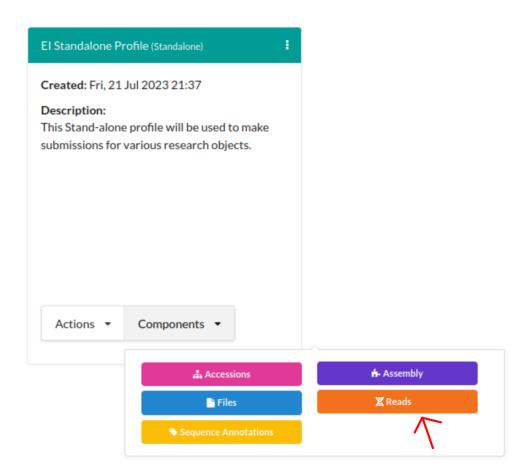


Fig. 1: Stand-alone Profile Components: Reads component button

E	l Standalone Pro	Standalone Profile (Standalone)					
D TI	reated: Wed, 23 escription: his Stand-alone ubmissions for v	profilev	vill be used				
	Actions 🝷	Comp	onents 💌				
	Upload Files						
ho	Submit Reads	<		_			
	Submit Assem	bly					
Submit Annotation							

Fig. 2: Stand-alone Profile Actions: 'Submit Reads' action

## 16.1.2 Upload Reads

Hint: To download a blank **Reads'** manifest template, click the **b**utton.

Important: The Reads checklist dropdown menu is only available for Standalone profiles.

If you are submitting Reads for a profile other than a Standalone profile, please proceed to upload the Reads from your

local file system after you have clicked the 🕮 button.

1. On the **Reads'** web page, click the checklist dropdown to view a list of available checklists that support **Reads'** submission as shown below:

<b>≜</b> C(	OPO				٠	8	M	0	🌣 tester1 👻
Profile	: El Standalone Profile		🛔 🛉 🗎 🔖	Info					
Reads	ERC000046 : Pan Prostate sample checklist	V) 🖽 🛃							
	ERC000053 : Tree of Life Checklist								
	ERC000046 : Pan Prostate sample checklist								
Read -	ERC000042 : ENA RNA-Seq Checklist								
The Re	a ERC000043 : ENA Marine Microalgae Checklist								
	ERC000040 : ENA UniEuk_EukBank Checklist								
	<sup>#</sup> ERC000039 : ENA parasite sample checklist								
downlo	<sup>2</sup> ERC000035 : ENA Crop Plant sample enhanced annotation checklist								
After h	ERC000034 : ENA mutagenesis by carcinogen treatment checklist								
Andri	ERC000047 : GSC MIMAGS								
	ERC000036 : ENA sewage checklist								
	ERC000051 : PDX Checklist								
	ERC000049 : GSC MIUVIGS								
	ERC000048 : GSC MISAGS								
	ERC000050 : ENA binned metagenome								
	ERC000037 : ENA Plant Sample Checklist								
	ERC000032 : ENA Influenza virus reporting standard checklist								
	ERC000031 : GSC MIXS built environment								
	ERC000030 : ENA Tara Oceans								
	ERC000033 : ENA virus pathogen reporting standard checklist								
	CDC000000 - ENA CITET MULTER HILLIGHT - HELLIGHT - HELI								

Fig. 3: Reads' web page: Checklist dropdown menu with checklist options displayed

An overview of each **Reads** checklist option is explained in the *Reads' checklist section*.

2. Click U button to add **Reads'** from a spreadsheet for the chosen checklist as shown below:

**Note:** The colour of the button is based on the type of profile that you are submitting a Reads for. See the *Profile Types Legend* section regarding the colour code for the various types of project profiles on COPO.

3. An **Upload Read Manifest** dialogue is displayed. Click the your local system.

button to choose a file from

4. The uploaded manifest is shown in a table in the **Upload Read Manifest** dialogue as shown below. Click the Finish button to submit the reads manifest.

<b><sup>≜</sup>COPO</b>			٠	2	0	✿ tester1 →
Profile: El Standalone Profile Reads (ERC000046 : Pan Prostate sample checklist	) 🖽 🛃	Image: A state of the state				
Read - Getting started						
The Read component of a profile						
Select the desired checklist from the dropdown menu then, click the 🛓 button to download the blank mannest.						
After having completed the manifest, click the 🙃 button to upload the manifest.						

### Fig. 4: Reads' upload: Click 'Add Reads' from Spreadsheet' button

#COPO					٠	8	0	🗘 tester 1 👻
2001 0	Upload Read Manifest $ imes$	-						
Profile: El Standalone Profile Reads (ERC000046 : Pan Prostate sample checklist	ENA Reads Manifest Validation for ERC0000046 : Pan Prostate sample checklist	6- B	•	Info				
Read - Getting started The Read component of a profile	Upload a completed manifest for validation							
Select the desired thecklist from the dropdown menu then, click the 💽 button to download the blank manifest.	Upload Read Manifest Finish Close	J						

### Fig. 5: Reads' upload: 'Upload Read Manifest' dialogue

5. The new read(s) will be displayed on the **Reads** web page after a successful submission.

**Hint:** Reads records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

### 16.1.3 Submit Reads

Hint: The submitted read record will be highlighted green.

Click the desired reads records from the list of reads displayed on the **Reads'** web page. Then, click the **Submit** button (located in the top-right corner of the table) as shown below:

Upload Read Manifest		
ENA Reads Manifest Validation for ERC000046 : Pan checklist Upload a completed manifest for validation	Prostate sample	
Spreadsheet is valid		
Show 10 v entries	Search:	
₹ File checksum	$\tilde{\bar{\forall}}$ File name	Instr mod
61df53f6dc6a88b8c564378365e354f8, 5881289049072e1b69aa622b928f5144	small1_r1.fastq.gz, small2_r2.fastq.gz	Grid
92965fbe5532f5d05ac27c1b98e043c5	Cafeteria_transcriptome_1.fasta.gz	Grid
92965fbe5532f5d05ac27c1b98e043c5, 0f4e1e5b258269a90c68b47117fdc94c	small3_r3.fastq.gz, small4_r4.fastq.gz	Grid
Showing 1 to 3 of 3 entries	Previous 1 Next	
Uploa	ad Read Manifest Finish Cl	ose

Fig. 6: Reads' upload: 'Upload Read Manifest' dialogue with uploaded manifest

ofile: El St	andalone Pro	file									4	÷.	•	Info	
ads (ERC	:000046 : Pai	n Prostate sa	ample ch	ecklist				<b>v</b> )	<b>B</b>					Read records are saved	
					Sel	ect all	ielect filtered	Clear selection	Export CSV		<b>i Submit</b> h Reads				
owing 1 to 3 c	of 3 records Click	beside a record	rd to view ext	ra details											
project name	sequencing ÷	subject_id 🕴	gender 🕴	phenotype 🍦	sample type	PPCG	PPCG sample \$ ID	Pipeline/UUID 🝦	preservation $\frac{4}{7}$	xenograft 🕴	Sample 🝦	Instrument model	Library name		
test 1		erererewr	female	dfdsf	bone metastases	dfdfd	DNA	dferererer	Fresh Frozen	No	xyzA3	GridION	abccc		
		rewrewrewrer	male	dfdsf	csf	adfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzB3	GridION	abcddd		
		rewrewrewrer	male	dfdsf	csf	adfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzC3	GridION	abcdddd		
w 10 ~	records														

Fig. 7: Reads' upload: Reads' web page displaying the uploaded read(s)

ofile: El St	andalone Pro	ofile									_		-	-	Info	
ads (ERC	000046 : Pa	n Prostate sa	mple ch	ecklist				<b>~</b> )			#	ġ.		•		
															Read records are saved	
					Sel	ect all S	Select filtered	Clear selection	Export CSV	🖹 Delete	i Submit	$\leftarrow$				
											ch Reads					
wing 1 to 3 o	of 3 records 1 rec	cord selected														
project name	sequencing method	subject_id 🕴	gender 🗘	phenotype 🕴	sample type	PPCG ID	PPCG sample ‡ ID	Pipeline/UUID	preservation $\frac{1}{2}$	xenograft 🕴	Sample 🕴	Instrume model		ibrary ame		
test 1		erererewr	female	dfdsf	bone metastases	dfdfd	DNA	dferererer	Fresh Frozen	No	xyzA3	GridION	a	bccc		
		rewrewrewrer	male	dfdsf	csf	adfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzB3	GridION	а	bcddd		
		rewrewrewrer	male	dfdsf	csf	ədfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzC3	GridION	a	bcdddd		
v 10 ~	records															

Fig. 8: Reads submission: Click the "Submit" button to submit the highlighted read from the profile

file: El	Standalone Pro	ofile							• •		A	÷. 1	•	
ads (El	RC000046 : Pa	n Prostate sa	ample che	ecklist	Sele	ect all S	elect filtered	) Clear selection	Export CSV		i Submit			Submission completed. • To view accessions, select View Accessions from the menu • An embargo is placed on this submission. Embargo will be automatically lifted on: Sin; 28 Sep 2025 00:00 • To release this study now, select Lift Embargo from the me
wing 1 to	3 of 3 records Clic	k 🛨 beside a recor	rd to view ext	ra details							h Reads			Info
project name	÷ sequencing method	subject_id 🕴	gender ≑	phenotype 🕴	sample ÷	PPCG	PPCG sample ‡	Pipeline/UUID ‡	preservation ‡	xenograft 🗄	Sample ÷	Instrument	Library	Submission has been added to the processing queue. Status update will be provided.
							ID							
test 1		erererewr	female	dfdsf	bone metastases	dfdfd	DNA	dferererer	Fresh Frozen	No	xyzA3	GridION	abccc	
		rewrewrewrer	male	dfdsf	csf	adfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzB3	GridION	abcddd	
		rewrewrewrer	male	dfdsf	csf	adfdfdf	DNA	dfdsfdsf	Fresh Never Frozen	No	xyzC3	GridION	abcdddd	

Fig. 9: Reads submission: The Read has been submitted

## SEVENTEEN

# SAMPLES SUBMISSION

The following are the types of sample manifests that can be submitted.

Click the links below to learn more about each type of manifest submission:

- Aquatic Symbiosis Genomics (ASG) manifests
- Darwin Tree of Life (DToL) manifests
- Darwin Tree of Life Environmental (DToL\_ENV) manifests
- European Reference Genome Atlas (ERGA) manifests

#### See also:

- · How to access Samples web page
- How to submit Assemblies
- Barcoding manifest submissions
- How to upload Files
- How to submit Reads
- How to submit Sequence Annotations

# 17.1 How to Download Submitted Sample Manifest

**Hint:** This is useful if you would like to update sample metadata for a manifest or retrieve the actual manifest that was submitted.

Samples can be updated by resubmitting the manifest with the updated metadata. See *Updating Samples* section for more information about which fields can be updated.

Note: At least one sample record (in a manifest) must be submitted before a manifest can be downloaded.

The following steps describe how to download a submitted sample manifest:

1. Navigate to the **Samples** web page.

See How to access Samples web page section for guidance.

2. On the **Samples** web page, select **only one** sample record from the sample record table displayed.

Then, click the **Download sample manifest** button to download the manifest.

**Hint:** The manifest will be automatically downloaded as a .xlsx file

rofile: [											Info		
	DTOL Test Profile							a a	III 📔 🗶	•			
ample	s 🚺 😐	🛃 🔁	(#)										
Select all	Select filtered	Clear selection	Export CSV		A Download permits	View images							
				$\sim$									
Showing 1	to 10 of 51 records	1 record selected											
Serie	Rack or Plate ld	Tube or Well Id	Specimen Id 🕴	Order or Group	FAMILY 0	GENUS 🔅	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPE			
01	FK00526540	FF03454481	MBA-190930-003A	Hymenoptera	Ichneumonidae	Itoplectis	2776046	Itoplectis maculator					
0 2	FK00526541	FF03454482	MBA-190930-003B	Diptera	Tipulidae	Tipula	2881124	Tipula confusa					
			MBA-190930-003C	Isopoda	Porcellionidae	Porcellio	172005	Porcellio spinicornis					
<b>o</b> 3	FK00526542	FF03454483	110/11/07/00 0000										
03 04	FK00526542 FK00526543	FF03454483	MBA-190930-003D	Opiliones	Phalangiidae	Oligolophus	2979189	Oligolophus hansenii					
-				Opiliones POLYDESMIDA	Phalangiidae Polydesmidae	Oligolophus PROPOLYDESMUS	2979189 1569497	Oligolophus hansenii PROPOLYDESMUS TESTACEUS					
<b>o</b> 4	FK00526543	FF03454484	MBA-190930-003D		-								
04 05	FK00526543 FK00526544	FF03454484 FF03454485	MBA-190930-003D MBA-190930-003E	POLYDESMIDA	Polydesmidae	PROPOLYDESMUS	1569497	PROPOLYDESMUS TESTACEUS					
• 4 • 5 • 6	FK00526543 FK00526544 FK00526545	FF03454484 FF03454485 FF03454486	MBA-190930-003D MBA-190930-003E MBA-190930-003F	POLYDESMIDA CHORDEUMATIDA	Polydesmidae CHORDEUMATIDAE	PROPOLYDESMUS Melogona	1569497 2979188	PROPOLYDESMUS TESTACEUS Melogona scutellaris					
04 05 06 07	FK00526543           FK00526544           FK00526545           FK00526545           FK00526546	FF03454484 FF03454485 FF03454486 FF03454487	MBA-190930-003D MBA-190930-003E MBA-190930-003F MBA-190930-003G	POLYDESMIDA CHORDEUMATIDA Lepidoptera	Polydesmidae CHORDEUMATIDAE Lyonetiidae	PROPOLYDESMUS Melogona Lyonetia	1569497 2979188 753195	PROPOLYDESMUS TESTACEUS Melogona scutellaris Lyonetia clerkella					

Fig. 1: Samples web page: Pointer to 'Download sample manifest' button

## EIGHTEEN

# **SEQUENCE ANNOTATIONS SUBMISSION**

#### Note:

• Reads must be uploaded before a Sequence Annotation can be submitted.

#### See also:

- How to Update Sequence Annotations
- How to Delete Sequence Annotations

# **18.1 How to Submit Sequence Annotations**

### 18.1.1 Accessing the Sequence Annotations' Web Page

The **Sequence Annotations**<sup>1</sup> web page can be accessed from the **Components** button or **Actions** button associated with a profile<sup>2</sup>.

### Use Components' Button to Navigate to Sequence Annotations' Web Page

Click the button associated with a profile. Then, click the from the popup from the popup from the popup

### Use Actions' Button to Navigate to Sequence Annotations' Web Page

<sup>&</sup>lt;sup>1</sup> See: Sequence Annotation.

<sup>&</sup>lt;sup>2</sup> Also known as COPO profile. See: *COPO profile or work profile*.



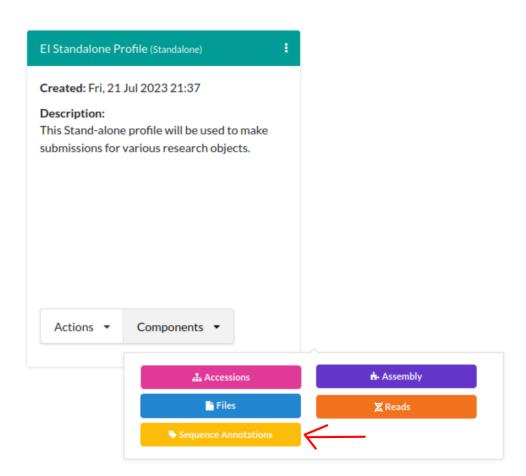


Fig. 1: Stand-alone Profile Components: Sequence Annotations' component button

E	l Standalone Pr	ofile (Sta	ndalone)		÷
D TI	reated: Wed, 2 escription: his Stand-alone ubmissions for v	profile	will be u	sed to	
	Actions •	Comp	onents	•	
	Upload Files				
ho	Submit Reads				
	Submit Assem	bly			
	Submit Annot	ation <del>&lt;</del>	$\leq$		

Fig. 2: Stand-alone Profile Actions: 'Submit Annotation' action

### **18.1.2 Submit Sequence Annotations**

1. Click • button to add **Sequence Annotations**' as shown below:

<sup>≜</sup> COPO							<b>A</b> <i>E</i>	1	s 0	✿ tester1 -
Profile: El Standalone Profile Sequence Annotations		#	ň.	Ľ	X	Info				
Sequence Annotations - Getting started										
The sequence annotation's page provides a platform to marking specific features in a Deoxyribonucleic acid (DNA), Ribonucleic acid (RNA) or protein sequence with descriptive information about structure or function. It is usally performed after a genome is sequenced and assembled.										
To add annotations, click the + icon.										

#### Fig. 3: Sequence Annotations' submission: Click 'Add Record' button

2. An Add Sequence Annotation dialogue is displayed. Provide the details then, click the Submit Annotation button.

Select a sample accession from the **SAMPLE** dropdown field menu. The dropdown menu will display the reads that were previously uploaded.

3. The new sequence annotation(s) will be displayed on the **Sequence Annotations** web page after a successful submission.

**Hint:** Sequence annotation records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful automatic submission.

Sequence Annotations' submission: Sequence Annotations' web page displaying the submitted sequence annotation(s)

# **18.2 How to Delete Sequence Annotations**

Note: Sequence annotations can only be deleted before they have been submitted.

Click the desired sequence annotation from the list of sequence annotations displayed on the **Sequence Annotations** web page. Then, click the **Delete** button (located in the top-right corner of the table) as shown below:

Submit annotatior	n		
Upload annotation files and fill ENA and have uploaded sample accessions.			
STUDY*			
PRJEB66432			
SAMPLE*			
None			~
RUN			
EXPERIMENT			
ANNOTATION TITLE*			
DECEMINATION			
DESCRIPTION			
DESCRIPTION Free text description of annotationannotation			
		TYPE*	lik
	f the sequenc		
Firee text description of annotationannotation	f the sequenc	TYPE*	~
Free text description of annotationannotation	f the sequence	TYPE*	~
Free text description of annotationannotation	f the sequenc	TYPE* None TYPE*	~
Free text description of annetationannotation FILE* None FILE* Non	f the sequence	TYPE* None TYPE* None	•
Free test description of annotationannotation FILE* None FILE* None FILE*	f the sequence	TYPE* None TYPE* None TYPE*	· ·

Fig. 4: Sequence Annotations' submission: 'Submit Annotation' dialogue with no sample accession chosen from SAMPLE dropdown menu

Add Sequence Annotation				
Submit annotation				
Upload annotation files and fill in m ENA and have uploaded samples ar accessions.				dy in
STUDY*				
PRJEB66432				
SAMPLE*				
ER516431676			~	
RUN				
ERR12080504				
EXPERIMENT				
ERX11462871				
ANNOTATION TITLE*				
Annotation title user-provided DESCRIPTION				
FILE*		TYPE*	ltr.	
None	~	None	*	
FILE*		TYPE*		
None	~	None	*	
FILE*		TYPE*		
None	~	None	¥	
		Submit	Annotation	Close

Fig. 5: Sequence Annotations' submission: 'Submit Annotation' dialogue with sample accession chosen from SAMPLE dropdown menu

±COPO		A P Z O ¢tester1 -
Profile: El Standalone Profile Sequence Annotations 💡 💠	<u>.</u>	Image: Sequence annotation submitting
	Select all Select filtered Clear selection Export CSV + Add 27 Edit @ De Search Sequence Ar	netations
Showing 1 to 1 of 1 records Click 🕐 beside a record to view extra details		Annotation submission has been scheduled, you will be notified when it is complete
STUDY 🔅 SAMPLE 🔅 RUN 🔅 EXPERIMENT 🔅 T	TLE	AISSION ERROR
• PRJEB66432 ERS16431676	Cafeteria_transcriptome_1.fasta.gz	
show 10 v records	Previous 1	Next

Fig. 6: Sequence Annotations' submission: Sequence Annotations' web page displaying the (pending) uploaded sequence annotation(s)

ofile: El Standalone equence Annotatio												h é		X	Last Sequence Annotation Submitted: - Seq Annotation Acces
quence Annotatio															ERZ21822618
					Select all	Select filter	ed	Clear selection	Export CSV	+ Add	🕼 Edit	Delete	i Sub	mit	Info
											earch Seque	nce Anno			Annotation submission has been scheduled, you will be notified
wing 1 to 1 of 1 records	Click 🔂 beside a re	cord to view	extra details												when it is complete
STUDY 🕴	SAMPLE \$	RUN 🕴	EXPERIMENT	† TIT	LE ÷	DESCRIPTIO	DN 🕴	FILES		÷ AC		SUBMI	SION ERF	ROR	
• PRJEB66432	ERS16431676			Tes	t Annotation			Cafeteria_tra	scriptome_1.fas	a.gz ER	Z21822618				
											Previou	s 1	lext		
COPO											Previou	s 1	lext		<b>▲ # ≥ 0 o</b>
COPO ofile: El Standalono	e Profile													X	
		)									Previou			X	
ofile: El Standalone		)			Select all	Select filtere	ed C	-lear selection	Eport CSV	<b>+</b> Add St		Delete			Sequence annotation submitting Info Annotation submission has been scheduled, you will be notified
ofile: El Standalone	ns 😢 🛨	)			Select all	Select filtere	rd C	Clear selection	Export CSV		al Z Edit	Delete			Sequence annotation submitting_
ofile: El Standalone quence Annotatio	ns 😢 🛨	RUN ¢	EXPERIMENT	÷TITL		Select filtere		Clear selection	Export CSV	S	al Z Edit	B Delete acce Annot		mit	Sequence annotation submitting Info Annotation submission has been scheduled, you will be notified

Fig. 7: Sequence annotation deletion: Click the "Delete" button to remove the highlighted sequence annotation from the profile

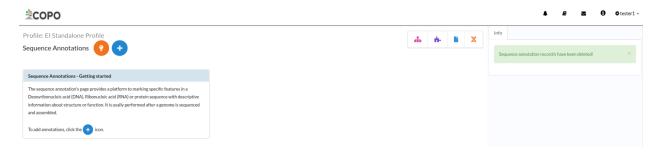


Fig. 8: Sequence annotation deletion: Sequence annotation record has been deleted

## CHAPTER

# NINETEEN

# **UPDATING PROFILES**

**Warning:** Profile types cannot be changed or updated once they have been created. If you need to change the profile type, you will need to delete the profile and create a new one.

### See also:

## **Deleting** Profiles

To edit a profile, click the  $\cdot$  icon that is associated with the desired profile. The option to edit or delete a profile record will be displayed once clicked.

Fifth ASG Profile (ASG)	K 🕼 Edit 🖉 Edit
<b>Created:</b> Thu, 20 Jul 2023 09:30 <b>Description:</b>	Edit record
This is the fifth ASG profile to be created.	
Actions • Components •	

Fig. 1: COPO Profile: Click the Edit button

Edit Profile	
Title required 3	
Fifth ASG Profile	
Description required (	
This is the fifth ASG profile to be created today.	
	1
Profile Type 🚯	
Aquatic Symbiosis Genomics (ASG)	~
Associated Profile Type 🚯	
Select associated type(s)	
	Cancel 🛓 Save ┥

Fig. 2: COPO Profile: Edit the existing details. Click the Save button to update the profile.

1	COPO				🛔 🖉 🗷 🗘 🗘 tester1 -
w	ork Profiles <u> </u>	Info			
			Record updated!		
			Web page will refresh in 3 seconds.		
	Eighteenth ERGA Profile (ERGA)	Fifth ASG Profile (ASG)	Seventheen ERGA Profile (ERGA)	Sixtheen ERGA Profile (ERGA)	
	<b>Created:</b> Thu, 20 Jul 2023 23:38	Created: Thu, 20 Jul 2023 09:30	<b>Created:</b> Thu, 29 Jun 2023 13:02	Created: Thu, 29 Jun 2023 10:49	
	Description: This is the eighteen ERGA profile to be created.	Description: This is the fifth ASG profile to be created.	Description: This is the seventheen profile to be created	Description: This is the sixtheen ERGA profile to be created.	Profile Types Legend
	View more				• ERGA
					🔁 ASG 🔹
	Actions  Components	Actions • Components •	Actions • Components •	Actions • Components •	

Fig. 3: COPO Profile: Profile record has been updated. Wait 3 seconds for the web page to be automatically reloaded.

# **19.1 Deleting Profiles**

Note:

- Deleting a profile will **not** delete the associated COPO user account. The user account will still be able to log into the system.
- Only profiles that have no associated research objects such as samples, reads, assemblies or files etc. can be deleted.
- If you need to have a profile deleted that has associated research objects, please contact the .

To delete a profile, click the  $\cdot$  icon that is associated with the desired profile. The option to edit or delete a profile record will be displayed once clicked.

Seventheen ERGA Profile (ERGA)	🕼 Edit	Delete GA)
<b>Created:</b> Thu, 29 Jun 2023 13:02		Delete record
<b>Description:</b> This is the seventheen profile to be created		
Actions • Components •		

Fig. 4: COPO Profile: Click the Delete button

Delete Profile
<b>Are you sure that you would like this profile to be deleted?</b> You <b>would not</b> be able to retrieve the profile after it has been deleted.
Cancel Confirm

Fig. 5: COPO Profile: A confirmation dialog will appear. Click the Confirm button to confirm the deletion.

Profile deletion - error										
Profile couldn't be removed. Only profiles that have no dataf can be deleted.	iles or sample	es associated								
Please contact <u>EI.COPO@earlham.ac.uk</u> if you would like this	profile to be d	eleted.								
	Cancel	Confirm								

Fig. 6: COPO Profile: An error will occur if you try to remove a profile that that has associated samples or datafiles.

Profile deleted	×
Profile has been deleted. Web page will reload in 3 seconds.	
You <b>would not</b> be able to retrieve the profile after it has been	n deleted.
	Cancel Confirm

Fig. 7: COPO Profile: Profile record has been deleted. Wait 3 seconds for the web page to be automatically reloaded.

## CHAPTER

## TWENTY

## **UPDATING SAMPLES**

Samples can be updated by reuploading/resubmitting the manifest that was used to create them with the amended changes **before** or **after** the samples have been accepted by a sample manager and submitted to ENA (European Nucleotide Archive)<sup>1</sup>.

Please note that not all field values of existing samples can be updated via the manifest resubmission update method. The fields that can be updated with that method are listed below. Those fields are known as *non-compliance fields* while the fields that are not listed or cannot be updated are known as *compliance fields*<sup>2</sup>.

See the *How to Download Submitted Sample Manifest* section for guidelines about how to download a manifest that was already submitted.

**Hint:** To view a list of fields that can be updated for a particular project, collapse the list of fields by clicking the button below.

**Important:** The amended manifest or updated spreadsheet file **must** be uploaded to the same profile that was initially used to upload the manifest (before any modifications were done).

An error will occur if you perform one of the following actions:

- Upload the amended manifest to a different profile<sup>3</sup> (other than the one used to upload the manifest to initially)
- Upload the amended manifest to a new profile
- · Delete a profile that already has samples associated with it

Note:

- The manifest must be uploaded again with the amendments included for the change or update to occur.
- You **cannot** reupload a manifest with some of the existing samples removed. The removed samples (from the reuploaded manifest) will not be automatically removed from the manifest sample record. If you would like existing samples to be removed or deleted from the manifest record, please contact for assistance detailing the profile title and reason for the removal.
- Fields are also referred to as columns in the manifest.

<sup>&</sup>lt;sup>1</sup> See term: *ENA*.

<sup>&</sup>lt;sup>2</sup> See term: *Compliance field*.

<sup>&</sup>lt;sup>3</sup> Also known as COPO profile. See term: *COPO profile*.

- BARCODE HUB
- BARCODE\_PLATE\_PRESERVATIVE
- COLLECTOR SAMPLE ID
- CULTURE\_OR\_STRAIN\_ID
- DATE\_OF\_PRESERVATION
- DEPTH
- DIFFICULT OR HIGH PRIORITY SAMPLE
- ELEVATION
- HAZARD GROUP
- IDENTIFIED\_BY
- IDENTIFIED\_HOW
- IDENTIFIER\_AFFILIATION
- INFRASPECIFIC\_EPITHET
- LIFESTAGE
- PARTNER\_SAMPLE\_ID
- BARCODE\_HUB
- BARCODE PLATE PRESERVATIVE
- COLLECTOR\_SAMPLE\_ID
- CULTURE\_OR\_STRAIN\_ID
- DATE\_OF\_PRESERVATION
- DEPTH
- DIFFICULT\_OR\_HIGH\_PRIORITY\_SAMPLE
- ELEVATION
- GAL SAMPLE ID
- HAZARD GROUP
- IDENTIFIED\_BY
- IDENTIFIED\_HOW
- IDENTIFIER\_AFFILIATION
- INFRASPECIFIC\_EPITHET
- LIFESTAGE
- ASSOCI-
- ATED\_TRADITIONAL\_KNOWLEDGE\_CONTACT
- ASSOCI-
- ATED\_TRADITIONAL\_KNOWLEDGE\_OR\_BIOCULTURIAEVARIOUNCT\_ID ASSOCI-
- ATED\_TRADITIONAL\_KNOWLEDGE\_OR\_BIOCULTURAHLGSCHERSMARPLEICEBABME
- BARCODE HUB
- BARCODING\_STATUS
- BARCODE\_PLATE\_PRESERVATIVE
- BIOBANKED\_TISSUE\_PRESERVATIVE
- COLLECTED BY
- COLLECTION\_LOCATION
- COLLECTOR\_AFFILIATION
- COLLECTOR\_SAMPLE\_ID
- COMMON\_NAME
- CULTURE\_OR\_STRAIN\_ID
- DATE\_OF\_COLLECTION
- DATE\_OF\_PRESERVATION
- DECIMAL\_LATITUDE
- DECIMAL\_LONGITUDE
- DEPTH

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DESCRIPTION\_OF\_COLLECTION\_METHOD

- PLATE ID FOR BARCODING
- PRESERVED BY
- PRESERVER AFFILIATION
- PURPOSE\_OF\_SPECIMEN
- RELATIONSHIP
- SEX
- SIZE OF TISSUE IN TUBE
- SPECIMEN\_ID\_RISK
- TIME\_ELAPSED\_FROM\_COLLECTION\_TO\_PRESERVATION TIME\_OF\_COLLECTION
- TISSUE\_FOR\_BARCODING
- TISSUE\_REMOVED\_FOR\_BARCODING
- TUBE\_OR\_WELL\_ID\_FOR\_BARCODING
- VOUCHER\_ID
- PLATE\_ID\_FOR\_BARCODING
- PRESERVED BY
- PRESERVER\_AFFILIATION
- PURPOSE OF SPECIMEN
- RELATIONSHIP
- SEX
- SIZE\_OF\_TISSUE\_IN\_TUBE
- SPECIMEN IDENTITY RISK
- - TIME ELAPSED FROM COLLECTION TO PRESERVATION
- TIME\_OF\_COLLECTION
- TISSUE\_FOR\_BARCODING
- TISSUE\_REMOVED\_FOR\_BARCODING
- TUBE\_OR\_WELL\_ID\_FOR\_BARCODING
- VOUCHER\_ID
- DIFFICULT\_OR\_HIGH\_PRIORITY\_SAMPLE
- DNA\_REMOVED\_FOR\_BIOBANKING
- DNA VOUCHER ID FOR BIOBANKING
- - ETHICS PERMITS DEF
  - - ETHICS\_PERMITS\_REQUIRED
    - FAMILY
    - GAL
    - GAL\_SAMPLE\_ID
    - GENUS
    - GRID\_REFERENCE
    - HABITAT
    - HAZARD\_GROUP
    - IDENTIFIED BY
    - IDENTIFIED\_HOW
    - IDENTIFIER\_AFFILIATION
    - IDENTIFIER\_AFFILIATION

• INDIGENOUS RIGHTS DEF

INDIGENOUS\_RIGHTS\_DEF

• INFRASPECIFIC\_EPITHET

INDIGENOUS\_RIGHTS\_APPLICABLE

**Chapter 20. Updating Samples** 

- LIFESTAGE
- NAGOYA\_PERMITS\_DEF
- NAGOYA PERMITS FILENAME
- NAGOYA\_PERMITS\_REQUIRED
- ORDER OR GROUP
- ORGANISM PART
- ORIGINAL COLLECTION DATE
- ORIGINAL\_GEOGRAPHIC\_LOCATION
- OTHER INFORMATION
- PRESERVATION\_APPROACH
- PRESERVATIVE\_SOLUTION
- PRESERVED\_BY
- PRESERVER AFFILIATION
- - PROXY\_TISSUE\_VOUCHER\_ID\_FOR\_BIOBANKING• TISSUE\_REMOVED\_FOR\_BARCODING
- PROXY\_VOUCHER\_ID
- PROXY\_VOUCHER\_LINK
- PURPOSE OF SPECIMEN
- REGULATORY COMPLIANCE
- RELATIONSHIP
- SAMPLE COORDINATOR
- SAMPLE\_COORDINATOR\_AFFILIATION

- SAMPLE COORDINATOR ORCID ID
- SAMPLING\_PERMITS\_FILENAME
- SAMPLING PERMITS REQUIRED
- SCIENTIFIC NAME
- SEX
- SIZE OF TISSUE IN TUBE
- SPECIMEN IDENTITY RISK
- TAXON ID
- TAXON REMARKS
- TIME\_ELAPSED\_FROM\_COLLECTION\_TO\_PRESERVATION
- TIME\_OF\_COLLECTION
- TISSUE FOR BARCODING
- TISSUE\_FOR\_BIOBANKING
- TISSUE\_REMOVED\_FOR\_BIOBANKING
- TISSUE\_REMOVED\_FROM\_BARCODING
- TISSUE VOUCHER ID FOR BIOBANKING
- TUBE\_OR\_WELL\_ID\_FOR\_BARCODING
- VOUCHER ID
- VOUCHER\_INSTITUTION
- VOUCHER LINK

CHAPTER

## TWENTYONE

# **UPDATING SEQUENCE ANNOTATIONS**

This section describes how to update **Sequence Annotations**<sup>1</sup>. The **Sequence Annotations** update process is similar to the **Sequence Annotations** submission process. Therefore, please refer to the *Sequence Annotations Submission* section for more information.

#### Note:

• Sequence Annotations must be uploaded before they can be updated.

#### See also:

- How to Submit Sequence Annotations
- How to Delete Sequence Annotations
- 1. Click the desired sequence annotation from the table of uploaded sequence annotations to highlight it.

Then, click the **Edit** button to update or edit the annotation as shown below:

<b>≜COPO</b>		🜲 🖉 🔁 🤁 🕏 tester1 -
Profile: EI Standalone Profile Sequence Annotations	(	info         Info
Showing 1 to 1 of 1 records 1 record selected		I Deter i Submi
STUDY	TLE	SUBMISSION ERROR
O         PRJEB68229         ERS27581995         Test	st Annotations Cafeteria_transcriptome_1.fasta.gz	
show 10 v records	Pre	vious 1 Next

Fig. 1: Sequence Annotations' update: Click 'Edit' button after having clicked the desired sequence annotation

- 2. An Add Sequence Annotation dialogue is displayed. Provide the updated details then, click the Submit Annotation button.
- 3. The updated sequence annotation(s) will be displayed on the **Sequence Annotations** web page after a successful update.

<sup>&</sup>lt;sup>1</sup> See: Sequence Annotation.

Submit annotation				
Ipload annotation files and fill in metada NA and have uploaded samples and rea				
STUDY*				
PRJEB68229				
SAMPLE*				
ERS27581995			~	
RUN				
ERR12208020				
EXPERIMENT				
ERX11618893				
Test Annotations DESCRIPTION				
This sequence annotation desc in the protein sequence namely modifications and binding sites	/ post-			
FILE*		TYPE*		
Cafeteria_transcriptome_1.fast	a.( ~	fasta	~	
FILE*		TYPE*		
None	~	None	~	
FILE*		TYPE*		
None	~	None	~	
FILE*		TYPE*		
None	~	None	~	

Fig. 2: Sequence Annotations' update: 'Submit Annotation' dialogue with updated information

**Hint:** Sequence annotation records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful automatic submission.

⊉co																A S O Otester1 ~
	I Standalone	ns 🕐								đ	÷	•		2	ζ	Annotation submission has been scheduled, you will be notified X when it is complete
						Select all Select filtered Clear selection	Expor		e De	lete i	Submit Anno1	_				
Showing 1	to 1 of 1 records	Click 😝 beside a	record to	view extra details												
	STUDY 🕴	SAMPLE \$	RUN 🔅	EXPERIMENT \$	TITLE \$			FILES &	AC	CESSION		UBM	IISSIOI R	N		
0	PRJEB68229	ERS27581995			Test Annotations	This sequence annotation describes sites of interest in the protein sequence namely post- translational modifications and binding sites.		Cafeteria_transcriptome_1.fasta.gz								
show 10	~ records															
									Pr	evious	1	Next				

Fig. 3: Sequence Annotations' update: Sequence Annotations' web page displaying the (pending) updated sequence annotation(s)

<b>≜cc</b>	PO																•	8	M	0	🗢 tes	ster1 +
Profile: E	I Standalone I	Profile								<u>њ</u>				z	Info							
Sequen	ce Annotatio	ins 👩 🕻	F)							-				-								
						Select all Select filtered Clear selection Exp	xport (		🔒 Delete	<b>i s</b> ience A	ubmit nnotal											
Showing 1	to 1 of 1 records	Click 🚯 beside	a record to	view extra details																		
	STUDY 🔅	SAMPLE \$	RUN \$	EXPERIMENT \$	TITLE \$		-	FILES ÷	ACC	SSION		UBM RROF	ISSIOI R	N ș								
•	PRJEB68229	ERS27581995			Test Annotations	This sequence annotation describes sites of interest in the protein sequence namely post- translational modifications and binding sites.	(	Cafeteria_transcriptome_1.fasta.gz														
show 10	~ records								Previ	ous 1	Ne	ext										

Sequence Annotations' update: Sequence Annotations' web page displaying the updated sequence annotation(s) after it has been submitted

# CHAPTER

## TWENTYTWO

# **UPDATING READS**

This section describes how to update **Reads** for a given checklist. The **Reads** update process is similar to the **Reads** submission process. Therefore, please refer to the *Reads Submission* section for more information.

#### Note:

• Reads must be uploaded before they can be updated.

#### See also:

- How to Submit Reads
- Explore Various Types of Reads Checklist
- How to Submit Files
- 1. On the **Reads'** web page, click the checklist dropdown then, choose a desired checklist from the list of available checklists that you would like to update a **Reads** for.

**Note:** The colour of the button is based on the type of profile that you are updating a Reads for.

See the *Profile Types Legend* section regarding the colour code for the various types of project profiles on COPO.

	ofile										a 6-	
Reads ERC000046 : Pan Prostate sample checklist					🔍 ( 🖿 🛃							
								K				
				s	elect all	Select filtered	Clear selection	Export CSV		ubmit		
										Search Read		
nowing 1 to 2 of 2 records Clic	k 🔂 beside a reco	rd to view ext	ra details									
project sequencing				sample	PPCG	PPCG					Instrument	Library
name sequencing method	subject_id 🕴	gender ≑	phenotype 🍦	type	ID ÷	sample 👙 ID	Pipeline/UUID 🔅	preservation 🔅	xenograft 🍦	Sample 🍦	model	name ÷
	erererewr	female	dfdsf	bone metastases	dfdfd	DNA	dferererer	Fresh Frozen	No	xyzA3	GridION	abccc

Fig. 1: Reads' update: Click 'Add Reads' from Spreadsheet' button to upload an amended reads manifest

2. An **Upload Read Manifest** dialogue is displayed. Click the <sup>Upload Read Manifest</sup> button to choose an updated file from your local system.

The uploaded manifest is shown in a table in the Upload Read Manifest dialogue as shown below. Click the

button to complete the update process of the reads manifest.

Upload I	Upload Read Manifest X						
for E cheo	ENA Reads Manifest Validation for ERC000046 : Pan Prostate sample checklist Upload a completed manifest for validation						
Sprea	Spreadsheet is valid						
Show 10 v entries Search:							
CG nple	Pipeline/UUID	Sample	gender	phenotype	preservation		
١A	dferererer	xyzA3	female	dfdsf	Fresh Frozen		
JA	dfdsfdsf	xyzB3	female	dfdsf	Fresh Never Frozen		
Showing	Showing 1 to 2 of 2 entries Previous 1 Next						
Upload Read Manifest Finish Close							

### Fig. 2: Reads' update: 'Upload Read Manifest' dialogue with updated manifest

3. The update read(s) will be displayed on the **Reads** web page after a successful update.

**Hint:** Reads records that are highlighted **yellow** indicate that the records are pending submission. The records will be highlighted **green** after a successful submission.

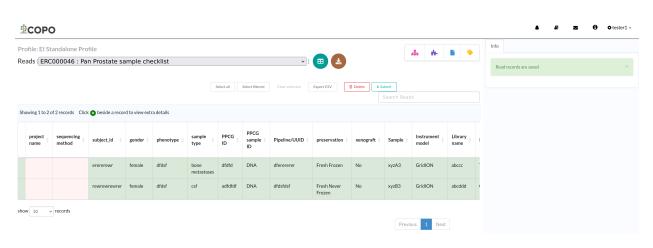


Fig. 3: Reads' update: Reads' web page displaying the updated read(s)

CHAPTER

# TWENTYTHREE

# ADDING CHILDREN PROJECTS TO PARENT PROJECTS

# 23.1 In COPO

See *Choose associated profile type(s)* section when creating a profile for more details.

# 23.2 In Public Repositories

Please contact the if you would like child projects (subprojects) to be added to parent (main) projects in public repositories like ENA<sup>1</sup> or NCBI<sup>2</sup>.

Please provide the parent project accession and the child project accession(s) when making the email request.

<sup>&</sup>lt;sup>1</sup> See term: *ENA*.

<sup>&</sup>lt;sup>2</sup> See term: *NCBI*.

CHAPTER TWENTYFOUR

# DOWNLOADING MANIFEST TEMPLATES & STANDARD OPERATING PROCEDURES (SOPS)

In COPO, manifests refer to Microsoft Excel spreadsheets that are used to record metadata about a biological research.

## 24.1 Downloading Manifest Templates

Blank manifest templates are available for download below or on the Manifests web page.

In addition, click the <sup>1</sup> button located on the COPO **Samples** web page to download a manifest template. See samples-component component for more details about accessing the **Samples** web page.

ASG manifest template<sup>1</sup> DToL manifest template<sup>2</sup> ERGA manifest template<sup>3</sup> Barcoding manifest template (within Tree of Life profiles) Reads manifest template (within Tree of Life profiles)

Note:

- The manifest templates for reads within Stand-alone profiles are available for download on the **Reads web page** for those profiles. See *Reads Submission* section for more details.
- Barcoding manifest templates are available for download on the Barcoding manifest web page. See *Barcoding Manifest Submission* section for more details.

<sup>&</sup>lt;sup>1</sup> See term: ASG (Aquatic Symbiosis Genomics).

<sup>&</sup>lt;sup>2</sup> See term: *DToL* (*Darwin Tree of Life*).

<sup>&</sup>lt;sup>3</sup> See term: ERGA (European Reference Genome Atlas).

# 24.2 Recording Data in Manifests

Each manifest follow a manual known as *Standard Operating Procedure*  $(SOP)^4$  which provides a detailed guidance on how to record metadata in the manifest.

The SOP for the various manifests are available below.

In addition, click the <sup>1</sup> button located on the COPO **Samples** web page to download the SOP. See samplescomponent component for more details about accessing the **Samples** web page.

## 24.2.1 ASG SOP

This follows most of the instructions outlined in the DToL SOP, with some minor changes and omissions.

ASG SOP

ASG Project

## 24.2.2 DToL (Darwin Tree of Life) SOP

DToL SOP DToL SOP GitHub repository DToL Project

## 24.2.3 DToL\_ENV (Darwin Tree of Life Environmental Samples) SOP

This will be made available soon.

## 24.2.4 ERGA SOP

ERGA SOP ERGA SOP GitHub repository

## 24.2.5 POP\_GENOMICS (Population Genomics) SOP

POP\_GENOMICS SOP

ERGA SOP GitHub repository

See also:

• Using manifest wizard to prefill manifests

<sup>&</sup>lt;sup>4</sup> See term: *SOP*.

# CHAPTER TWENTYFIVE

# **USING COPO API**

The COPO API is a RESTful website service that allows users to interact with the COPO system. The API is built using the Django REST (REpresentational State Transfer)<sup>1</sup> Framework.

	Servers	
<b>Hint:</b> The button,	/api - Current Website Server 🗸	, indicates that the API method endpoints will produce results
· · · · · · · · · · · · · · · · · · ·		· 1 1
from the website ho	st server i.e. if the live COPO web	site is used to query the endpoint, then, the live results will be

retrieved while the opposite occurs if one uses the demo website to query the API method endpoints.

# 25.1 API End-points

The COPO API (Application Programming Interface)<sup>2</sup> comprises manifest, sample, statistics and profile endpoints. Their results are available for download in csv, json or ro-crate<sup>3</sup> file formats depending on the record type as shown in the table below.

Each endpoint results contain metadata provided by the submitter.

Table 1: Available Result Formats for Records				
File Format	Available Record Types			
csv	Study, Sample, Manifest			
json	Study, Sample, Manifest			
ro-crate	Sample			

Note: The live COPO website API endpoints are used in the examples below.

To use the demo website API endpoints, replace https://copo-project.org/api/ with https://demo. copo-project.org/api/ in the examples below.

<sup>&</sup>lt;sup>1</sup> See term: *REST* 

<sup>&</sup>lt;sup>2</sup> See term: *API* 

<sup>&</sup>lt;sup>3</sup> See term: *RO-Crate* 

## 25.1.1 Audit Endpoints

## Fetch Sample Updates Between Dates

```
https://copo-project.org/api/audit/sample/{from}/{to}
```

OR

\$ curl -X GET "https://copo-project.org/api/audit/sample/{from}/{to}" -H "accept:\_ →application/json"

This results in a list of sample updates that occurred between a given date period.

## Fetch Sample Updates by Manifest ID

https://copo-project.org/api/audit/sample/manifest\_id/{manifest\_id}

OR

This results in a list of sample updates by manifest IDs (Identifications)<sup>4</sup>.

## Fetch Sample Updates by COPO ID

https://copo-project.org/api/audit/sample/{copo\_id}

OR

\$ curl -X GET "https://copo-project.org/api/audit/sample/copo\_id/{copo\_id}" -H "accept:\_ →application/json"

This results in a list of sample updates based on {copo\_id}.

## Fetch Sample Updates by Update Type

https://copo-project.org/api/audit/sample/update\_type/{update\_type}

OR

This results in a list of sample updates based who performed the update. The update\_type can be system or user.

A **system** update occurs when the update was performed by COPO while a **user** update occurs when a user reuploads a manifest with amended sample metadata.

Please note that not all sample information that has been uploaded already can be updated when the manifest is reuploaded. Only fields that are updatable are updated when a manifest is reuploaded.

<sup>&</sup>lt;sup>4</sup> See term: *Manifest ID* 

See the Updating Samples section for more information as well as the Fetch updatable fields by project API method.

## Fetch Sample Updates by Field and Field Value

https://copo-project.org/api/audit/sample/{field}/{field\_value}

## OR

\$ curl -X GET "https://copo-project.org/api/audit/sample/{field}/{field\_value}" -H
\$
\$ -# accept: application/json"

This results in a list of sample updates based on a sample field value and one of the following sample fields:

- RACK\_OR\_PLATE\_ID
- SPECIMEN\_ID
- TUBE\_OR\_WELL\_ID
- biosampleAccession
- public\_name
- sraAccession

## Fetch Sample Updates by ASG Sample Type

https://copo-project.org/api/audit/sample/asg

OR

This results in a list of updates for ASG<sup>8</sup>. sample types.

## Fetch Sample Updates by DTOL Sample Type

https://copo-project.org/api/audit/sample/dtol

OR

This results in a list of updates for DToL<sup>9</sup>. sample types.

<sup>8</sup> See term: *DToL* 

<sup>9</sup> See term: *ENA* 

## Fetch Sample Updates by ERGA Sample Type

#### https://copo-project.org/api/audit/sample/erga

OR

This results in a list of updates for ERGA<sup>10</sup>. sample types.

## 25.1.2 Manifest Endpoints

### **Fetch Manifests**

https://copo-project.org/api/manifest

OR

\$ curl -X GET "https://copo-project.org/api/manifest" -H "accept: application/json"

This results in a list of all manifest IDs<sup>Page 128, 4</sup>. The manifest identification can be used to retrieve records in the other endpoints.

#### **Fetch Current Manifest Versions**

https://copo-project.org/api/manifest/current\_version

OR

\$ curl -X GET "https://copo-project.org/api/manifest/current\_version" -H "accept:\_ →application/json"

This displays the current or latest manifest version of each manifest project brokered through COPO.

## Fetch Sample Records by Manifest ID

https://copo-project.org/api/manifest/{manifest\_id}

OR

\$ curl -X GET "https://copo-project.org/api/manifest/{manifest\_id}" -H "accept:\_ →application/json"

This results in a list of sample records for the given manifest IDs<sup>Page 128, 4</sup>.

<sup>&</sup>lt;sup>10</sup> See term: Sample manager

### Fetch Manifests between Dates

https://copo-project.org/api/manifest/{from}/{to}

OR

\$ curl -X GET "https://copo-project.org/api/manifest/{from}/{to}" -H "accept:\_ →application/json"

This results in a list of all manifest IDs<sup>Page 128, 4</sup> recorded in the given date period.

### Fetch Manifests between Dates for a Project

https://copo-project.org/api/manifest/{project}/{from}/{to}

OR

\$ curl -X GET "https://copo-project.org/api/manifest/{project}/{from}/{to}" -H "accept:\_ →application/json"

This results in a list of all manifest IDs<sup>Page 128, 4</sup> recorded in the given date period for a given project.

### Fetch Sample Record Status in a Manifest

https://copo-project.org/api/manifest/{manifest\_id}/sample\_statuses

OR

This results in minimal sample status information for each sample contained in the given {manifest\_id}.

## Validate Manifest by Profile ID

**Note:** Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

https://copo-project.org/api/manifest/validate

This results in the ID of the validation report to be queried.

## Validate Manifest by Report ID

**Note:** Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

https://copo-project.org/api/manifest/validate/report/

OR

This gives the status and/or validation errors for a manifest based on the manifest report ID.

### Validate Manifest

**Note:** Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

https://copo-project.org/api/apiKey

https://copo-project.org/api/manifest/validations

OR

\$ curl -X POST "https://copo-project.org/api/manifest/validations/" -H "accept: \*/\*" -d
\_\_""

This checks whether a given manifest passes or fails validation for the authorised user.

## 25.1.3 Sample Endpoints

#### **Fetch Sample Records by Project**

```
https://copo-project.org/api/sample/{project}
```

OR

This results in a list of all the samples of a project in COPO.

### Fetch Sample Records by Associated Project Type

**Hint:** The associated project type is the project type that the sample is subproject of. For example, a sample may be associated with a project type of "BGE" but the sample itself may be an "ERGA" sample.

In sample records, the associated project type is referred to as **associated\_tol\_project** whereas in profile records, it is referred to as **associated\_type**.

https://copo-project.org/api/sample/associated\_tol\_project/{values}

OR

This results in a list of all sample records of a given associated project type(s) in COPO.

#### Fetch Sample Records between Dates

https://copo-project.org/api/sample/project/manifest\_version/fields

OR

\$ curl -X GET "https://copo-project.org/api/sample/project/manifest\_version/fields}" -H
\$
\$
"accept: application/json"

This results in a list of fields of a project for a given manifest version.

### Fetch Sample Records between Dates

https://copo-project.org/api/sample/{from}/{to}

OR

This results in a list of all samples recorded in the given date period.

### Fetch Updatable Fields by Project

https://copo-project.org/api/sample/updatable\_fields/{project}

OR

This results in list of fields that can be updated when a manifest is reuploaded/resubmitted in COPO based on the given {project}`.

## Fetch Sample Records by COPO ID

### Hint:

- Sample records IDs are referred to as copo\_id in COPO and alias in ENA.
- Multiple copo\_id can be provided as a comma separated list in this endpoint.

https://copo-project.org/api/sample/copo\_id/{copo\_ids}

OR

\$ curl -X GET "https://copo-project.org/api/sample/copo\_id/{copo\_ids}" -H "accept:\_ application/json"

This results in full sample information for the sample records returned from the given {copo\_ids}.

## Fetch Sample Records by Biosample ID

#### Note:

- Biosample accession IDs are assigned to sample records by ENA<sup>Page 129, 9</sup> after the samples have been approved by a sample manager<sup>Page 130, 10</sup>.
- The biosample\_id is referred to as biosampleAccession in COPO and biosample\_id in ENA.

https://copo-project.org/api/sample/biosample\_id/{biosample\_ids}

OR

This results in full sample information for the sample records returned from the given {biosample\_ids}.

#### Fetch Sample Records by Field and Values

#### Hint:

• Multiple values can be provided as a comma separated list in this endpoint.

https://copo-project.org/api/sample/sample\_field/{field}/{values}

OR

This results in full sample information for the sample records returned from the given {field}/{values}.

### Fetch Study Records by Sample ID

### Hint:

• Multiple sample\_ids can be provided as a comma separated list in this endpoint.

https://copo-project.org/api/sample/StudyFromSampleAccession/{sample\_ids}

OR

This results in full sample information for the sample records returned from the given {sample\_ids}.

### Fetch Sample Records by Study ID

#### Hint:

Multiple biostudyAccessions can be provided as a comma separated list in this endpoint.

https://copo-project.org/api/sample/SampleFromStudyAccession/{biostudyAccessions}

OR

```
$ curl -X GET "https://copo-project.org/api/sample/SampleFromStudyAccession/

$$ {biostudyAccessions}" -H "accept: application/json"
```

This results in full sample information for the sample records returned from the given {biostudyAccessions}.

## 25.1.4 Profile Endpoints

### **Create Profile Record**

**Note:** Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

https://copo-project.org/api/apiKey

https://copo-project.org/api/profile//make\_profile

OR

\$ curl -X POST "https://copo-project.org/api/profile//make\_profile" -H "accept: \*/\*" -d
\_\_\_\_""

This creates a profile record for the authenticated user.

## **Fetch Profile Records**

**Note:** Authentication is required in order to use this API method. Obtain an API token from the following endpoint before using this method:

https://copo-project.org/api/apiKey

https://copo-project.org/api/profile/get\_for\_user

OR

\$ curl -X POST "https://copo-project.org/api/profile/get\_for\_user" -H "accept: \*/\*" -d "
\_\_\_\_"

This results in a list of all profiles for the authenticated user.

## 25.1.5 Statistics' Endpoints

## Fetch Number of COPO Users

https://copo-project.org/api/stats/number\_of\_users

OR

\$ curl -X GET "https://copo-project.org/api/stats/number\_of\_users" -H "accept:\_ →application/json"

This results in the total number of registered users in COPO.

### Fetch Number of Sample Records by Sample Type

https://copo-project.org/api/stats/number\_of\_samples/{sample\_type}

OR

This results in the total number of registered sample records in COPO by a given sample type.

## Fetch Tree of Life (ToL) Projects Brokered by COPO

```
https://copo-project.org/api/stats/tol_projects
```

OR

This results in a list of all main/primary projects brokered by COPO.

## Fetch Associated Tree of Life (ToL) Projects Brokered by COPO

```
https://copo-project.org/api/stats/associated_tol_projects
```

OR

\$ curl -X GET "https://copo-project.org/api/stats/associated\_tol\_projects" -H "accept:\_ →application/json"

This results in a list of all child projects/ subprojects brokered by COPO.

CHAPTER TWENTYSIX

# **EXPLORING MANIFEST WIZARD**

The manifest wizard is a tool to help you populate a manifest with common data values. It is a simple wizard that will ask a few questions then, generate the manifest file for you.

The manifest wizard can be accessed via the **Prefilled template** download dropdown menu option on the Manifests web page.

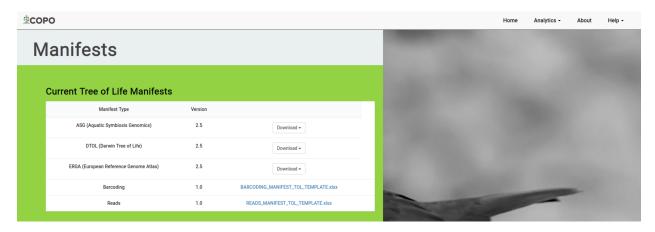


Fig. 1: Manifests web page: Tabular information for various manifest types and their current versions

PO					Home	Analytics -	About	н
lanifests				100000000000000000000000000000000000000				
lannests								
Current Tree of Life Manifests								
Manifest Type	Version							
ASG (Aquatic Symbiosis Genomics)	2.5	Download -						
DTOL (Darwin Tree of Life)	2.5	Download +						
	2.5	Blank template						
ERGA (European Reference Genome Atlas)								
ERGA (European Reference Genome Atlas)		Prefilled template		and the second se				
EKGA (European kererence Genome Attas) Barcoding	1.0	Prefilled template Standard Operating Procedure (SOP)	EMPLATE.xlsx					

Fig. 2: Manifests web page: Manifest download template options - Blank template and Prefilled template with option to download, Standard Operating Procedure (SOP)

Blank manifest templates can be downloaded via the **Blank template** dropdown menu option or from the *Download Manifest Templates* section.

# 26.1 Prefill Manifests

1. Navigate to the Manifests web page. Then, click the Prefilled template option from the dropdown menu.

PO			Home	e Analytics -	About	Help
/lanifests						
Oursel Trace of Life Marifactor		Carlo and				
Current Tree of Life Manifests Manifest Type	Version					
ASG (Aquatic Symbiosis Genomics)	2.5	Download -				
DTOL (Darwin Tree of Life)	2.5	Download -				
ERGA (European Reference Genome Atlas)	2.5	Blank template Prefiled template				
Barcoding	1.0	Standard Operating Procedure (S Launch DTOL_MANIFEST_v2.5 wizard			-	

## Fig. 3: Manifests web page: Click 'Prefilled template' dropdown menu option

2. In the **Tree of Life Manifest Wizard** displayed, enter the number samples that you would like to describe then, input a common value for a field by selecting the field name from the dropdown list.

**Note:** The manifest wizard will only display fields that are associated with the type of manifest that you would like to prefill.

Once you have inputted a value for a common field, that value will be prefilled according to the number of samples that you have inputted.

- 3. Click the  $\xrightarrow{\text{Next}}$  to proceed to the next step of the manifest wizard.
- 4. Click the button to download the prefilled manifest file.
- 5. Preview of downloaded manifest with prefilled metadata

## See also:

- Standard Operating Procedure (SOP) guidelines for manifests
- Download Manifest Templates

Tree of Life Manifest Wizar	rd
Samples 2 Download	2 Reset Next
low many samples would you like to describe?	
1	\$
are there common values for these fields? <b>O</b>	
	~

Fig. 4: Manifests web page: Tree of Life Manifest wizard

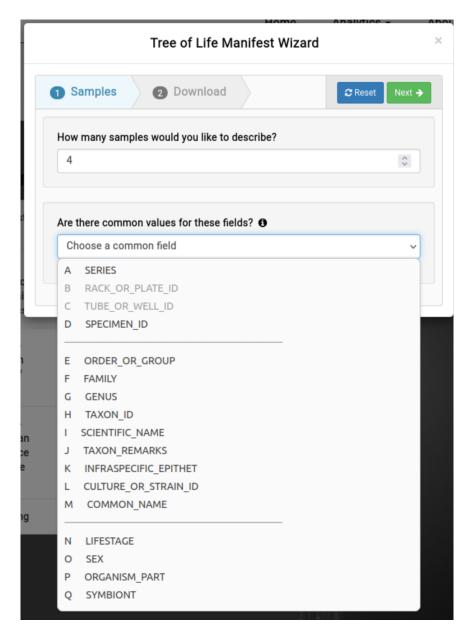


Fig. 5: Tree of Life Manifest wizard: Common field dropdown menu

Tree	of Life Manifest Wizard		
1 Samples 2	Download	<b>₽</b> Reset	Next 🗲
How many samples would	d you like to describe?		
4			\$
Are there common values Choose a common field	_		~
ORDER_OR_GROUP	Lepidoptera	<b>D</b>	
FAMILY	Lyonetiidae	Đ	
GENUS	Lyonetia	圃	
TAXON_ID	753195	Đ	
SCIENTIFIC_NAME	Lyonetia clerkella	Ē	
LIFESTAGE	ADULT	<ul> <li>✓ ÎII</li> </ul>	

Fig. 6: Tree of Life Manifest wizard: Inputted common field values

Tree of Life Manifest Wizard	х Х
1 Samples 2 Download	← Prev Finish
The manifest template is ready to be generated finish button to generate it.	I. Click the

Fig. 7: Tree of Life Manifest wizard: Download prefilled manifest by clicking the 'Finish' button

								DTO	DL_MANIFEST	TEMPLATE_v2.	4.1.xlsx - Lit	oreOffice Calc					
le Edit Vie	w Insert For	mat Style	s Sheet	Data	Tools	Window	Help										
• 🗖 • 🖻	- 🖸 🖶	R X	D 🖻 1	<u> </u>			<u>a</u> /		<u>₩</u> - ↓ <sub>↑</sub> ‡	. 🗤 🖓 屋	11 🕄	Ω • 😤 🗔	🗆 🗋 🖬 = 🖽	1.			
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A	В			с			D		Е	F	G	н			К		
SERIES	RACK_OR_P	ATE_ID	TUBE_C	DR_WE	LL_ID	SPECI	MEN_ID	ORDER	_OR_GROUP	FAMILY	GENUS	TAXON_ID	SCIENTIFIC_NAME	TAXON_REMARKS	INFRASPECIFIC	EPITHET	
								Lepidopt	era	Lyonetiidae	Lyonetia	753195	Lyonetia clerkella				
								Lepidopt	era	Lyonetiidae			Lyonetia clerkella				
								Lepidopt	era	Lyonetiidae	Lyonetia	753195	Lyonetia clerkella			U	
								Lepidopt	era	Lyonetiidae	Lyonetia	753195	Lyonetia clerkella				P.
K4 MH →	🔒 Metadata E	e de la compañía de	a Validation		an ison Darah (	Seficitions											
	💦 Metadata E	ntry Dat	a vaudation	Orga	anismParci	Definitions											
					- C	and Die	alan 🗆 M	atch Case									

Fig. 8: Tree of Life Manifest wizard: Prefilled manifest

# CHAPTER TWENTYSEVEN

# TREE OF LIFE DASHBOARD

The Tree of Life (ToL) dashboard can be explored on the Tol dashboard web page .

Note: Few information will be displayed on the Tree of Life dashboard if you are not logged into COPO.

## Hint:

- The Tree of Life dashboard provides an overview of COPO statistics, abbr:*ToL*(*Tree of Life*)<sup>1</sup> inspection, manifest submission and world map of Genome Acquisition Labs (GAL)s and partners.
- Click a card item on the dashboard to explore the data further.
- Click a map location on the world map to view more details about a GAL or Partner.

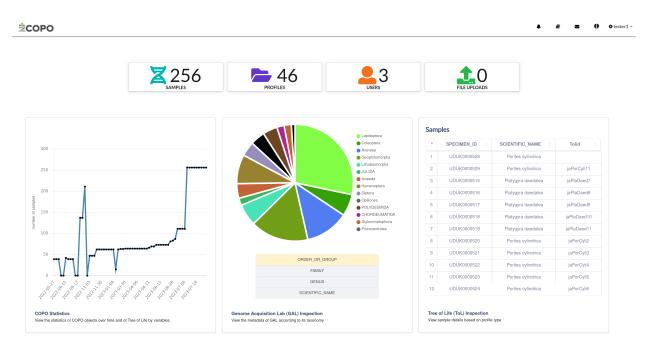
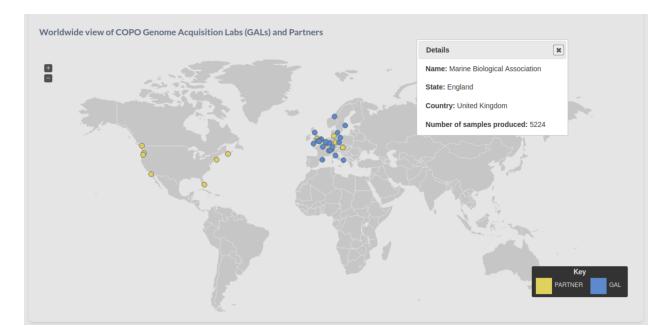


Fig. 1: ToL Dashboard: Overview of COPO statistics and ToL inspection

<sup>&</sup>lt;sup>1</sup> See term: *Tree of Life (ToL)* 



Fig. 2: ToL Dashboard: Geographical location of all GALs and Partners and an overview of manifest submissions



## Fig. 3: ToL Dashboard: Popup dialogue with more information about one of the GALs

To view more details about a GAL or Partner, click one of the map locations on the world map. A popup dialogue will be displayed information about the GAL or Partner such as name, state, country, and number of samples produced.

# 27.1 Tree of Life Inspection

A ToL inspection analyses the sample metadata of COPO profile records and facilitates search faceting and data discovery of the results.

ree of Life (ToL) Ins	spection 🕕 🙆		SAMPLES			Statu	s	
						Idie		
ASG DTOL ERGA			Samples					
	Search:		Show 10	~ entries	Show all fields:	] Query in CO	PO record: Search:	
Profile Title	🕴 Date Created 🍦	Number of Samples  🍦	+	SPECIMEN_ID	SCIENTIFIC_NAME		tolid	
ifth ASG Profile	20/07/2023	0	1	UDUK0000528	Porites cylindrica			
ourth ASG Profile	20/04/2023	90	2	UDUK0000529	Porites cylindrica		jaPorCyli11	
'hird ASG Profile	15/04/2023	0	3	UDUK0000515	Platygyra daedalea		jaPlaDaed7	
econd ASG Profile	20/02/2023 05/08/2022	0	4	UDUK0000516	Platygyra daedalea		jaPlaDaed8	
in all AGO I TOILLE	03/00/2022	1.5	5	UDUK0000517	Platygyra daedalea		jaPlaDaed9	
			6	UDUK0000518	Platygyra daedalea		jaPlaDaed10	
			7	UDUK0000519	Platygyra daedalea		jaPlaDaed11	
			8	UDUK0000520	Porites cylindrica		jaPorCyli2	
			9	UDUK0000521	Porites cylindrica		jaPorCyli3	
			10	UDUK0000522	Porites cylindrica		jaPorCyli4	

Fig. 4: Tree of Life (ToL) Inspection web page

# 27.2 Tree of Life Inspection by Genome Acquisition Lab

A ToL inspection by GAL analyses the sample metadata of COPO profile records by GALs<sup>2</sup> based on their taxonomy.

See also:

• COPO statistics section

<sup>&</sup>lt;sup>2</sup> See term: *Genome Acquisition Lab (GAL)*. Also referenced as Partner.

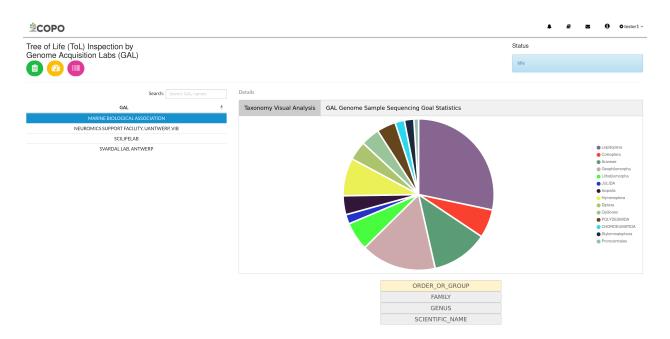


Fig. 5: Tree of Life (ToL) Inspection by Genome Acquisition Lab (GAL) web page

## CHAPTER

# TWENTYEIGHT

# **RETRIEVING ACCESSIONS**

Approved submissions result in accessions being created. The accessions can be explored on the Accessions' dashboard , on the ENA browser<sup>1</sup> or NCBI Biosamples<sup>2</sup> (after they become public).

The types of accessions that are created are:

- Stand-alone submissions
  - Project accessions
  - Experiment accessions
  - Run accessions
  - Read accessions
  - Assembly accessions
  - Sequence annotation accessions
- ToL<sup>Page 149, 3</sup> submissions
  - Biosample accessions
  - SRA accessions
  - Submission accessions

## Note:

• The <sup>(=)</sup> button will only appear on the web page if you are granted permission to be a sample manager.

### See also:

- Stand-alone profile components
- ToL profile components
- Accessions profile component

<sup>&</sup>lt;sup>1</sup> See term: *ENA*.

<sup>&</sup>lt;sup>2</sup> See term: *NCBI*.

<sup>&</sup>lt;sup>3</sup> See term: *Tree of Life (ToL)*.

ccessions							Info		
					ts' Accessions Stand-a	lone Projects' Accessions			
cientific Name 🎍	Specimen ID	Taxon ID ∲	Biosample Accession	Manifest ID		Submission Accession	Filter /		
Acropora aff. formosa JVB	UDUK0000440	2916800	SAMEA130680128	e35fd278-9605-4c22-b67f- b9331ef2aada	ERS15977473	ERA24682572	🗹 ASG 🕻	•	
Acropora aff. formosa FJVB	UDUK0000441	2916800	SAMEA130680129	e35fd278-9605-4c22-b67f- b9331ef2aada	ERS15977474	ERA24682572			
toplectis maculator	MBA-190930-003A	2776046	SAMEA130680124	3899a32e-03bc-4791-acc2- bba9108e35c4	ERS15977469	ERA24682569			
epus europaeus	ERGA_BCE_9858_102	9983	SAMEA130675209	940c7c04-2e8a-48a6- b744-05389650fb5e	ERS15951273	ERA24635733			
.epus timidus	ERGA_BCE_9858_101	62621	SAMEA130675213	940c7c04-2e8a-48a6- b744-05389650fb5e	ERS15951277	ERA24635736			
Tetrastemma	ERGA_FAFA_7377_002	307678	SAMEA130602965	550676fd-0bb3-4b38-	ERS14895786	ERA21817969			

Fig. 1: Accessions' Dashboard: Tree of Life projects' accessions

<b>COPO</b>					▲ ₽	<b>Z</b> 0	¢tester1 ∗
Accessions				Info			
	Export CSV Other Project	ts' Ac	cessions Stand-alone Projects' Accessions				
			ch Accessions	Fil	ter Accession Types		
Accession $\Rightarrow$	Alias	÷.	Profile Title	🗹 Pr	roject <b>O</b>		
PRJEB48570	649e1016619c1c83c87f8d10		Twentieth Standalone Profile	🔽 Sa	Imple		
ER58420342	copo-reads-649e1016619c1c83c87f8d10:sample:transcriptome		Twentieth Standalone Profile	🔽 As	ssembly		
GCA_915070445.1	649e1016619c1c83c87f8d10_reads_641a023ddf1044ecc84da218		Twentieth Standalone Profile	🗹 Ex	xperiment <b>()</b>		
ERX6793970	copo-reads-649e1016619c1c83c87f8d10_reads_641a023ddf1044ecc84da912		Twentieth Standalone Profile	🗹 Ru	in		
ERR7224569	copo-reads-649e1016619c1c83c87f8d10_reads_641a023ddf1044ecc84da912		Twentieth Standalone Profile				
show 10 v records							
			Previous 1 Next				

Fig. 2: Accessions' Dashboard: Stand-alone projects' accessions

# CHAPTER TWENTYNINE

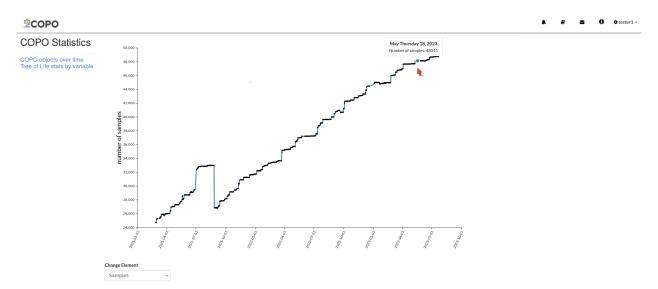
# **COPO STATISTICS**

Statistics are generated for each COPO instance over time and by a variable. The statistics are automatically updated and can be accessed on the Statistics web page.

## 29.1 Statistics over Time

Statistics can be generated for the following research object elements over time:

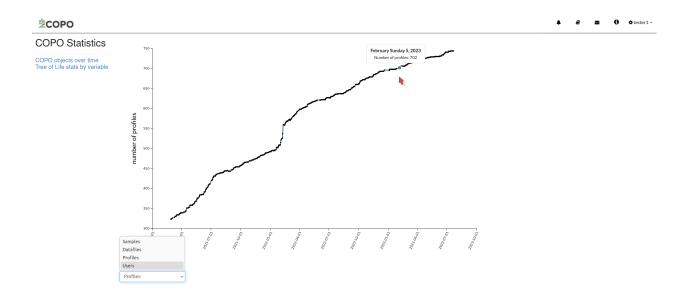
- Samples
- Datafiles
- Profiles
- Users



COPO Statistics: Line graph illustrating the number of samples recorded over time

COPO Statistics: Dropdown menu of research object elements that can be queried to get statistics of the number of samples over time

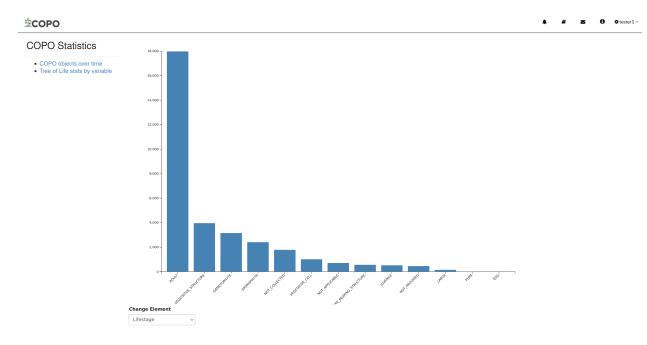
## Collaborative OPen Omics (COPO) Project Documentation, Release 1.0



# 29.2 Statistics by Variable

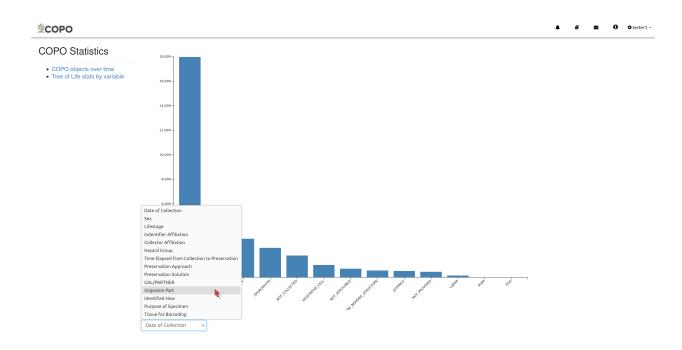
Statistics can be generated for the number of samples submitted based on the research elements or variables such as -

- Date of Collection
- Sex
- Harzard Group
- Organism Part



COPO Statistics: Bar graph illustrating total number of samples recorded for various Lifestage elements

COPO Statistics: Dropdown menu of elements/variables that can be queried to get statistics of the number of samples



# **MANIFEST CHECKLIST**

Hint: To view the entire description of a checklist, collapse the description by clicking the **b** button below.

The manifest checklist<sup>1</sup> is a combination of the default European Nucleotide Archive  $(ENA)^2$  checklist and additional checklists that are specific to projects. The manifest checklist is used to generate the manifest file which can be a Microsoft Excel (MS) spreadsheet file, Comma-separated values (CSV) file or a form that is required to be uploaded to ENA.

An overview of each manifest checklist is given below. It was adapted from ENA sample checklists and annotation checklists.

# **30.1 Barcoding Manifest Checklists**

For mitochondrial cytochrome oxidase subunit 1 genes.

For ribosomal RNA genes from prokaryotic, nuclear or organellar DNA. All rRNAs are considered partial.

# **30.2 Sample Manifest Checklists**

Minimum information required for the sample

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

<sup>&</sup>lt;sup>1</sup> See term: *Manifest checklist*.

<sup>&</sup>lt;sup>2</sup> See term: ENA.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

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Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information about a Micro B3 sample. A checklist for reporting metadata of marine microbial samples associated with genomics data. NOTE: Non-genomics data, i.e. oceanographic environmental data and morphologybased biodiversity data, should be submitted to the appropriate National Oceanographic Data Centre according to established reporting practices maintained by oceanographic community experts. Major National Oceanographic Data Centres from countries bordering the North-East Atlantic, and its adjacent seas: the Mediterranean, the Black Sea, the Baltic, the North Sea and the Arctic are listed at http://www.seadatanet.org/Overview/Partners.

For the Ocean Sampling Day campaign, non-genomics data shall be reported to the PANGAEA (http://www.pangaea. de/submit/).

Minimum information required for a prokaryotic pathogen sample

Minimum Data for Matching (MDM). A checklist for reporting metadata of pathogen samples for the Global Microbial Identifier (GMI) reporting system. More about GMI can be found here

Minimum information about a Tara Oceans sample. A checklist for reporting metadata of oceanic plankton samples associated with genomics data from the Tara Oceans Expedition.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information about an Influenza virus sample. A checklist for reporting metadata of Influenza virus samples associated with genomic data. This minimum metadata standard supports submission of avian, human and mammalian

surveillance data as well as serology and viruse isolate information (where available). The ENA Influenza sample checklist is based on standards in use at the Influenza Research Database.

Minimum information about a virus pathogen. A checklist for reporting metadata of virus pathogen samples associated with genomic data. This minimum metadata standard was developed by the COMPARE platform for submission of virus surveillance and outbreak data (such as Ebola) as well as virus isolate information.

Minimum Information required for reporting samples associated with genomic data, derived from carcinogen induced animal tumours. This minimum metadata standard was developed in collaboration with Duncan Odom lab for the Mouse Liver Cancer Evolution Project.

The ENA Crop sample enhanced checklist has been developed in collaboration with a number of EMBL-EBI teams to capture enriched annotation of published crop plant samples that lack sufficient reported metadata and are typically associated with systematic transcriptomic realignment-based analyses.

Minimum information about sewage samples. A checklist for reporting of sewage surveillance samples associated with sequence data from metagenomic sequencing projects. This minimum metadata standard was developed by the COMPARE platform.

ENA implementation of plant specimen contextual information associated with molecular data. The checklist has been developed in collaboration with the NCBI-GenBank and iPlant data resources under the umbrella of the Genomic Standards Consortium.

Shellfish contextual information associated with molecular data. The checklist has been developed in collaboration with EMBRIC Project partners.

GMinimum information about parasite samples. A checklist for reporting metadata of parasite samples associated with molecular data. This standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from protozoan parasites (e.g. Cryptosporidium) and also multicellular eukaryotic parasites (e.g. Platyhelminthes and Nematoda).

Minimum information required for reporting samples associated with the UniEuk EukBank initiative. This checklist aims to capture contextual metadata associated with V4 18S SSU rRNA molecular data.

Minimum information to standardise metadata related to samples used in GMI PT (Global Microbial Identifier Proficiency Test). A checklist for reporting metadata of GMI PT samples associated with molecular data. This minimum metadata standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from Campylobacter coli, Campylobacter jejuni, Listeria monocytogenes, Klebsiella pneumoniae, Salmonella enterica, Escherichia coli and Staphylococcus aureus.

Marine microalgae contextual information. The checklist has been developed in collaboration with EMBRIC Project partners and is suitable for reporting metadata related to environmental samples and those in culture collections.

A checklist for reporting metadata of human-associated pathogen samples for the COMPARE-ECDC-EFSA reporting system.

A checklist for reporting metadata of food-borne pathogen samples for the COMPARE-ECDC-EFSA reporting system.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Minimum information to standardise metadata of binned metagenome samples. Ensures binned and MAG metagenome assembly metadata is compatible.

Minimum information required for reporting samples associated with patient-derived xenograft (PDX) models or patient samples

Minimum information required for reporting HoloFood samples. HoloFood is a 'hologenomic' approach that will improve the efficiency of food production systems by understanding the biomolecular and physiological processes affected by incorporating feed additives and novel sustainable feeds in farmed animals

Minimum information required for reporting samples associated with the Tree of Life Programme.

CHAPTER

THIRTYONE

# SETTING UP COPO PROJECT LOCALLY WITH DOCKER

The central instance of COPO runs on a pool of three virtual machines. The following set up instructions are structured in a similar manner using one node. Feel free to make changes for a bigger or smaller pool.

Clone the GitHub COPO project repository.

Visual Studio Code (VSCode) is recommended for running the COPO project after having sat up the Docker environment. You can download VSCode from here for your local machine.

**Note:** There are a number of parameters in the command below that need to be updated or you may want to change for your local deployment. Please read through carefully.

**Hint:** A Python virtual environment is not required to run the COPO project application locally since the project is running via Docker containers. However, if you would like to run the project locally without Docker and within a Python virtual environment, please refer to the *COPO project setup with PyCharm documentation*.

**Warning:** The **ENA\_SERVICE** environment variable is set to the ENA development server. All submission to this server will be deleted after 24 hours. To submit to the production ENA server remove dev and set prod.

## **31.1 Install Docker**

Follow the official Docker installation documentation for your distribution.

Make changes to your firewall, iptables and security groups to serve a website, use Docker swarm and redis. The port number will depend on your setup and if you choose to use the default ports for each service.

## 31.2 Initialise Docker Swarm

Listing	1:	Start a	Docker	swarm
---------	----	---------	--------	-------

docker swarm init --advertise-addr <the IP of the machine you want to advertise>

e.g. \$ docker swarm init 127.0.0.1 where 127.0.0.1 is the IP address of localhost.

This command will return a token. You need this token to make the other VMs join the swarm if you plan to use more than one one node. On the other machines run:

Listing 2: Command to make other VMs join the swarm manager

docker-swarm join --token <the token returned by the previous command> <the IP<sub>→</sub> advertised previously>:2377

Check out the Docker documentation if you want to change the default port.

**Note:** You may need to change the following instructions depending on the server you are deploying to. Please consider which services need to run in the backend or frontend network.

## 31.2.1 Add Docker Node Labels

Label the node as a web service, nginx service, mongo service, postgres service and backup service. The web service and nginx service will be deployed on the frontend network. The mongo service, postgres service and backup service will be deployed on the backend network.

### Adding One Docker Node Label

**Hint:** \$HOSTNAME is a bash variable that returns the hostname of the machine. You can use the hostname of the machine instead of the variable. In a Linux OS, you can run \$ echo \$HOSTNAME to get the hostname.

If you are using more than one node, you will need to label the other nodes as well.

### Listing 3: Documentation for the Docker swarm command

```
docker node update \
    --label-add web-service=true \
    --label-add nginx-service=true \
    --label-add mongo-service=true \
    --label-add postgres-service=true \
    --label-add backup-service=true \
    $HOSTNAME
```

### Adding More than Docker One Node Labels

If you are using more than one Docker node, you can label the other nodes as follows:

Node 1

Listing 4: Node 1 Docker label command

```
docker node update \
    --label-add web-service=true \
    --label-add nginx-service=true \
    --label-add mongo-service=false \
    --label-add postgres-service=false \
    --label-add backup-service=false \
    copo-0
```

## Node 2

Listing 5: Node 2 Docker label command

```
docker node update \
    --label-add web-service=false \
    --label-add nginx-service=false \
    --label-add mongo-service=false \
    --label-add postgres-service=true \
    --label-add backup-service=true \
    copo-1
```

Node 3

Listing 6	: Node 3	Docker	label	command
-----------	----------	--------	-------	---------

```
docker node update \
    --label-add web-service=false \
    --label-add nginx-service=false \
    --label-add mongo-service=true \
    --label-add postgres-service=false \
    --label-add backup-service=false \
    copo-2
```

## **Create Docker Volumes**

Docker volumes are used to persist data via the plugin, **local-persist**. This ensures that the data is not lost when the containers are restarted. Volumes are created on the swarm manager.

Substitute the paths in commands before running it.

**Hint:** You may need to install curl before running the command below. You can install curl by running \$ sudo apt-get install curl.

You may need to install the **local-persist** plugin to persist volumes before running the command below. You can install it by running: \$ curl -fsSL https://raw.githubusercontent.com/MatchbookLab/local-persist/master/scripts/install.sh | sudo docker

Listing 7: Commands to create Docker volumes

### **Create Networks on Docker Swarm Manager**

On the swarm manager create two networks - one for the frontend and one for the backend. The front-end network will be used by the web service and the nginx service while the backend network will be used by the database services.

#### Listing 8: Commands to create Docker networks on the swarm manager

docker network create -d overlay copo-frontend-network
docker network create -d overlay copo-backend-network

#### Listing 9: View networks created on Docker swarm manager

docker network ls	
-------------------	--

### **Create Secrets on Docker Swarm Manager**

All secrets are file based. You will need to create some of the keys with third parties and choose passwords before proceeding with the COPO setup.

Listing 10: Commands to create secrets on Docker swarm manager

```
docker secret create copo_mongo_initdb_root_password copo_mongo_initdb_root_password
docker secret create copo_mongo_user_password copo_mongo_user_password
docker secret create copo_postgres_user_password copo_postgres_user_password
docker secret create copo_web_secret_key copo_web_secret_key
docker secret create copo_orcid_secret_key copo_orcid_secret_key
docker secret create copo_orcid_client_id copo_orcid_client_id
docker secret create copo_figshare_consumer_secret_key copo_figshare_consumer_secret_key
docker secret create copo_figshare_client_id_key copo_figshare_client_id_key
docker secret create copo_figshare_client_secret_key copo_figshare_client_secret_key
docker secret create copo_google_secret_key copo_google_secret_key
docker secret create copo_twitter_secret_key copo_twitter_secret_key
docker secret create copo_facebook_secret_key copo_facebook_secret_key
docker secret create copo_webin_user copo_webin_user
docker secret create copo_webin_user_password copo_webin_user_password
docker secret create copo-project.crt copo-project.crt
docker secret create copo-project.key copo-project.key
docker secret create copo_nih_api_key copo_nih_api_key
docker secret create copo_public_name_service_api_key copo_public_name_service_api_key
docker secret create copo_mail_password copo_mail_password
docker secret create copo_bioimage_path copo_bioimage_path
docker secret create ecs_secret_key ecs_secret_key
```

Listing 11: View secrets created on Docker swarm manager

docker secret ls

### **Build COPO Project Docker Image**

Download the Dockerfile\_local. for your local machine.

Place the downloaded Dockerfile in the COPO project root directory.

Alternatively, you can use the Dockerfile present in the root project directory Dockerfile for demonstration environment.

**Note:** The Dockerfile is configured to build the **local\_copo\_web** container image with the tag, v1.0.1. If you have a different tag and container name, you will need to change the Dockerfile accordingly.

If you are using a Mac OS, download the Dockerfile\_mac.

Visit here for more information on how to build an application with a Docker image.

Listing 12: Navigate to COPO project root directory

cd <path-to-project-root-directory>/COP0

Listing 13: Build Docker image

docker build . -f Dockerfile\_local -t local\_copo\_web:v1.0.1

### **Deploy Docker Image on Docker Swarm Manager**

The **redis**, **postgres** and **mongo** Docker services are created on the swarm manager. Download the local compose file file to create the services.

Alternatively, you can download compose file for demonstration environment.

Replace the <path-to-project-root-directory> with the absolute path to the COPO project root directory.

**Note:** The Docker compose file is configured to use the secrets and volumes created above. If you have used different names for the secrets and volumes, you will need to change the compose file accordingly.

If you are using a Mac OS, download the Mac compose file.

The following commands should be run from the root directory of the COPO project.

**Warning:** The **ENA\_SERVICE** environment variable is set to the ENA development server. All submission to this server will be deleted after 24hours. To submit to the production ENA server remove "dev"

Listing 14: Edit Compose file to container tag e.g. local\_copo\_web:v1.0.1

nano local\_copo.compose.yaml

Update the tag, save the file then, exit by inputting: CTRL + 0 then, ENTER then, CTRL + X

Listing 15: Command to deploy Docker image, local\_copo\_web:v1.0.1

docker stack deploy --compose-file '<path-to-file>/local\_copo.compose.yaml' copo

Listing 16: Local Compose file for COPO project application

```
version: "3.8"
services:
 web:
   image: local_copo_web:v1.0.1
   command: >
     bash -c "code-server serve-local --disable-telemetry --auth none --host 0.0.0.0 --
→port 8100"
   ports:
      - "8000:8000"
      - "8100:8100"
   volumes:
      - <path-to-project-root-directory>/COPO:/copo
   environment:
      - ENVIRONMENT_TYPE=prod
      - ASPERA_PLUGIN_DIRECTORY=aspera_linux_plugin
      - SECRET_KEY_FILE=/run/secrets/copo_web_secret_key
      - MEDIA_PATH=media/
      - DEBUG=true
      - REDIS_HOST=copo_redis
      - REDIS_PORT=6379
      - WEBIN_USER_FILE=/run/secrets/copo_webin_user
      - WEBIN_USER_PASSWORD_FILE=/run/secrets/copo_webin_user_password
      - ENA_SERVICE=https://wwwdev.ebi.ac.uk/ena/submit/drop-box/submit/
      - MONGO_USER=copo_user
      - MONGO_USER_PASSWORD_FILE=/run/secrets/copo_mongo_user_password
      - MONGO_DB=copo_mongo
      - MONGO_HOST=copo_mongo
      - MONGO_PORT=27017
      - MONGO_MAX_POOL_SIZE=100

    POSTGRES_DB=copo

      - POSTGRES_USER=copo_user
      - POSTGRES_PORT=5432
      - POSTGRES_SERVICE=copo_postgres

    POSTGRES_PASSWORD_FILE=/run/secrets/copo_postgres_user_password

      - ORCID_SECRET_FILE=/run/secrets/copo_orcid_secret_key
      - ORCID_CLIENT_FILE=/run/secrets/copo_orcid_client_id

    FIGSHARE_CONSUMER_SECRET_FILE=/run/secrets/copo_figshare_consumer_secret_key

      - FIGSHARE_CLIENT_ID_FILE=/run/secrets/copo_figshare_client_id_key
      - FIGSHARE_CLIENT_SECRET_FILE=/run/secrets/copo_figshare_client_secret_key
      - GOOGLE_SECRET_FILE=/run/secrets/copo_google_secret_key
```

```
(continued from previous page)
  - TWITTER_SECRET_FILE=/run/secrets/copo_twitter_secret_kev
  - FACEBOOK_SECRET_FILE=/run/secrets/copo_facebook_secret_key
  - NIH_API_KEY_FILE=/run/secrets/copo_nih_api_key

    PUBLIC_NAME_SERVICE_API_KEY_FILE=/run/secrets/copo_public_name_service_api_key

  - MAIL_PASSWORD_FILE=/run/secrets/copo_mail_password
  - MAIL_PORT=587
  - MAIL ADDRESS=data@earlham.ac.uk
  - MAIL_SERVER=outlook.office365.com

    MAIL USERNAME=eidata@nbi.ac.uk

  – ALLOWED_HOSTS=
  - PUBLIC_NAME_SERVICE=https://id.tol.sanger.ac.uk/api/v2/
  - ENA_ENDPOINT_REPORT=https://wwwdev.ebi.ac.uk/ena/submit/report/samples
  - ASPERA_PATH=/root/.aspera/cli
  - BIOIMAGE_PATH_FILE=/run/secrets/copo_bioimage_path
  - BIOIMAGE_SERVER=bsaspera_w@hx-fasp-1.ebi.ac.uk
  - ECS_SECRET_KEY_FILE=/run/secrets/ecs_secret_key
  - ECS_ACCESS_KEY_ID=copo@nbi.ac.uk
  - ECS_ENDPOINT=http://ei-copo.obj-data.nbi.ac.uk
  - ENA_V2_SERVICE_SYNC=https://wwwdev.ebi.ac.uk/ena/submit/webin-v2/submit
  - ENA_V2_SERVICE_ASYNC=https://wwwdev.ebi.ac.uk/ena/submit/webin-v2/submit/queue
  - B2DROP_PERMITS=/copo/b2drop/permits
depends on:
  - redis

    postgres

  - mongo
networks:

    copo-frontend-network

    copo-backend-network

deploy:
  replicas: 1
  restart_policy:
    condition: on-failure
  placement:
    constraints:
      - "node.labels.web-service==true"
  resources
    limits:
      cpus: '4'
      memory: 7GB
    reservations:
      cpus: '2'
      memory: 2GB
  update_config:
    parallelism: 1
    delay: 10s
secrets:

    copo_web_secret_key

  - copo_postgres_user_password
  - copo_mongo_user_password
  - copo_google_secret_key

    copo_facebook_secret_key

  - copo_twitter_secret_key
```

```
- copo_orcid_secret_key
    - copo_orcid_client_id
    - copo_figshare_client_id_key
    - copo_figshare_client_secret_key
    - copo_figshare_consumer_secret_key
    - copo_webin_user
    - copo_webin_user_password
    - copo_nih_api_key
    - copo_public_name_service_api_key
    - copo_mail_password
    - copo_bioimage_path
    - ecs_secret_key
redis:
 image: copo/copo-redis:redis-v6.2.6.18
 networks:
    - copo-frontend-network
 deploy:
    replicas: 1
    endpoint_mode: dnsrr
    restart_policy:
      condition: on-failure
    placement:
      constraints:
        - "node.labels.web-service==true"
    update_config:
      parallelism: 1
      delay: 10s
    resources:
      limits:
        cpus: "0.5"
        memory: 1GB
      reservations:
        cpus: "0.3"
        memory: 512mb
postgres:
 image: postgres:9.6
 networks:
    - copo-backend-network
 volumes:
    - postgres-data:/var/lib/postgresql/data
 secrets:

    copo_postgres_user_password

 ports:
    - "5432:5432"
 environment:

    POSTGRES_DB=copo

    POSTGRES_USER=copo_user

    POSTGRES_PASSWORD_FILE=/run/secrets/copo_postgres_user_password

 deploy:
    replicas: 1
```

```
endpoint_mode: dnsrr
    restart_policy:
      condition: on-failure
    placement:
      constraints:
        - "node.labels.postgres-service==true"
    update_config:
     parallelism: 1
      delay: 10s
    resources:
      limits:
        cpus: "0.5"
        memory: 1GB
      reservations:
        cpus: "0.3"
        memory: 512mb
mongo:
 image: copo/copo-mongo:20
 networks:
    - copo-backend-network
 volumes:
    - mongo-data:/data/db
 secrets:
    - copo_mongo_initdb_root_password
    - copo_mongo_user_password
 ports:
    - "27017:27017"
  environment:
    - MONGO_INITDB_ROOT_USERNAME=copo_admin
    - MONGO_INITDB_ROOT_PASSWORD_FILE=/run/secrets/copo_mongo_initdb_root_password
    - MONGO_USER=copo_user

    MONGO_USER_PASSWORD_FILE=/run/secrets/copo_mongo_user_password

    - MONGO_DB=copo_mongo
 deploy:
    replicas: 1
    #endpoint_mode: dnsrr
    restart_policy:
      condition: on-failure
    placement:
      constraints:
        - "node.labels.mongo-service==true"
    update_config:
     parallelism: 1
      delay: 10s
    resources:
      limits:
        cpus: "0.8"
        memory: 2GB
      reservations:
        cpus: "0.4"
        memory: 512mb
```

networks: copo-backend-network: external: true copo-frontend-network: **external**: true secrets: copo\_web\_secret\_key: **external**: true copo\_postgres\_user\_password: **external**: true copo\_mongo\_user\_password: **external**: true copo\_google\_secret\_key: external: true copo\_figshare\_client\_id\_key: external: true copo\_facebook\_secret\_key: external: true copo\_twitter\_secret\_key: external: true copo\_orcid\_secret\_key: external: true copo\_orcid\_client\_id: external: true copo\_figshare\_client\_secret\_key: **external**: true copo\_figshare\_consumer\_secret\_key: **external**: true copo\_webin\_user: external: true copo\_webin\_user\_password: **external**: true copo\_nih\_api\_key: **external**: true copo\_public\_name\_service\_api\_key: external: true copo\_mail\_password: **external**: true copo\_mongo\_initdb\_root\_password: **external**: true copo-project.crt: external: true copo-project.key: **external**: true copo\_bioimage\_path: external: true ecs\_secret\_key: external: true volumes: web-data: external: true

static-data:	
<b>external:</b> true	
submission-data:	
<b>external</b> : true	
logs-data:	
<b>external:</b> true	
mongo-backup:	
<pre>external: true</pre>	
postgres-backup:	
<pre>external: true</pre>	
mongo-data:	
<b>external</b> : true	
postgres-data:	
<b>external:</b> true	
b2drop-permits:	
<b>external:</b> true	

Listing 17: View services created on Docker swarm manager

docker service ls docker ps docker ps -a

### Listing 18: Inspect created image and check if it is running

docker image inspect local\_copo\_web:v1.0.1

#### Listing 19: Start copo\_web Docker container (if it is not started)

docker service scale copo\_web=1

### Listing 20: Command to stop copo\_web Docker container

docker service scale copo\_web=0

### Set up PostgreSQL database

In the terminal, navigate to the root directory of the COPO project application then, run the following commands.:

**Hint:** Retrieve the **local\_copo\_web** container ID by running the \$ **docker ps** command below in the root project directory of the COPO project application in the terminal for the **local\_copo\_web:v1.0.1** Docker image.

Listing 21: Install PostgreSQL database version 9.6 in terminal

docker run --name postgresql -e POSTGRES\_USER=<postres-username> -e POSTGRES\_PASSWORD= →<postres-password> -p 5432:5432 -v /data:/var/lib/postgresql/data -d postgres:9.6

Replace <postgres-username> and <postgres-password> with the username and password for PostgreSQL database respectively.

Listing 22: Enter the **local\_copo\_web** container

docker exec -it <local\_copo\_web-container-id> bash

Listing 23: Setup scripts to be run in the **local\_copo\_web** Docker container

python manage.py makemigrations python manage.py makemigrations chunked\_upload python manage.py makemigrations allauth python manage.py migrate python manage.py setup\_groups python manage.py setup\_schemas python manage.py createcachetable python manage.py social\_accounts

Listing 24: Install Python requirements for the project

python manage.py makemigrations python manage.py makemigrations chunked\_upload python manage.py makemigrations allauth python manage.py migrate python manage.py setup\_groups python manage.py setup\_schemas python manage.py createcachetable python manage.py social\_accounts

Listing 25: Create a Django admin/superuser

python3 manage.py createsuperuser

Enter the required details to create the Django admin/superuser. The Django admin/superuser can log into the COPO project application from the local Django admin website.

CTRL	+	Р
CTRL	+	Q
exit		

The commands above can be accessed in the 3\_db\_setup.sh script. This file is located in the set\_up\_scripts directory of the COPO project root directory.

In the following steps, we will create the PostgreSQL database for the COPO project application in the root directory of the project.

**Hint:** Retrieve the PostgreSQL container ID by running the command below in the root project directory of the COPO project application in the terminal for the **postgres:9.6** Docker image: **\$ docker ps** 

Listing 27: Enter the PostgreSQL container

docker exec -it <postgres-container-id> bash

```
Listing 28: Run setup scripts in the PostgreSQL Docker container
```

```
psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM socialaccount_socialapp_

→sites'

psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM django_site'

psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'DELETE FROM socialaccount_socialapp'

psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c "INSERT INTO django_site (id, domain,

→ name) VALUES (1, 'www.copo-project.org', 'www.copo-project.org')"

psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c "INSERT INTO socialaccount_socialapp_

→ (id, provider, name, client_id, secret, key) VALUES (1, 'orcid', 'Orcid', '$ORCID_

→ CLIENT_ID', '$ORCID_SECRET', '')"

psql -h 'localhost' -U $POSTGRES_USER -d 'copo' -c 'INSERT INTO socialaccount_socialapp_

→ sites (id, socialapp_id, site_id) VALUES (1, 1, 1)'
```

The commands above can be accessed in the 3\_db\_setup.sh script. This file is located in the set\_up\_scripts directory of the COPO project root directory.

## 31.2.2 Updating COPO Website Service

The COPO project is updated frequently and as such is under active development. To update your instance to a newer (or the latest) version, download the local compose file or the compose file for demonstration environment on the swarm manager or root directory of the project if you have one node.

Then, run the following commands in the terminal:

**Note:** The Docker tag below needs to be changed to reflect the most recent version available in DockerHub. Please check the latest version there. You can safely ignore the \*feature tags as they are not stable releases. For stable releases look for **\*rc**.

### Hint:

- Retrieve the **copo-web** container ID by running the \$ docker ps command below in the root project directory of the COPO project application in the terminal for the **copo/copo-web:v1.0.1** Docker image.
- To check if the web service is running, run the command below in the root project directory of the COPO project application in the terminal for the **copo/copo-web:v1.0.2** Docker image: \$ docker logs -f <container-ID-for-updated-copo-web>
- If you update often we recommend taking care of removing old docker images regularly.

Listing 29: Edit Compose file by updating the Docker container tag on the Docker swarm manager

nano local\_copo.compose.yaml

Update the Docker tag, save the file then, exit it by inputting: CTRL + 0 then, ENTER then, CTRL + X

Listing 30: Command to deploy updated Docker image: local\_copo\_web:v1.0.2 on the Docker swarm manager

docker stack deploy --compose-file '<path-to-file>/local\_copo.compose.yaml' copo

## 31.2.3 Launch COPO Website

The COPO project application can be accessed locally on port 8100 via the VSCode browser extension.

Within the VSCode IDE browser, add a new configuration by following the steps below:

- 1. Navigate to Run -> Add Configuration
- 2. Edit the **launch.json** file that is created with the following file contents:
  - Listing 31: VSCode launch.json configuration file contents

```
{
        "version": "0.2.0".
        "configurations": [
            {
                "name": "Python: Django",
                "type": "python",
                "request": "launch",
                "program": "${workspaceFolder}/manage.py",
                "env" : {
                    "PYTHONPATH1" : "${workspaceFolder}/lib:${PYTHONPATH}"
                },
                "args": [
                    "runserver",
                    "0.0.0:8000"
                ],
                "django": true,
                "justMyCode": false
            },
            {
                "name": "Python: Django makemigration",
                "type": "python",
                "request": "launch",
                "program": "${workspaceFolder}/manage.py",
                "env" : {
                    "PYTHONPATH" : "${workspaceFolder}/lib:${PYTHONPATH}"
                },
                "args": [
                    "makemigration"
                J,
                "django": true,
                "justMyCode": false
            },
            {
                "name": "Python: Celery Workers",
                "type": "python".
```

```
"request": "launch",
                 "module": "celery",
                 "console": "integratedTerminal",
                 "env" : {
                     "GEVENT SUPPORT": "True"
                 },
                 "args": ["-A", "web", "worker", "-1", "debug", "-P", "gevent", "--
\hookrightarrow concurrency", "10", "-Q", "celery", "-E"],
                 "justMyCode": true
            },
            {
                 "name": "Python: Celery Beat",
                 "type": "python",
                 "request": "launch",
                 "module": "celery",
                 "console": "integratedTerminal".
                 "args": ["-A", "web", "beat", "-1", "debug"]
             }
        ]
}
```

The COPO project application can be accessed locally on on port 80000 or on port 81000.

Note: Install required VSCode extensions for the COPO project application by following the steps below:

- 1. Navigate to the Extensions tab on the left-hand side of the VSCode IDE
- 2. Search for and install the following extensions:
  - Python (required)

If your local machine is restarted, you will need to start the Docker container again at startup. To do this, run the following command in the terminal: \$ docker start <container-ID-for-copo-web>. You can retrieve the container ID by running the command below in the root project directory of the COPO project application in the terminal for the copo/copo-web:v1.0.2 Docker image: \$ docker ps

## 31.2.4 Tips

- Enable Manage Unsafe Repositories in Source Control in VSCode browser application to allow VSCode to access the COPO GitHub project repository.
- Install the following VSCode extensions:
  - GitHub Copilot
  - Prettier Code formatter
  - Git Extension Pack

Listing 32: Set GitHub configuration in terminal

```
git config --global user.name "<GitHub-username>"
git config --global user.email "<GitHub-email-address>"
```

Listing 33: Create a tag via the terminal

git tag <tagname>

### Listing 34: Push a particular tag to GitHub via the terminal

git push origin <tagname>

Listing 35: Remove an existing tag from GitHub via the terminal

git tag -d <tag-name>

Listing 36: Docker command used to list all the running Docker containers

docker ps

Listing 37: Docker command used to start, stop and restart a Docker service

sudo systemctl start docker
sudo systemctl stop docker
sudo systemctl restart docker

Listing 38: Docker command used to start, stop and restart a container respectively

docker start docker stop docker restart

Listing 39: Docker command used to execute a command in a running container

docker exec it <container-ID> bash

Listing 40: Docker command used to find the installed version of docker

docker version

Listing 41: Docker command used to know the details of all the running, stopped, or exited containers

docker ps -a

Listing 42: Docker command used to create a volume so that the docker container can use it to store data

docker volume create <volume-name>

CHAPTER THIRTYTWO

# SETTING UP COPO PROJECT LOCALLY WITHOUT DOCKER

The COPO project is built on the Django framework and uses MongoDB, Redis, and PostgreSQL databases. Python is the main programming language used in the project.

The open source project is hosted on GitHub.

According to your OS, please choose the appropriate link below for instructions on how to set up the project on your local machine:

# 32.1 Set Up COPO Project on Linux

**Note:** If you are using a different OS (Operating system) other than Ubuntu, you can skip this step. See *COPO project guidelines for Windows users* if Windows is your preferred OS.

### 32.1.1 Install Python

```
sudo apt -y install software-properties-common
sudo add-apt-repository ppa:deadsnakes/ppa
sudo apt update
sudo apt -y install python3.8
```

### 32.1.2 Install Python Development Tools

### 32.1.3 Install Required Packages

Listing 1: Install required packages and enable the databases to start on boot

sudo apt -y install supervisor sudo gem install sass sudo apt -y install redis mongodb postgresql sudo systemctl enable mongodb sudo systemctl enable postgresql sudo systemctl enable redis

Listing 2: Install MongoDB on your local machine

### 32.1.4 Install Integrated Development Environment (IDE)

Any IDE (Integrated Development Environment) can be used to work on the project. However, we recommend using one of the following IDEs:

#### **PyCharm Professional**

A cross-platform IDE that provides consistent experience on the Windows, macOS, and Linux operating systems.

sudo snap install pycharm-professional --classic

#### OR

Visit PyCharm website to download an appropriate version for your OS or download it from the Ubuntu Software Center.

### Visual Studio Code

VSCODE (Visual Studio Code) is a lightweight but powerful source code editor which runs on your desktop and is available on Windows, macOS and Linux.

It comes with built-in support for JavaScript, TypeScript and Node.js and has a rich ecosystem of extensions for other languages (such as C++, C#, Java, Python, PHP, Go) and runtimes (such as .NET and Unity).

Visit VSCode website to download an appropriate version for your OS or download it from the Ubuntu Software Center

### 32.1.5 Configure IDE

### **PyCharm**

Note: If using VSCode IDE, you can skip this step.

**Warning:** If you encounter the error, Error: Please enable Django support for the project, navigate to File->Settings->Languages & Frameworks->Django->Enable Django to enable Django support for the project.

If using PyCharm IDE, add a new configuration by following the steps below: #. Navigate to Add New Configuration #. Select **Django server** #. Click **Save** 

Visit Run/debug configurations to learn how to create a configuration in PyCharm.

### VSCode

If using VSCode IDE, add a new configuration by following the steps below: #. Navigate to Run -> Add Configuration #. Edit the **launch.json** file that is created with the following file contents:

Listing 3: VSCode **launch.json** configuration file contents

```
{
        "version": "0.2.0",
        "configurations": [
            {
                "name": "Python: Django",
                "type": "python",
                "request": "launch",
                "program": "${workspaceFolder}/manage.py",
                "env" : {
                    "PYTHONPATH1" : "${workspaceFolder}/lib:${PYTHONPATH}"
                },
                "args": [
                    "runserver".
                    "0.0.0.0:8000"
                ],
                "django": true,
                "justMyCode": false
            },
            {
                "name": "Python: Django makemigration",
                "type": "python",
                "request": "launch",
                "program": "${workspaceFolder}/manage.py",
                "env" : {
                    "PYTHONPATH" : "${workspaceFolder}/lib:${PYTHONPATH}"
                },
                "args": [
```

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```
"makemigration"
                 ],
                 "django": true,
                 "justMyCode": false
            },
            {
                 "name": "Python: Celery Workers",
                "type": "python",
                 "request": "launch",
                 "module": "celery",
                 "console": "integratedTerminal",
                 "env" : {
                     "GEVENT_SUPPORT": "True"
                 },
                 "args": ["-A", "web", "worker", "-1", "debug", "-P", "gevent", "--
                , "10", "-Q", "celery", "-E"],
\rightarrow concurrency"
                 "justMyCode": true
            },
            {
                 "name": "Python: Celery Beat",
                 "type": "python",
                 "request": "launch",
                 "module": "celery",
                 "console": "integratedTerminal".
                 "args": ["-A", "web", "beat", "-l", "debug"]
             }
        ]
}
```

### 32.1.6 Declare Environment Variables

Set secrets in the environment variables in your **.bashrc** file. Activate **.bashrc** file by running the command: source .bashrc

If using PyCharm IDE, declare the environment variables in the following places: \* Edit Configurations > Environment variables \* File->Settings->Build, Execution, Deployment->Console->Python console \* File->Settings->Build, Execution, Deployment->Console->Django console \* File->Settings->Languages & Frameworks->Django->Enable Django

### 32.1.7 Set up Python virtual environment

Run the following commands within the project directory to set up a Python virtual environment for the project

Alternatively, you can create a virtual environment for the project with the command: python3 -m venv venv

Listing 4: Install packages with pip3 and Python3

```
sudo apt install -y python3-virtualenv
source venv/bin/activate
pip3 install -r requirements/base.txt
pip3 install celery
```

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```
python manage.py migrate && python manage.py social_accounts && python manage.py setup_

→groups && python manage.py setup_schemas && python manage.py createcachetable &&_

→supervisord -c celery.conf && supervisorctl -c celery.conf start all

python manage.py createsuperuser
```

**Warning:** Here are solutions to possible errors that you might encounter after having ran the above commands: • Possible error #1: TypeError: 'Collection' object is not callable. If you meant to call the 'authenticate' method on a 'Database' object it is failing because no such method exists. Solution #1: Run the command: \$ pip3 install pymongo==3.11.4 Reason: pymongo versions >4 is incompatible with the COPO project • Possible error #2: Issues related to importlib, rdlib, lxml, numpy, pandas and cffi Python packages Solution #2: #. In the requirements/base.txt file located in the project directory, change the version numbers for the following packages so that all packages can be compatible with each other - asgiref==3.7.2 - cffi==1.15.1 - importlib-metadata==1.6.1 -1xml = 4.9.3- numpy==1.20.0 – pandas==1.2.2 1. Change line 12 in wizard\_helper.py file from pandas.io.json import json\_normalize to from pandas import json\_normalize 2. Run the command: pip3 install -r requirements/base.txt again to install the packages • **Possible error #2**: text index required for \$text query Solution #3: Create an index in the SampleCollection in mongoDB: db.SampleCollection. createIndex( { "\$\*\*": "text" } )

### 32.1.8 Set Up Mongo Database in COPO Project

Note: Replace the username and password for MongoDB with your own username and password

Run the 4\_mongo\_setup.sh MongoDB set up script to configure the MongoDB database on your machine

### Set up MongoDB in Studio3T

**Note:** Replace the <username> and <password> for MongoDB with your MongoDB username and password By default, the username for MongoDB is copo\_user. The hostname, ``localhost``,, can also be substituted with the IP address of 127.0.0.1

Create a new MongoDB connection manually with the following details: **\* Connection Name**: copo\_mongo **\* Connection Type**: Standalone Connection **\* Hostname**: localhost **\* Port**: 27017 **\* Authentication**: Username and Password **\* Username**: copo\_user **\* Password**:

OR

MongoDBURI:mongodb://copo\_user:password@localhost:27017/copo\_mongo?retryWrites=true&connectTimeoutMS=10000&authSource=admin&authMechanism=SCRAM-SHA-1

### 32.1.9 Set Up PostgreSQL Database in COPO Project

**Note:** Replace the username and password of PostgreSQL with your own username and password

Run the 3\_db\_setup.sh PostgreSQL set up script to configure the PostgreSQL database on your machine

### 32.1.10 Launch COPO Website

Listing 5: Launch COPO website using the following command

python manage.py runserver

Alternatively, click on the **Run** button (i.e the green play button) on the top-right corner of the PyCharm IDE to launch the website.

# 32.2 Set Up COPO Project on Windows

### 32.2.1 Option 1: Using Ubuntu Terminal

Set up Ubuntu terminal on Windows by enabling the Windows Subsystem for Linux through the following steps.

# Navigate to Control Panel->Programs-> Turn Windows Features On Or Off # Enable the Windows Subsystem for Linux option in the list # Click the OK button # Click Restart now when you're prompted to restart your computer # Open Microsoft Store (MS) from the Start menu, and search for Linux in the store or open this link to find the Ubuntu app on MS store: # Click Get the apps under the Linux on Windows? banner. # Search and click Ubuntu Linux distribution to get "Get" or "Install" it # Launch Ubuntu app

**Note:** The first time that the Linux environment is launched, one is prompted to enter a UNIX username and password. These don't have to match your Windows username and password, but will be used within the Linux environment.

**Hint:** In the Ubuntu terminal (which can be found in the Microsoft Store or from the **Start** menu or by searching for **Ubuntu** using the search bar): \* To copy text: highlight desired text then, right-click \* To paste text: right-click

#### Warning:

- Error #1: 0x800701bc WSL 2 requires an update to its kernel component. For information please visit https://aka.ms/wsl2kernel Solution: Go to Manual installation steps for older versions of WSL | Microsoft Docs to download WSL 2Set WSL 2 as default version: wsl –set-default-version 2
- Error #2: WslRegisterDistribution failed with error: 0x80370102. Error: 0x80370102 The virtual machine could not be started because a required feature is not installed. Solution: \* Run Windows PowerShell under Administrator rights (Right-click on the Windows 10 Start button and select "Windows PowerShell (Admin)" \* Copy-paste the following command: \* Enable-WindowsOptionalFeature -Online -FeatureName VirtualMachinePlatform \* Restart the PC or laptop

### 32.2.2 Option 2: Using Windows Terminal

#### Note:

- Commands are entered in the command prompt
- Cloning a GitHub repository enables the branches to show and gives access to committing, pushing etc to the remote repository
- Repeat steps 1 to 19 under Ubuntu section in setting up COPO project on Ubuntu

#### Hint:

- To open the command prompt in Windows, open the **Start menu** and search for cmd.. Press **Enter** or click the result to open a command window or right-click the option to run it as an administrator
- To view all environment variables in the terminal:C:Users<username> SET
- 1. Download and install Python:
- 2. Download PyCharm: Python IDE for Professional Developers by JetBrains
- 3. Install Django: >``py -m pip3 install Django``
- 4. Download PyCharm IDE for Professional Edition:
- 5. Setup PyCharm Professional with a JetBrains account and a school email
- 6. Add/Authorise GitHub account to PyCharm
- 7. Clone the COPO project GitHub repository instead of downloading it as a .zip file from the GitHub repository
- 8. Open the cloned COPO project in PyCharm
- 9. In PyCharm, add a new configuration by navigating to Add Configurations->Add new->Django Server
- Set up or copy and paste environment variables in the following four places in PyCharm: \* Edit Configurations \* File->Settings->Build, Execution, Deployment->Console->Python console \* File->Settings->Build, Execution, Deployment->Console->Django console \* File->Settings->Languages & Frameworks->Django->Enable Django

11. Set system environment variables \* On the Windows taskbar, right-click the Windows icon and select System. \* In the Settings window, under R\*\*elated Settings\*\*, click Advanced system settings. \* On the Advanced tab, click Environment Variables \* Click New\* to create a new environment variable \* Click \*\*Edit to modify an existing environment variable \* After creating or modifying the environment variable, click Apply and then, OK to have the change take effect

### OR

Set environment variables in the terminal \* To set environment variables in the terminal replace "export" with "set"

e.g. Replace > export ENVIRONMENT\_TYPE="dev" with > set ENVIRONMENT\_TYPE="dev"

CHAPTER

# THIRTYTHREE

# **BROKERING DATA IN COPO WITH FAIR DATA PRINCIPLES**

*Findable, Accessible, Interoperable and Reusable (FAIR)* data enables data consumers (people or machines) to find, aggregate and analyse data that would otherwise be private or invisible, building on the existing web of linked data.

In COPO, the FAIR principles are applied as follows:

# 33.1 Findable

### 33.1.1 Using DataTables' search engine

COPO uses *DataTables* to display tabular data. The data are indexed in the DataTables' *smart* search engine and the search box is accessible within each table of data; it is located at the top right of the table. The search engine is updated automatically when metadata is added or updated.

### The search box provides the following abilities:

- Match words out of order
- Partial word matching
- Preserved text

See here for more information about searching for data in DataTables.

### 33.1.2 Using COPO API

Metadata can also be found via the COPO API.

# 33.2 Accessible

The required data can be retrieved freely with unrestricted access or via authentication and authorisation mechanisms, where necessary.

# 33.3 Interoperable

Data are integrated and available on ENA and NCBI. Data can be exported in csv, json or ro-crate format using the COPO API.

# 33.4 Reusable

Metadata are well-described with a plurality of accurate and relevant attributes. They are published to public repositories and can be accessed with the COPO API via a clear and accessible data usage.

# 33.5 FAIR Webinars

Webinar: COPO: Extending the frontiers of "FAIR" Data in Agriculture as part of RDA/IGAD webinar series

Date: February 12th July, 2020.

Host: Research Data Alliance/Improving Global Agricultural Data (RDA/IGAD)

Featured:

- Dr. Anthony Etuk , former Research Software Engineer of the COPO team
- Dr. Felix Shaw , Research Software Engineer of the COPO team

https://youtu.be/33Ozdpdfyh0

### See also:

Visit FAIR website for more information about FAIR principles.

# CHAPTER THIRTYFOUR

# LICENCE

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CHAPTER

### THIRTYFIVE

# CONTRIBUTOR COVENANT CODE OF CONDUCT

# 35.1 Our Pledge

We as members, contributors, and leaders pledge to make participation in our community a harassment-free experience for everyone, regardless of age, body size, visible or invisible disability, ethnicity, sex characteristics, gender identity and expression, level of experience, education, socio-economic status, nationality, personal appearance, race, religion, or sexual identity and orientation.

We pledge to act and interact in ways that contribute to an open, welcoming, diverse, inclusive, and healthy community.

# 35.2 Our Standards

Examples of behaviour that contributes to a positive environment for our community include:

- · Demonstrating empathy and kindness toward other people
- · Being respectful of differing opinions, viewpoints, and experiences
- Giving and gracefully accepting constructive feedback
- Accepting responsibility and apologising to those affected by our mistakes, and learning from the experience
- Focusing on what is best not just for us as individuals, but for the overall community

Examples of unacceptable behaviour include:

- The use of sexualised language or imagery, and sexual attention or advances of any kind
- Trolling, insulting or derogatory comments, and personal or political attacks
- · Public or private harassment
- Publishing others' private information, such as a physical or email address, without their explicit permission
- · Other conduct which could reasonably be considered inappropriate in a professional setting

# 35.3 Enforcement Responsibilities

Community leaders are responsible for clarifying and enforcing our standards of acceptable behaviour and will take appropriate and fair corrective action in response to any behaviour that they deem inappropriate, threatening, offensive, or harmful.

Community leaders have the right and responsibility to remove, edit, or reject comments, commits, code, wiki edits, issues, and other contributions that are not aligned to this Code of Conduct, and will communicate reasons for moderation decisions when appropriate.

# 35.4 Scope

This Code of Conduct applies within all community spaces, and also applies when an individual is officially representing the community in public spaces. Examples of representing our community include using an official e-mail address, posting via an official social media account, or acting as an appointed representative at an online or offline event.

# 35.5 Enforcement

Instances of abusive, harassing, or otherwise unacceptable behaviour may be reported to the community leaders responsible for enforcement at . All complaints will be reviewed and investigated promptly and fairly.

All community leaders are obligated to respect the privacy and security of the reporter of any incident.

# 35.6 Enforcement Guidelines

Community leaders will follow these Community Impact Guidelines in determining the consequences for any action they deem in violation of this Code of Conduct:

### 35.6.1 1. Correction

**Community Impact**: Use of inappropriate language or other behaviour deemed unprofessional or unwelcome in the community.

**Consequence**: A private, written warning from community leaders, providing clarity around the nature of the violation and an explanation of why the behaviour was inappropriate. A public apology may be requested.

### 35.6.2 2. Warning

**Community Impact**: A violation through a single incident or series of actions.

**Consequence**: A warning with consequences for continued behaviour. No interaction with the people involved, including unsolicited interaction with those enforcing the Code of Conduct, for a specified period of time. This includes avoiding interactions in community spaces as well as external channels like social media. Violating these terms may lead to a temporary or permanent ban.

### 35.6.3 3. Temporary Ban

Community Impact: A serious violation of community standards, including sustained inappropriate behaviour.

**Consequence**: A temporary ban from any sort of interaction or public communication with the community for a specified period of time. No public or private interaction with the people involved, including unsolicited interaction with those enforcing the Code of Conduct, is allowed during this period. Violating these terms may lead to a permanent ban.

### 35.6.4 4. Permanent Ban

**Community Impact**: Demonstrating a pattern of violation of community standards, including sustained inappropriate behaviour, harassment of an individual, or aggression toward or disparagement of classes of individuals.

Consequence: A permanent ban from any sort of public interaction within the community.

# 35.7 Attribution

This Code of Conduct is adapted from the Contributor Covenant, version 2.0, is available at https://www. contributor-covenant.org/version/2/0/code\_of\_conduct.html.

Community Impact Guidelines were inspired by Mozilla's code of conduct enforcement ladder.

For answers to common questions about this code of conduct, see the FAQ or Translations.

Last reviewed on: 08-01-2024

# CHAPTER

# THIRTYSIX

# **PRIVACY NOTICE**

This Privacy Notice explains what data is collected by the **Collaborative OPen Omics** (**COPO**) website service, its purposes, how the data is processed and how COPO keeps it secure.

Please view our Terms of Use regarding the rules and requirements for the use of the service.

# 36.1 Consent

Processing your data is necessary for our legitimate interest of allowing the operation and functioning of COPO. By using our website, you hereby consent to our Privacy Notice and agree to its terms.

### 36.1.1 Data Collected

COPO adopts appropriate data collection, validation, storage and processing practices as well as security measures to protect against unauthorised access, alteration, disclosure or destruction of your personal information, Orcid credentials and metadata provided on our service.

### Information collected:

- Internet Protocol (IP) address
- Operating system
- Browser
- · First name, last name and username after you sign into the service with your Orcid credentials
- Email address (after you input it in the dialog shown after a first-time access to the service)
- Date and time when a profile record and manifests are created or updated
- Metadata submitted. Metadata is the essential information about when, where, how and why data has been collected. It can relate to research elements like samples, assemblies, sequencing annotations, barcoding, experiments, reads or runs
- If you contact us via email, we may receive additional information about you such as the contents of the message and/or attachments you may send us and any other information you may choose to provide

### Usage of information collected:

- To utilise Google Fonts, an interactive web directory via Cascading Style Sheets (CSS), which is embedded in the service
- To provide the user access to the service
- To answer support request sent by the user
- To monitor errors and exceptions that may occur during metadata submission
- To register your email address with your COPO user account and to submit your email address to public repositories after manifest submissions
- To send email notifications when submitted samples have been accepted or rejected by a sample manager

# 36.2 Data Access

- Authorised COPO team developers
- Public metadata repositories that COPO relies on to provide the service. They are:
  - BioImage Archive (BIA)
  - $ENA^1$
  - NCBI<sup>2</sup>

# 36.3 Data Retention

- Any personal data (name and email address) and metadata obtained from you will be retained as long as the service is live, even if you stop using the service.
- COPO obscures your email address and omits your name from the COPO Application Programming Interface (API) method results after a manifest submission. However, your email address will be submitted to public repositories and will be visible on public records as a metadata submitter.
- · Access to the web and security logs containing personal data are restricted to the relevant COPO team developers

# 36.4 Cookies

This service uses "cookies" to store information about the web pages that the visitor has accessed or visited.

The information is used to log any errors or exceptions that may occur and user sessions.

<sup>&</sup>lt;sup>1</sup> See term: *ENA*.

<sup>&</sup>lt;sup>2</sup> See term: *NCBI*.

# 36.5 Questions

Any questions or comments concerning this Privacy Notice can be addressed to us by

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# CHAPTER

# THIRTYSEVEN

# **TERMS OF USE**

- The **Collaborative OPen Omics (COPO)** website service promotes *Findable, Accessible, Interoperable and Reusable (FAIR)* metadata brokerage through the submission of research objects (raw or processed data, reads, samples, images etc.) which are made public to the research community and public repositories like -
  - BioImage Archive (BIA)
  - $ENA^1$
  - NCBI<sup>2</sup>
- This service uses cookies to record information about your website session to enable the website to function well. You can control your use of cookies from your web browser but if you choose not to accept cookies from the COPO website service, you will not be able to take full advantage of all of the website's features.
- This service also uses Google Fonts, a website font service that is owned by Google LLC or by Google Ireland Limited, to provide an interactive web directory via Cascading Style Sheets (CSS) throughout the service.

The Google server needs to collect your Internet Protocol (IP) address in order to send you the Google Font files from the Google servers when you access the service. Through the use of Google Fonts, the website performance is optimised and is displayed more beautiful.

Even though our service self-host Google Fonts on some web pages in order to eliminate violating General Data Protection Regulation (GDPR), there are other web pages in our service that do not. By using the service, you consent for the service to use your IP address so that it can load the Google Fonts from the Google servers.

- COPO will make all reasonable effort to maintain continuity of its service and provide adequate warning of any changes or discontinuities. However, COPO accepts no responsibility for the consequences of any temporary or permanent discontinuity of the service.
- If you email or submit offensive, inappropriate or objectionable content on our website or to us, or engage in any disruptive behaviour on our service, we may use your personal information from our security logs to stop such behaviour. We may also use your personal information to inform relevant third parties about the content and your behaviour where we reasonably believe that you are or may be in breach of any applicable laws.
- COPO imposes no additional restrictions on the use of the submitted data available on our service after they have been provided by the metadata submitter other than those provided by the metadata submitters like embargoed metadata.

However, there are restrictions imposed on the metadata submitter on the metadata after the metadata have been uploaded and submitted on the COPO service.

Some of these metadata submitter restrictions include but are not limited to the following:

• Profile records cannot be deleted after they have associated research objects like samples, reads, files, sequencing annotations, accessions, barcoding manifests etc..

<sup>&</sup>lt;sup>1</sup> See term: *ENA*.

<sup>&</sup>lt;sup>2</sup> See term: *NCBI*.

- Samples cannot be deleted after they have been submitted; they can only be updated. More details about what field values can be updated can be found in the *Updating Samples* section in our documentation.
- Please see our documentation on the various profile components for *Stand-alone Profile* and *Tree of Life Profile* for more information concerning the restrictions and possibilities of the various research objects.
- All scientific metadata will be made publicly available after data submission and we may store it permanently.
- The metadata submitted and the COPO Application Programming Interface (API) methods are generated in part from the data contributed by the community who remain the data submitters.
- COPO does not guarantee the accuracy of any provided metadata for any purpose. We, however, make all reasonable effort to ensure that the metadata submitted are validated according to the Standard Operating Procedure (SOP)<sup>3</sup> for each manifest type.

Please see our documentation regarding the SOP requirements for each manifest type for more information.

- The metadata submitted may be subject to embargoed rights or permits rights. It is the responsibility of users of this service to ensure that their exploitation of the data does not infringe any of the rights of such parties.
- We reserve the right to update these terms of use at any time. We will attempt to give reasonable notice of any changes by placing a notice on our website or by sending an email to any email address you may have provided to us, but you may wish to check the terms of use each time you use the website.

The date of the most recent revision will appear at the bottom of this web page, the 'Terms of Use' web page. If you do not agree to these changes, please do not continue to use our service.

- Any feedback provided to COPO about its service will be treated as non-confidential unless the individual or organisation providing the feedback states otherwise.
- Any questions or comments concerning these terms of use can be addressed to us by . More details about the data that we collect from you when you browse the website, make manifest submissions and how we process the data are detailed in our *Privacy Notice*.

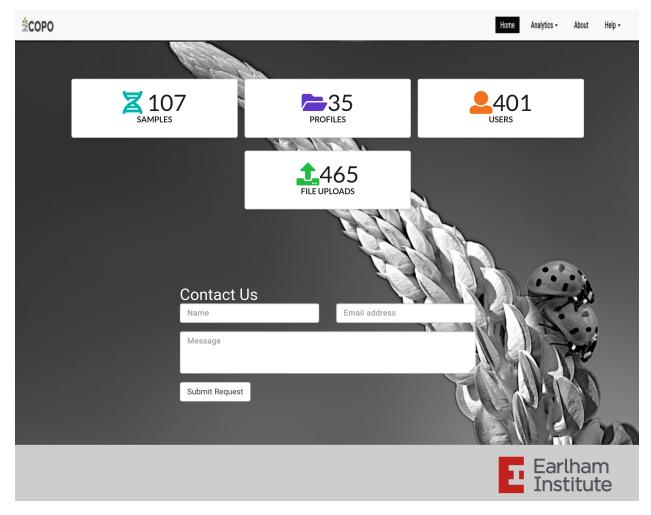
Last revised: 28-10-2023

<sup>&</sup>lt;sup>3</sup> See term: *SOP*.

# CHAPTER THIRTYEIGHT

# CONTACT COPO

Send an email to the COPO team at , indicating your enquiry or request. The COPO team will respond as soon as possible.



Alternatively, you can input your enquiry or request in the Contact form on the COPO homepage



Alternatively, click the envelope icon located in the top-right section of the top navigation bar to be redirected to the contact form on the COPO homepage (if you are already logged into COPO)

### CHAPTER

### THIRTYNINE

# FREQUENTLY ASKED QUESTIONS

**Hint:** To view the entire answer to a question, collapse the answer by clicking the ▶ button below.

# 39.1 Dashboard

### 39.1.1 How can I view accessions after I have submitted samples, reads, or experiments in COPO?

- Click the button.
- The accessions dashboard will be displayed.
- Alternatively, navigate to the Accessions' dashboard.

### 39.1.2 Is there a way to analyse metadata submissions?

- 1. Tree of Life dashboard
  - Alternatively, click the button.
- 2. Tree of Life inspection web page
  - Alternatively, click the button.
- 3. Tree of Life inspection by Genome Acquisition Lab web page
  - Alternatively, click the <sup>1</sup>button.
- 4. Statistics web page

# 39.2 Manifest Update

### 39.2.1 How can I update values for samples that I have submitted in COPO?

#### Note:

- The manifest must be reuploaded in the same profile that the samples were submitted in.
- The desired value(s) will be updated once the field value is not a compliance field<sup>1</sup>.
- See the Updating Samples section for information about which field values can be updated.

# 39.3 Permits

### 39.3.1 Can I view or download permits that I have uploaded in COPO?

Yes, permits can be retrieved and downloaded by selecting the desired sample record(s) on the Samples web page

Then, clicking the 2 Download permits button on the web page.

### 39.3.2 Why am I unable to upload permit one after the other?

### Warning:

• 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 <sup>Upload Permits</sup> 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.

# **39.4 Profiles**

### 39.4.1 How can I be added to a profile group?

### 39.4.2 How can I create a profile on COPO?

• View the following video to see how to create a profile.

https://youtu.be/7xiVTNw6pPc

<sup>1</sup> See term: *Compliance field* 

# 39.4.3 How can I upload/submit research objects to a profile owned by another user or how can I create a group or how can I share my profile with others?

See *Sharing Profiles* section for more information.

### 39.4.4 How can I add a subproject to a profile on COPO?

- In the Add Profile form, choose the desired subproject(s) from the list of associated projects as shown below.
- See the Secondary Projects section for information about the available subprojects.

Add Profile
Title required
Description required (
Profile Type 🕕
Darwin Tree of Life (DTOL)
Associated Profile Type
Select associated type(s)
Aquatic Symbiosis Genomics (ASG)
Biodiversity Genomics Europe (BGE)
European Reference Genome Atlas (ERGA)
European Reference Genome Atlas - Pilot (ERGA_PILOT)

Fig. 1: Add Profile form: Selecting Associated Profile Type dropdown menu

# 39.4.5 How can I add a subproject or secondary project to a primary project in ENA/Biosamples?

• Contact the with the request providing the project accession of the child/subproject and the project accession of the parent/primary project.

### 39.4.6 How can I edit or delete a profile that I have created in COPO?

- Click the icon that is associated with the desired profile.
- The option to edit or delete a profile record will be displayed once clicked.
- The web page will refresh after the task has been completed successfully.

### 39.4.7 How many profiles can I have in COPO?

• For instance, you can create a profile to represent work done as part of a grant, subproject within a project or a PhD (Doctorate of Philosophy) project.

### 39.4.8 How can I view more profiles that I have created in COPO?

• More profiles that you have created will be loaded.

### 39.4.9 How can I view more information about a profile that I have created in COPO?



- The view more... button will only be associated with a profile if the profile has at least one of the following information.
- Click the <u>View more...</u> button associated with the profile.
- After the button is clicked, a popup dialog will show at least one of the following information if it is available:
  - Release Status (if applicable)
  - Release Date (if applicable)
  - Associated Profile Type(s)
  - Sequencing Centre

# 39.4.10 How can I navigate to the top of the web page after having loaded several work profiles?

• Alternatively, click the  $\circ$  button which automatically navigates to the top of the web page.

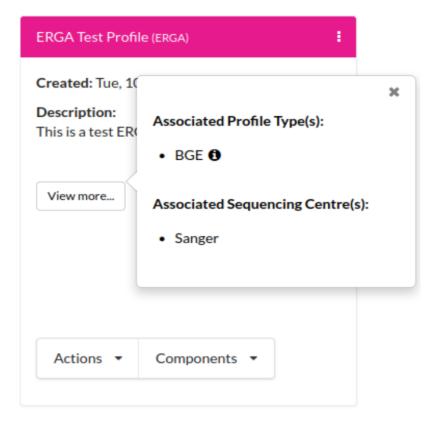


Fig. 2: Profile: View more information popup dialog

### 39.4.11 How can I create components for a profile?

- 1. Navigate to the work profile web page
- 2. Click the <sup>t</sup> button
- 3. Fill in then, save the form that is displayed
- 4. Click the <u>Actions</u> button associated with the created profile record to view a dropdown list of tasks that can be performed for that profile
- 5. Complete the action/task
- 6. Click the <u>components</u> button associated with the profile record to view the component of the action that was performed

# 39.5 Samples

### 39.5.1 Can I delete samples that have submitted?

No, samples cannot be deleted after the manifest have been submitted.

### 39.5.2 Can I retrieve samples or the manifest that have been submitted?

Yes, see the How to Download Submitted Sample Manifest section for more information.

### 39.5.3 How can I view images that have been uploaded?

See the View Submitted Images section for more information.

### 39.5.4 How can I download permits that have been uploaded?

See the Download Submitted Permits section for more information.

### 39.5.5 What are the formats that I download samples in?

The following are the formats that samples can be downloaded in:

- Microsoft Excel Spreadsheet format (.xlsx)
   See the *Downloading manifest in spreadsheet format* section for more information.
- Comma-separated values (csv) format (.csv)

On the **Samples** web page, click the button to download a manifest in csv format.

See How to access Samples web page section for guidance.

# **39.6 Sample Managers**

### 39.6.1 How can I be assigned as a sample manager?

- Make a request to the indicating the type of profile group that you would like to be assigned as a sample manager.
- The permission will be granted after the request has been approved.

### 39.6.2 How can I know if I have been assigned as a sample manager?

- The <sup>the button</sup> will be displayed on the web page.
- The accept/reject samples web page will be displayed once the button is clicked.
- Alternatively, if you can navigate to the Accept/Reject Samples' web page with an **Unauthorisation** error web page being displayed then, you are a sample manager.

### 39.6.3 How can I accept or reject samples that users have submitted?

**Note:** See *Accessing the Accept or Reject Samples web page* section for guidelines on accessing the **Accept or Reject Samples** web page.

See Accepting or Rejecting Samples section for more information.

### 39.6.4 Can I download permits that users have uploaded in COPO?

Yes, on the **Accept or Reject Samples** web page, permits can be downloaded by selecting the desired sample record(s) then, clicking the button on the web page.

See *Downloading permits* section for more information.

39.6.5 Can I view images that users have uploaded in COPO?

Yes, on the Accept or Reject Samples web page, images can be viewed by selecting the desired sample record(s) then,

clicking the <u>view Images</u> button on the web page.

See Viewing images section for more information.

# 39.6.6 If I belong to more than one sample manager manifest group, how can I view or accept samples that belong to them?

Note:

- The manifest dropdown menu will only be displayed on the Accept or Reject samples web page if you as a sample manager, belongs to more than one sample manager manifest group.
- If the *dtol* sample manager group dropdown menu option is selected, both Aquatic Symbiosis Genomics (ASG) profiles and Darwin Tree of Life (DToL) profiles will be displayed in the **All profiles** tab and/or **Profiles for My Sequencing Centre** the **Accept or Reject samples** web page will be displayed (if any exists).
- Choose desired sample manager group from the manifest group dropdown menu.
- Click the <sup>(=)</sup> button to accept or reject samples.

#COPO				8	0	🌣 tester 1 👻
	Add Email Address				 	
Work Profiles 🥊 🕂	An email address is required for your user account		Info			
	Enter email address					
COPO - Getting started	Please check the following box if you consent to your identifiable information being stored in COPO. The information will be submitted to public repositories and will be a					
Here are a few quick steps to get you started with COPO.	part of the public record. See our <u>Privacy Notice</u> for more details.					
1. COPO Profile:	I Agree					
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.	Colorite					
Use the + button on the page to create a new profile.	Submit					
2. Profile Components:						
Once you have created a work profile, you can start creating						
components within the profile. COPO provides templates for creating and managing different components such as Datafiles,						
Samples, 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.						

Fig. 3: Accept or Reject samples: Email address prompt shown when a user logs into COPO for the first time

See Viewing images section for more information.

### CHAPTER

## FORTY

# GLOSSARY

#### API

A software interface that allows two or more applications to communicate with each other.

#### ASG

A project that aims to provide the genomic foundations needed by scientists to answer key questions about the ecology and evolution of symbiosis in marine and freshwater species, where at least one partner is a microbe.

#### Assembly

Any sequence records from coding or non-coding regions to full assembled chromosomes.

### BGE

A project that undertakes a comprehensive application of genomic science to biodiversity research will drive fundamental advances in conservation science and policy.

#### **Biocuration**

The extraction of unstructured biological data from manifests into a structured, computable form.

#### **Compliance field**

A compliance field in COPO is a mandatory field that cannot be updated after a manifest has been uploaded or submitted before or after the samples have been accepted or rejected by a sample manager.

#### **COPO** (Collaborative OPen Omics)

COPO is a web-based tool for creating and managing metadata for research objects.

### **COPO** profile

Also known as work profile. A collection of 'research objects' or components that contain data generated on a biological research project or study.

There are two general types of profiles in COPO: *Stand-alone* profiles and ToL profiles. ASG, DToL and ERGA are the ToL (primary) projects brokered through COPO.

#### CRUD (Create, Read, Update and Delete) operations

Comprises posting data (creating and/or updating data ), reading data (e.g. making queries) and deleting data.

#### DataTables

A jQuery library plug-in that displays tabular data. They are used in COPO to display a list of research objects. See DataTables for more information.

### DB (Database)

A database is an organised collection of data, generally stored and accessed electronically from a computer system.

#### DNA (Deoxyribonucleic acide)

The molecule inside cells that contains the genetic information responsible for the development and function of an organism.

#### Docker

A set of platform as a service (PaaS) products that use OS-level virtualisation to deliver software in packages called containers. Containers are isolated from one another and bundle their own software, libraries and configuration files; they can communicate with each other through well-defined channels.

Docker Engine is the software that oversees the hosting of the containers.

#### Dockerfile

A text-based file with no file extension that contains a script of instructions. Docker uses this script to build a container image. See Dockerfile reference

### DToL

Aims to sequence the genomes of 70,000 species of eukaryotic organisms in Britain and Ireland.

It is one of the ToL projects brokered through COPO. The project is a collaboration between biodiversity, genomics and analysis partners that is transforming the manner by which biology, conservation and biotechnology are conducted.

DToL may sometimes be referred to as DTOL.

### **EBI** (European Bioinformatics Institute)

EBI is a UK (United Kingdom) government-funded public repository for biological data that provides free access to biomedical and genomic information.

### EI (Earlham Institute)

The Earlham Institute is a hub of life science research, training, and innovation focused on understanding the natural world through the lens of genomics. EI supports several projects including COPO project.

EI is is one of four Norwich BioScience Institutes (NBI) international centres that is based in the Norwich Research Park in Eastern England. It is also one of eight institutes that receive strategic funding from the Biotechnology and Biological Sciences Research Council (BBSRC), part of UKRI (United Kingdom Research and Innovation), as well as support from other research funders.

The other NBI (Norwich BioScience Institutes) centres are John Innes Centre (JIC), Sainsbury Laboratory (TSL) and Quadram Institute Bioscience (QIB).

### EMBL (European Molecular Biology Laboratory)

EMBL is a EU (European Union) intergovernmental organisation that performs basic research in molecular biology and provides services to the scientific community in its member states.

#### ENA

ENA is a repository for nucleotide sequence data that provides annotated DNA and RNA sequences. It also provides free and unrestricted access stores complementary information such as experimental procedures that details sequence assemblies and other metadata related to sequencing projects.

ENA is part of the International Nucleotide Sequence Database Collaboration (INSDC), which comprises the DNA DataBank of Japan (DDBJ), the European Molecular Biology Laboratory (EMBL), and GenBank at the National Center for Biotechnology Information (NCBI).

#### ERGA

A project that revolves around a pan-European scientific response to current threats to biodiversity by studying reference genomes which provide the most complete insight into the genetic basis that forms each species and represent a powerful resource in understanding how biodiversity functions.

#### FAIR

The ability to find, access, interoperate and reuse data with no or minimal human intervention.

#### GAL (Genome Acquisition Lab)

Partners or companies that perform genome sequencing.

#### Genome

A complete set of genetic material stored in long molecules of DNA in living organisms such as virus, oak tree or an elephant.

#### Genomics

The study of all or a substantial portion of the genes of an organism as a dynamic system, over time, to determine how those genes interact and influence biological pathways, networks, and physiology.

#### HTTP (Hypertext Transfer Protocol)

A protocol that allows communication between different systems. Similar to HTTPS (Hypertext Transfer Protocol Secure).

See also: HTTPS protocol

#### **IP** (Internet Protocol)

A protocol that allows communication between different systems.

#### MacOS

A series of proprietary graphical operating systems developed and marketed by Apple Inc. since 2001.

#### Manifest

A csv (comma-separated values) file or Microsoft (MS) Excel spreadsheet that contains metadata regarding a research object.

The manifest is used by scientists to upload metadata into COPO.

### Manifest checklist

A list of fields that are required to be filled in for a sample to be considered valid.

#### **Manifest ID**

A unique identifier assigned to each manifest record in COPO.

#### Metadata

In-depth and controlled contextual information about when, where, how and why data has been collected like geographical location, time of collection, tube or well identification and specimen identification. Metadata can relate to a research elements such as samples, assembles, annotations or experiments.

In life sciences, metadata facilitates *biocuration* which revolves around the structuring of datasets in a way that allows automated search, query and retrieval.

#### MIT (Massachusetts Institute of Technology) licence

A permissive free software license from the Massachusetts Institute of Technology that has limited restriction on the reuse of software.

### MongoDB

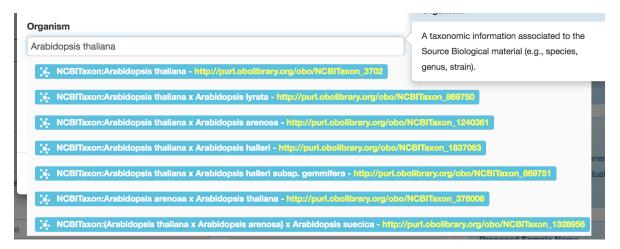
A document-oriented database program that uses JSON-like documents with optional schemas.

### NCBI (National Center for Biotechnology Information)

NCBI is a US (United States) government-funded public repository for biological data that provides free access to biomedical and genomic information.

### **Ontology field**

An ontology field in COPO is an auto-complete control, that maps user input to semantically-enriched values, which are explicit formal specifications of terms and their relationship to other terms in a domain.



### **Profile component**

Also known as *research object*. It forms part of a research project or study.

Templates for creating or describing research objects can be found here.

#### **Profile Types legend**

This describes the types of the profiles that have been created. It is located at the right of the \* *Work Profiles*\* web page.

#### **PyCharm**

A Python IDE (Integrated Development Environment) that provides code analysis, a graphical debugger, an integrated unit tester, integration with version control systems and supports web development with Django.

#### **Read the Docs**

A documentation hosting service based around Sphinx. COPO documentation is hosted on Read the Docs.

### Reads

A research object that holds raw read files and sequencing methods that refer to the DNA sequence from a small section of DNA.

It can be associated with one or more files, assemblies and sequence annotations.

#### Research

Systematic investigation, including research development, testing, and evaluation, designed to develop or contribute to generalisable knowledge.

#### REST

Relies on a stateless, client-server and cacheable communications *HTTP* request protocol. In COPO, it is used to communicate with the COPO API to perform *CRUD operations* using HTTP requests.

#### **RNA-seq** (Ribonucleic acid sequencing)

Analysis based on next-generation sequencing (NGS) data has recently become the de facto standard for the analysis of gene expression at the level of the whole transcriptome.

#### **RO-CRATE** (Research Object Crate)

RO-Crate is based on schema.org annotations in JSON-LD, and aims to make best-practice in formal metadata description accessible and practical for use in a wider variety of situations, from an individual researcher working with a folder of data, to large data-intensive computational research environments.

See more information about RO-Crate here.

#### Sample

Also known as *biosample*. A research object that represents biological samples collected and sequenced in real life.

#### Sample checklist

The checklist of metadata that the sample was registered with.

#### Sample manager

A sample manager is a person who is responsible for accepting or rejecting samples in a research project.

This person can also upload manifest on behalf of sample submitters.

#### Sample submitter

A sample submitter is a person who submits or uploads samples to a research project.

Sample submitters may also be referred to as manifest providers or manifest submitters.

#### **Sequence** annotation

A research object that is used to describe the process of marking specific features in a DNA, RNA or protein sequence with descriptive information about structure or function.

It can be associated with one or more files, reads and assemblies.

#### Singular stage

In datafile description, a **singular stage** is a stage of the description wizard in which all the files in the description bundle are constrained (by the system) to share the same metadata.

#### **SOP** (Standard Operating Procedure)

A manual compiled by various profile groups to help scientists fill in a manifest correctly.

See the *SOPs <fill-blank-manifests>* section for more information.

#### Specimen

Also known as biospecimen. It is a piece or portion of tissue, urine or other biologically derived material used for diagnosis and analysis.

#### SRA (Sequence Read Archive ) accession

A unique identifier assigned to a sample by the Sequence Read Archive (SRA) database. It usually starts with 'ERS' followed by a number.

### Studio3T

Studio3T, formerly known as Robo3T, is a GUI (Graphical User Interface) for MongoDB.

Visit Studio3T to download an appropriate version for your OS.

### ToL

A worldwide collaborative effort of biologists and nature enthusiasts to provide information about biodiversity, the characteristics of different groups of organisms and their evolutionary history (phylogeny).

### Ubuntu

A LINUX (Linux) distribution based on Debian and composed mostly of free and open-source software.

#### **URI (Uniform Resource Identifier)**

A string of characters that unambiguously identifies a particular resource.

#### See also: Uniform Resource Identifier

#### VSCode

VSCode is a lightweight but powerful source code editor which runs on your desktop and is available on Windows, macOS and Linux.

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