This document gives an overview on the order of events necessary to submit information on your experimental population to the Brassica Information Portal. This can be done using the wizard and the ruby client.

It further names all fields required for the submission of your new experimental plant population.

BIP user account

In order to submit content to the Brassica Information Portal, you need to sign in with your ORCiD account. If you don't have an ORCiD account yet, you will be referred to their services from our Sign in:
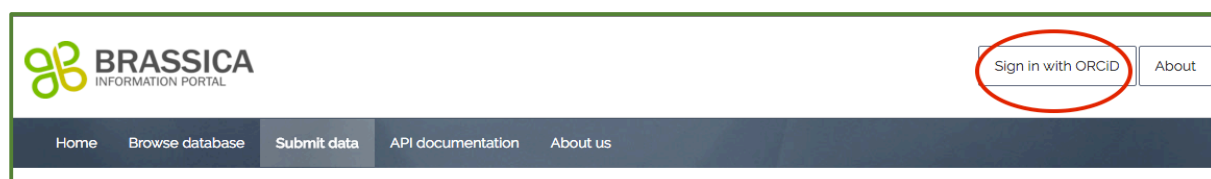
Your data submission to the Brassica Information Portal is split into two different submissions and need to be executed in the following order:
1) Population Submission
2) Trial Submission.

The Trial Submission documentation can be found in context with trial submissions, here: https://bip.earlham.ac.uk/submissions/new

Population Submission

You submit your experimental plant population first. This is the collection of the genetically different plant material used for your trial. In your trial submission you are asked for the name of your experimental population, which is why it is necessary to submit population information first. Go to bip.earlham.ac.uk and click on submit data. Choose "Plant population" and click "START!". Please note that the fields required for a population submission as shown in table 1 and the current configurations of the population submission client are specific to a diversity foundation set, not a crossing population.

This document describes
  A) Population Submission using the wizard
  B) Population Submission using the Ruby client

Population Submission using the wizard

The population submission wizard walks you through all steps of the submission. Information marked with a * is a compulsory field. This information is also shown in table 1. In the 4 submission steps described below you are asked for different information regarding your plant_population.
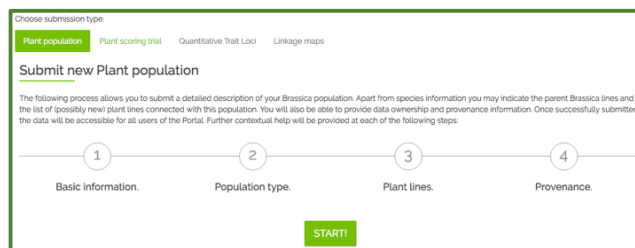

Figure 1 To access the population submission wizard, please go to https://bip.earlham.ac.uk/submissions/new

Step 1 - Basic information

Population Name*

Description

Population owned by

Step 2 - Population Submission

Taxonomy term

Population type*

Step 3 - Plant lines

Female parent line

Male parent line

Submission of plant line list (see below for template)

Step 4 - Provenance

Data owned by*

Data provenance

Comments

Visibility-public/private*

Step 1 asks for basic information on your population. Please follow this nomenclature when submitting the experimental plant population name: <Genus initials><Population type abbreviation> Nomenclature examples: BnaTNDH (Doubled Haploid mapping population derived from cross between Tapidor DH and Ningyou 7) or BnaDFS (a *Brassica napus* diversity foundation set).

In Step 2 the population will be further specified.

In step 3 you download a template for the submission of plant_lines and associated information. Then you are asked to fill out and submit the .csv file with the list of plant_lines used in your trial. Figure 2 shows an example of the layout of the .csv file.

Step 4 asks you to fill in some information about the provenance of the data you just submitted. You can choose to put an embargo on the data and wait with the submission until for example your paper is ready to be published.

Please Note that the wizard based population submission is still under construction and subject to change. You can however submit your data using the API or the ruby population submission client. We apologize for any inconvenience.

Figure 2 Population submission template that can be downloaded in step 3. Note that this feature is not yet implemented in the current version of our database.

Population Submission using the ruby client

The population submission client is a ruby script parsing information (objects) from a .csv spreadsheet provided by the user to the mapped location in the BIP database via the BIP-API. In order to understand the underlying resource and attribute names used in the script, please see the respective tables in the API-documentation.

During your submission you will be using the terminal. Therefore, you need to be familiar with the basics in navigating folders and moving and manipulating files. There is training material available to practice the upload with the ruby client using mock-data. You can find it here: https://github.com/TGAC/BIP_training

Install software:

-download ruby 2.3+

> -for OS X e.g. use brew:
> download brew following the instructions on the website:
> http://brew.sh/
>
> then type:
> brew install ruby
>
> -for Windows, use rubyinstaller:
> Download the installer by following the instructions on the website:
> http://rubyinstaller.org/

Files required:

Access the ruby client and an example .csv-file here:
https://github.com/TGAC/brassica/tree/master/public/population_submission

The population_submission.rb client currently enables the submission of all fields listed in table 2. If you are not familiar with ruby, the training material walks you through each step that needs to be taken in order to modify the client and input template for your own population submission. Some important file manipulation will be described below.

The .csv –file is an input template that goes with the current structure of the client. You have to change your input .csv file according to the information you have on your population.

File manipulation:

The ruby client

Open the file population_submission.rb and scroll through the client-file
Beneath " 1. Creating experimental plant_population ", you will see information as displayed in figure 3.
Please enter the following information on your population directly in the script:
- name,
- description
- establishing_organisation
- population_type_id
- taxonomy_term_id

```
puts " 1. Creating experimental plant_population "

plant_population_id = create_record('plant_population',
  name: 'BnaDFFS_1', # for workshop: put a random number behind the population,
  description: 'a BnaDFFS_1 description for data upload workshop ',
  establishing_organisation: 'JIC',
  population_type_id: 3 , # Dh segregating:1 ,DFS:2 , DFFS: 3,F3 pooled:4 , Rec
  taxonomy_term_id: 27 # Brassica napus id in BIP  27, Brassica oleracea: 32,
)
```

Figure 3 example text describing the plant population in population_submission.rb

Nomenclature examples for the plant_population.name are: BnaTNDH (Doubled Haploid mapping population derived from cross between Tapidor DH and Ningyou 7) or BnaDFS (a *Brassica napus* diversity foundation set).

The .csv file

With the help of the client population_submission.rb you are able to read in the content of your own .csv input file with your population metadata to the Brassica Information Portal.

The template PopSub_metadata_example.csv (Figure 2) reflects the current commands in the population_submission.rb client to read in data from that .csv file. It can be altered to the information available on your experimental plant population.

The template files (Figure 1 and 2) contain the minimal requirements of information for a population submission to the Brassica Information Portal. More fields are available in the database. To find out which information can be added, please go to our API-documentation.

Table 2. Fields required* for the submission of an experimental Population. They are presented below by <resource_name>.<attribute_name>.

- Plant_populations.name
- Plant_populations.population_type
- Plant_populations.description
- Plant_population.establishing_organization
- Plant_lines.plant_line_name
- Taxonomy_terms.id
- Plant_varieties.plant_variety_name
- Plant_accessions.plant_accession
- Plant_accessions.year_produced
- Plant_acessions.originating_organisation

*Note that more fields are available for submission of information to the BIP; to find the description of their names, please go to our API-documentation.

	A	B	C	D	E	F	G	H
1	Accession_name	Line_name	s-identidier	cultivar_nam	accession_type	accession_source	year_produced	
2	U.Nottm_BnASSYST-001	BnASSYST-001	SRR3134012	Alesi	Modern winter OSR	Nottingham	2013	
3	U.Nottm_BnASSYST-002	BnASSYST-002	SRR3134013	Remy	Modern winter OSR	Nottingham	2013	
4	U.Nottm_BnASSYST-003	BnASSYST-003	SRR3134014	Robust	Modern winter OSR	Nottingham	2013	
5	U.Nottm_BnASSYST-004	BnASSYST-004	SRR3134015	Alaska	Modern winter OSR	Nottingham	2013	
6	U.Nottm_BnASSYST-005	BnASSYST-005	SRR3134016	Pirola	Modern winter OSR	Nottingham	2013	
7	U.Nottm_BnASSYST-006	BnASSYST-007	SRR3134017	Milena	Modern winter OSR	Nottingham	2013	
8	U.Nottm_BnASSYST-007	BnASSYST-008	SRR3134018	Allure	Modern winter OSR	Nottingham	2013	
9	U.Nottm_BnASSYST-008	BnASSYST-009	SRR3134019	Agalon	Modern winter OSR	Nottingham	2013	
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Figure 3 template of a .csv file that corresponds to the population submission client's commands. If you have more metadata to submit in your .csv, you need to change the ruby client accordingly.

API key:

Sign in to BIP to retrieve your API key:
1) Click on API key in the popup bar under your user name.
2) Copy the API key and paste in your command to run the submission client (see below).
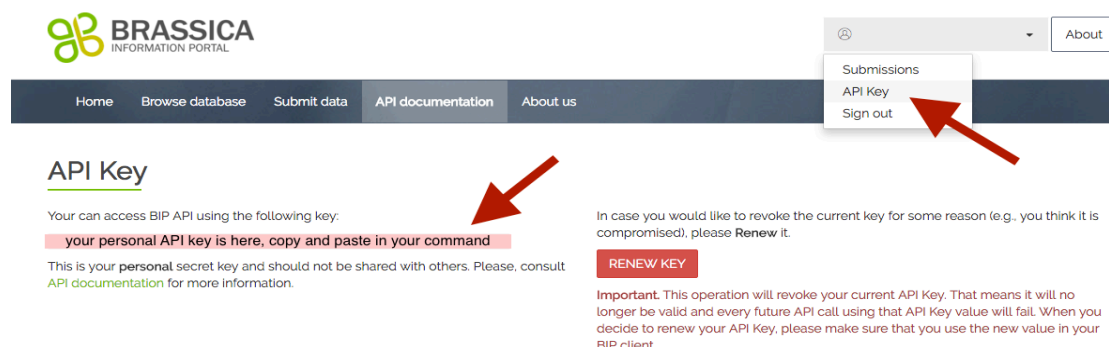
Run submission client:

After double-checking your submission file and script, use your terminal or command prompt to navigate into the folder your ruby- client and population metadata -.csv files are located in and run the command below. Make sure your input file and the submission script are located in the same folder or add the paths to their name:

ruby population_submission.rb <your_input_file.csv> <your_api_key>

If you are new to command line, click on the links for basic information on how to navigate your computer using terminal (OSX) or Command Prompt (Windows) .