

eLab Manuals

eLab Wizard

1. Introduction

The purpose of the eLab is to provide an overview over the data available within the EVOLTREE project. It can be used to get an insight on which data has been produced in the course of the project and by which EVOLTREE partner organisation.

The eLab collects the data available at partner organisations and formats it to enable search queries on it. No new data is created within the eLab. Every data item from the eLab database belongs to an EVOLTREE partner organisation.

2. Data Structure

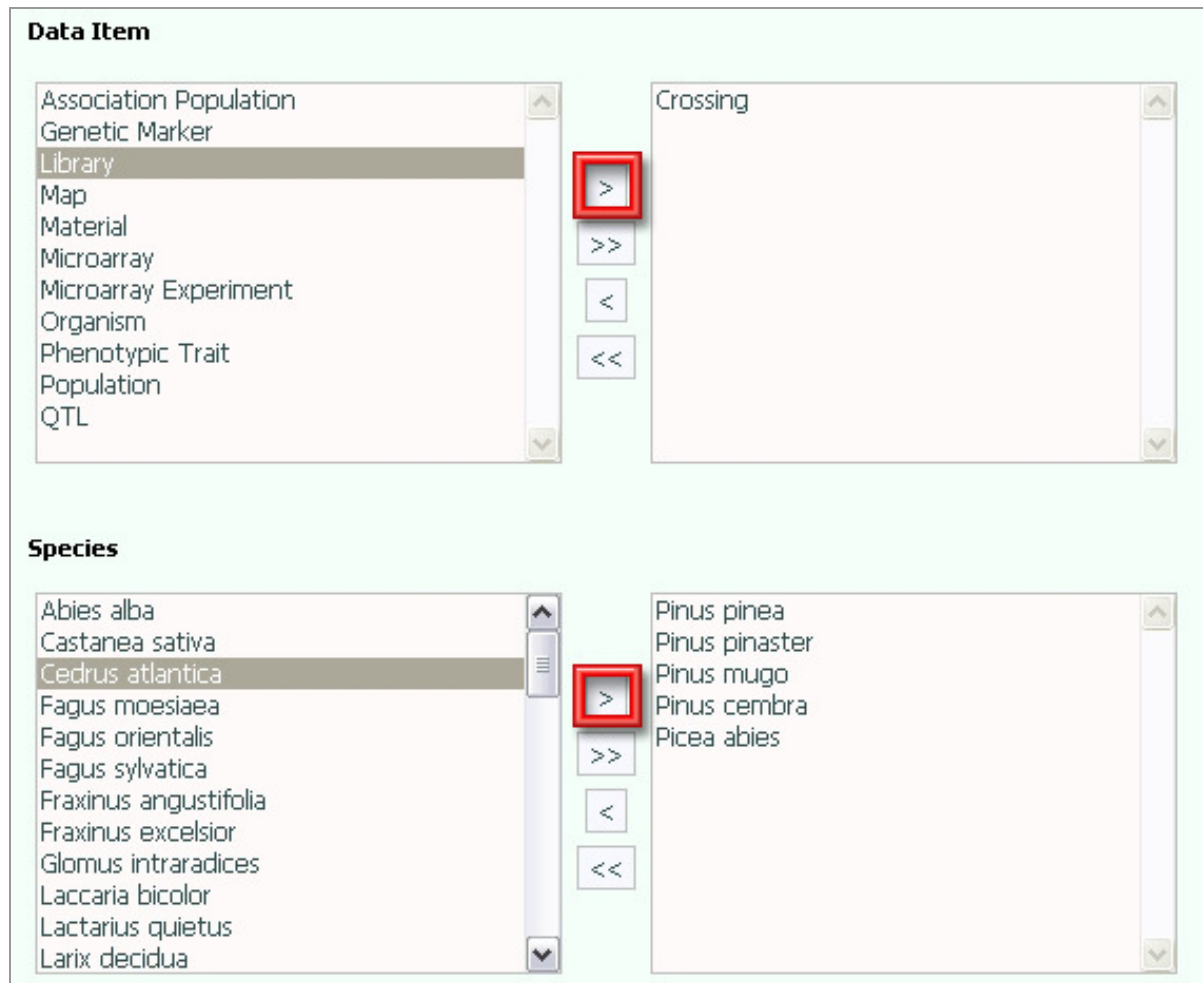
All data available within the project is organised in so-called data items. The list of data items represents the data types that are available within the EVOLTREE project. Therefore, the data items are supplemented every time new (not previously known) data is added to the eLab.

Currently 12 data items are available:

- Association Populations
group of genotypes selected for the study of one or more traits of interest
- Crossings
mapping pedigrees - group of genotypes with a fixed genealogy
- Genetic Markers
some are linked to maps, genotypic traits or diversity measurements
- Libraries
libraries of type cDNA, SSH, SSR, etc
- Maps
genetic and QTL maps
- Material
all materials available within the project - could be cDNA, gDNA, BACs, leaves, roots, etc
- Microarrays
- Microarray Experiments
- Organisms
all organisms available within the project (trees, insects, ...)
- Phenotypic Traits
some of them are linked to QTLs
- Populations (Natural Populations)
natural populations with linked genetic data, diversity measures and georeferenced data
- QTLs
some are linked to phenotypic traits

3. Search

When starting an eLab Search using the eLab Wizard, you are first asked to select the data items and (optionally) the species you are interested in. Mark the items and click the arrow button so that the items are shifted to the box on the right:



Then you can decide whether you would like to see the search result, or if you would like to refine your search parameters.

3.1. Refine Search

For each data item certain parameters are available which can be used to restrict the search. The parameters for the selected data items can be viewed by clicking on the button "Next":



Then the parameters are shown:

Crossing Parameters

Please specify detailed Parameters for Crossings:

Type: 3-generation outbred
diallel n1 x n1
F1
F2
Factorial 12 x 12
inter-species
Self F2 ✕

Genotypes are assigned to Genotypic Traits: -- All -- -- All --

Organisms are assigned to Phenotypic Traits: -- All -- -- All --

Map assigned to Crossing:

Library Parameters

Please specify detailed Parameters for Libraries:

Type: BAC library for BAC end sequencing
cDNA library
cDNA library (454)
Chloroplast genome library
Gene enriched genomic library
Genomic library
SSH
SSH library ✕

Tissue:

Current Stage:

In Repository Centre:

You can select the parameters you are interested. If all input items are left unchanged, all available data items are returned (without restrictions).

The search can be started by clicking on the search button:



3.2. Result View

The search result is shown in a new page:

eLab Search :: Results

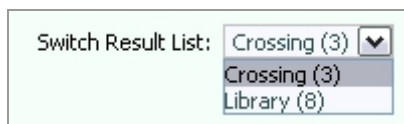
11 Data Items found Switch Result List: Crossing (3) ▼ Search Parameters: ⓘ

3 Crossings Page 1 / 1

ID	Species	Type	Size
NTB07-1	Pinus pinaster	F1	588
NTB07-2	Pinus pinaster	F1	588
NTB07-3	Pinus pinaster	F1	364

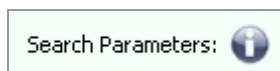
The following operations are available in the result view:

- After the search has finished, the results of the first data item (ordered alphabetically) are shown. If you would like to see the search results of the other data items, use the “Switch Result List” function:



All selected data items are shown in the list together with the number of results returned by the search query.

- If you would like to review you search parameters, you can use the “Search Parameters” function:



By clicking on the icon the search parameters can be reviewed in a pop window:

Your search parameters:

Species	
Pinus pinea, Pinus pinaster, Pinus mugo, Pinus cembra, Picea abies	

Data Item	Parameter
Library	Type: cDNA library, SSH, SSH library
Crossing	Type: F1, F2, inter-species


- If you would like to start a new search, use the following button on the right side:



3.3. Details View

Every item displayed in the result can be clicked to see more details about it.

For example when clicking on a crossing, the following page is shown:

eLab Search :: Details
Details of Crossing: **NTB07-2** **Data comes from:** INRA TreePop Database [Details](#) 

ID	NTB07-2
Species	Pinus pinaster
Type	F1
Size	588

Genotypes | Family Members | Phenotypic Traits | Genotypic Traits | Assigned Maps
588 Organisms Page 1 / 30

ID	Species	Genus	Family
ML001	Pinus pinaster	Pinus	Pinus
ML002	Pinus pinaster	Pinus	Pinus
ML003	Pinus pinaster	Pinus	Pinus
ML004	Pinus pinaster	Pinus	Pinus
ML005	Pinus pinaster	Pinus	Pinus
ML006	Pinus pinaster	Pinus	Pinus
ML007	Pinus pinaster	Pinus	Pinus
ML008	Pinus pinaster	Pinus	Pinus
ML009	Pinus pinaster	Pinus	Pinus
ML010	Pinus pinaster	Pinus	Pinus
ML011	Pinus pinaster	Pinus	Pinus
ML012	Pinus pinaster	Pinus	Pinus
ML013	Pinus pinaster	Pinus	Pinus

- In the header, the name of the crossing is shown:

Details of Crossing:
NTB07-2

- Beside the name the name of the database where the item comes from is shown:

Data comes from:
INRA TreePop Database [Details](#) 

If available, a link is displayed to view more details about the item (“Details”). When clicking on it, you are redirected to the partner database (and logged in automatically) to view the original data.

- In the table below the header the main parameters of the data item are shown:

ID	NTB07-2
Species	Pinus pinaster
Type	F1
Size	588


- At the bottom of the details view there is a list of tabs. There additional information for the current data item can be found:

Genotypes	Family Members	Phenotypic Traits	Genotypic Traits	Assigned Maps
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3.4. Application Properties

At every eLab view the so-called “Application Properties” are shown on the right side. This window contains some information about the current eLab session:

Application Properties

 You are logged in as:
Johanna Schmidt

 **Current Page:**
NTB07-2
(Crossing)

 **Previous Page:**
Result
[\[go back\]](#)

The first paragraph contains information about your user account - whether you are recognised as an EVOLTREE member, or as guest user.

The two paragraphs show the page which is currently viewed, and the page which was displayed before. By clicking on the link “[go back]”, you can jump back to the previous view.