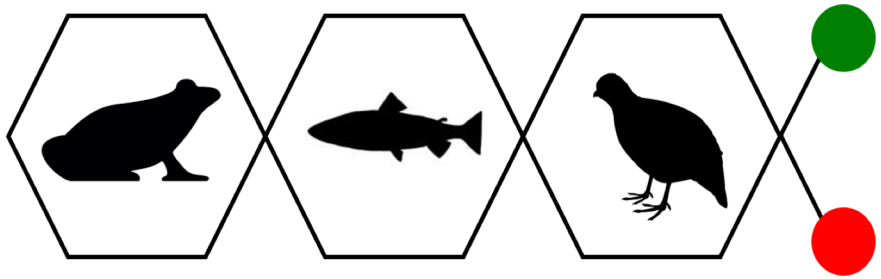
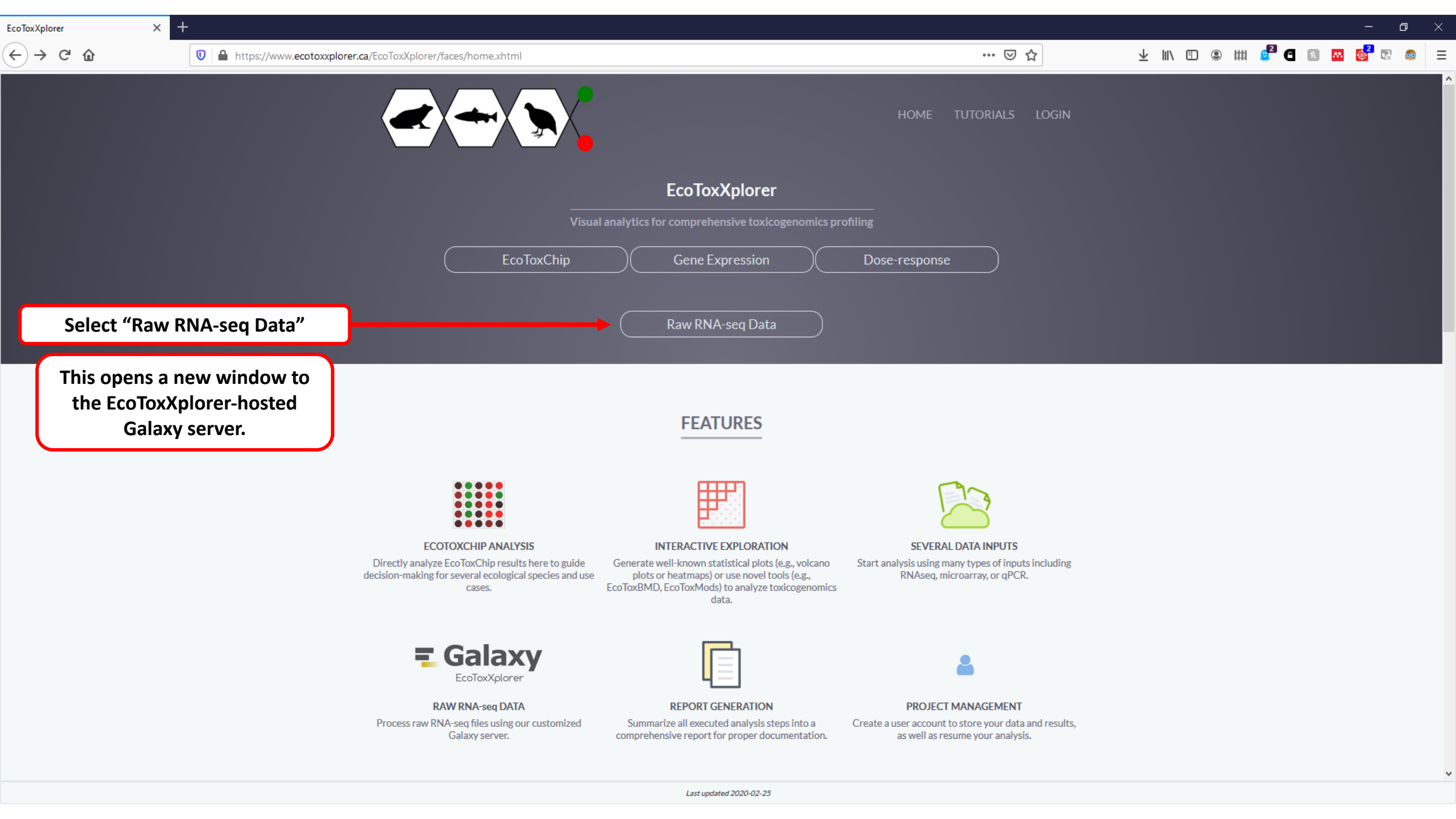


Tutorial #3

RNASeq Data Processing using Galaxy Module


EcoToxXplorer
https://www.ecotoxxplorer.ca/EcoToxXplorer/faces/home.xhtml
HOME
TUTORIALS
LOGIN
EcoToxXplorer
Visual analytics for comprehensive toxicogenomics profiling
EcoToxChip
Gene Expression
Dose-response
Raw RNA-seq Data
Select “Raw RNA-seq Data”
This opens a new window to the EcoToxXplorer-hosted Galaxy server.
FEATURES
ECOTOXCHIP ANALYSIS
Directly analyze EcoToxChip results here to guide decision-making for several ecological species and use cases.
INTERACTIVE EXPLORATION
Generate well-known statistical plots (e.g., volcano plots or heatmaps) or use novel tools (e.g., EcoToxBMD, EcoToxMods) to analyze toxicogenomics data.
SEVERAL DATA INPUTS
Start analysis using many types of inputs including RNAseq, microarray, or qPCR.
Galaxy
EcoToxXplorer
RAW RNA-seq DATA
Process raw RNA-seq files using our customized Galaxy server.
REPORT GENERATION
Summarize all executed analysis steps into a comprehensive report for proper documentation.
PROJECT MANAGEMENT
Create a user account to store your data and results, as well as resume your analysis.
Last updated 2020-02-25

Galaxy | EcoToxXplorer

https://galaxy.ecotoxxplorer.ca

Galaxy / EcoToxXplorer

Analyze Data | Workflow | Shared Data | Help | Login or Register | Using 0 bytes

Tools

search tools

Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
Column Join on Collections
Sequence operations

Workflows

- All workflows

Galaxy / EcoToxXplorer

Welcome to EcoToxXplorer Galaxy Server

This EcoToxXplorer Galaxy server is designed for mapping and quantification of raw RNA-seq data and it is integrated with EcoToxXplorer for statistical analysis and visualization.

How does it work?

If this is your first time to visit a Galaxy server and would like to gain more familiarity, please visit Galaxy 101 for an introduction of several fundamental concepts.

1) **Account registration:** you need to first register in order to upload files to our server.

2) **Loading data:** to load RNA-seq **fastq.gz** files from shared data for the desired species.

3) **Building collection:** this is a very practical step when you have tens or more of RNA-seq samples to process (details).

4) **Import workflow:** you need to first specify alignment program (details), sequencing type and organism. Click "View workflow". Then, just click on ico import the workflow.

Alignment program: Kallisto (faster) Organism: P. promelas (Fathead minnow) View workflow

5) **Run workflow:** after importing the workflow, you can directly start using it. You can visit the list of all imported workflows by clicking on All workflows. Fro attached to the workflow title, choose **run**.

6) Download your gene count table, add class labels and upload to EcoToxXplorer.

History

search datasets

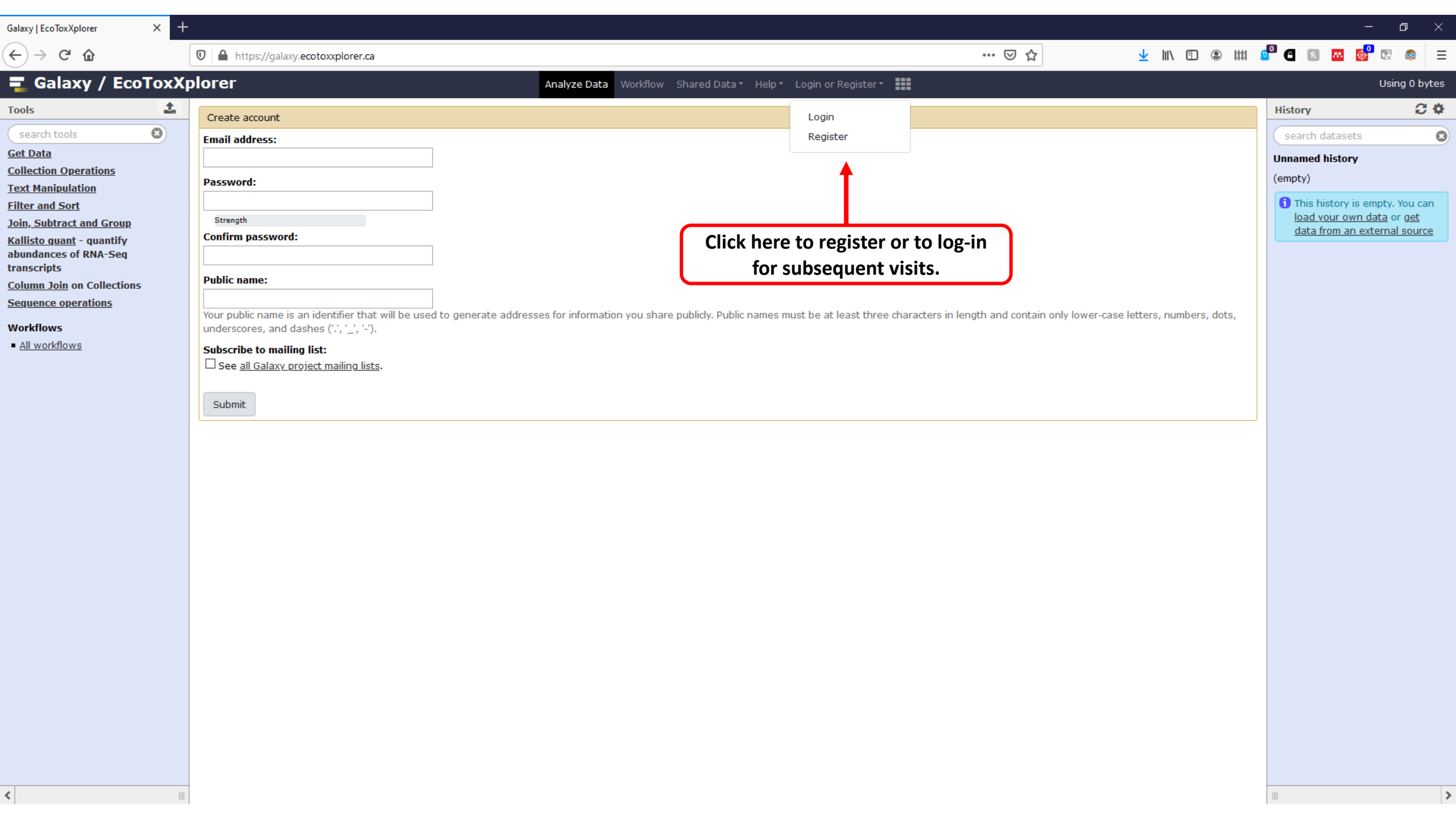
Unnamed history

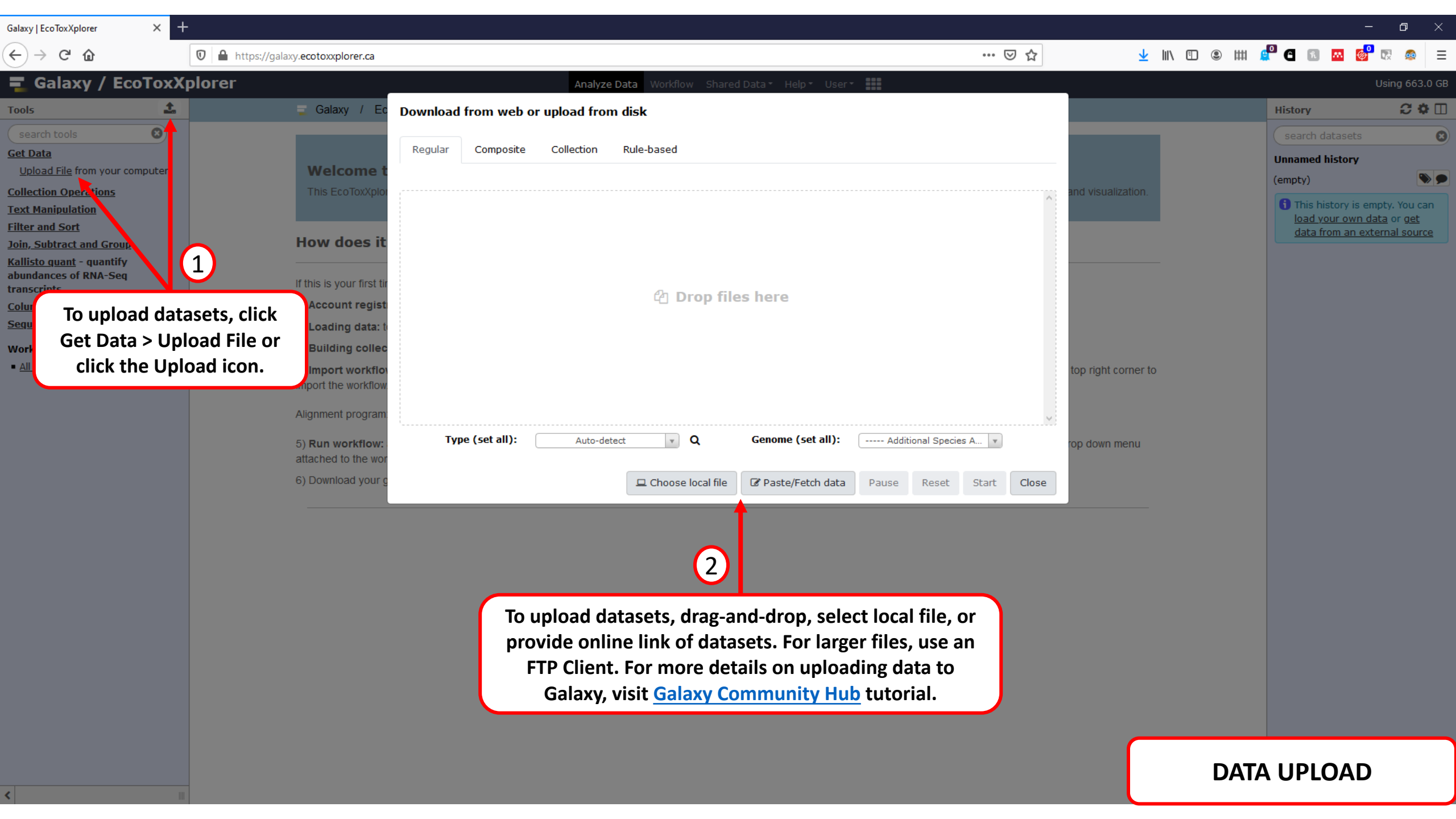
(empty)

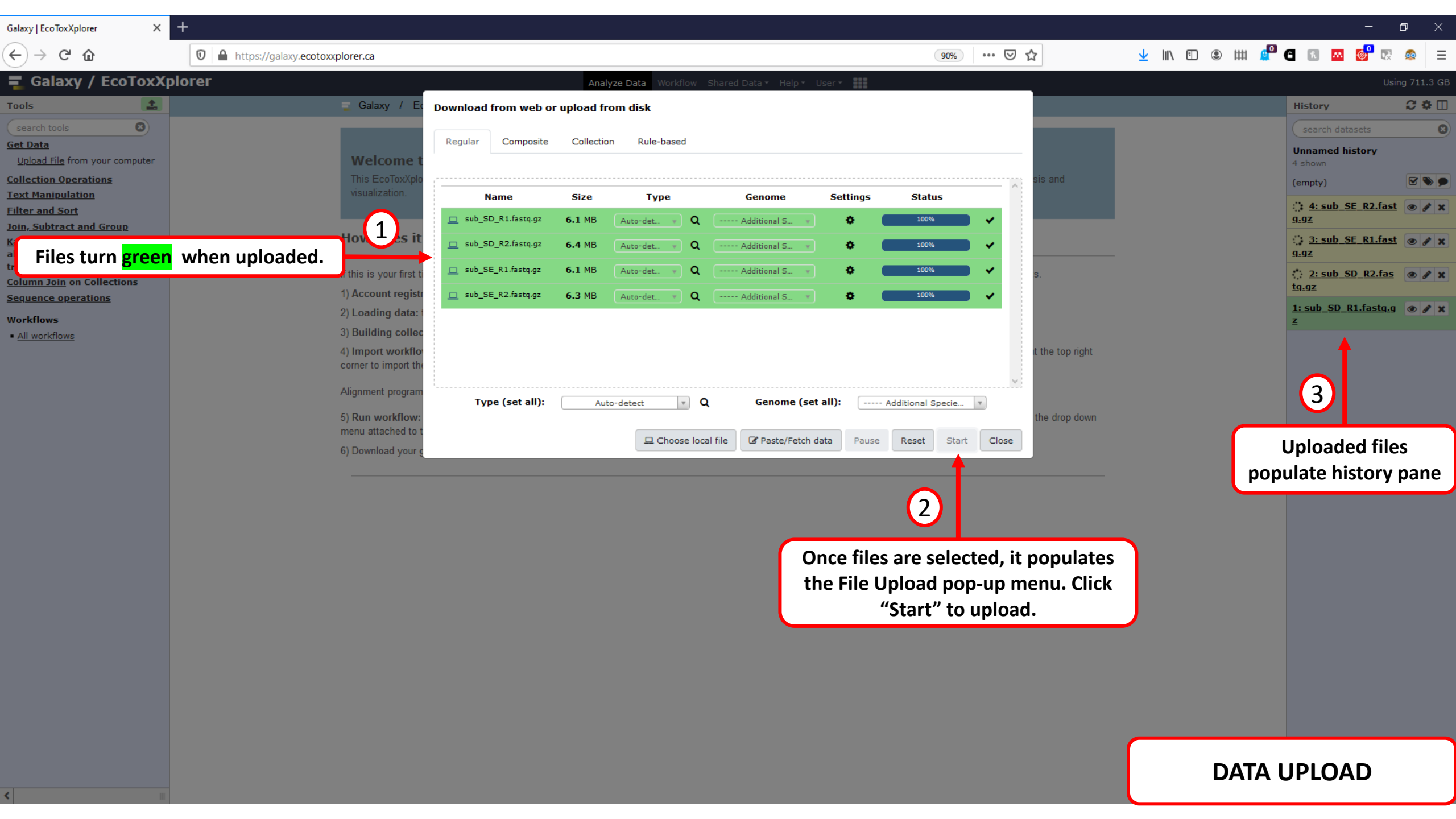
This history is empty. You can load your own data or get data from an external source

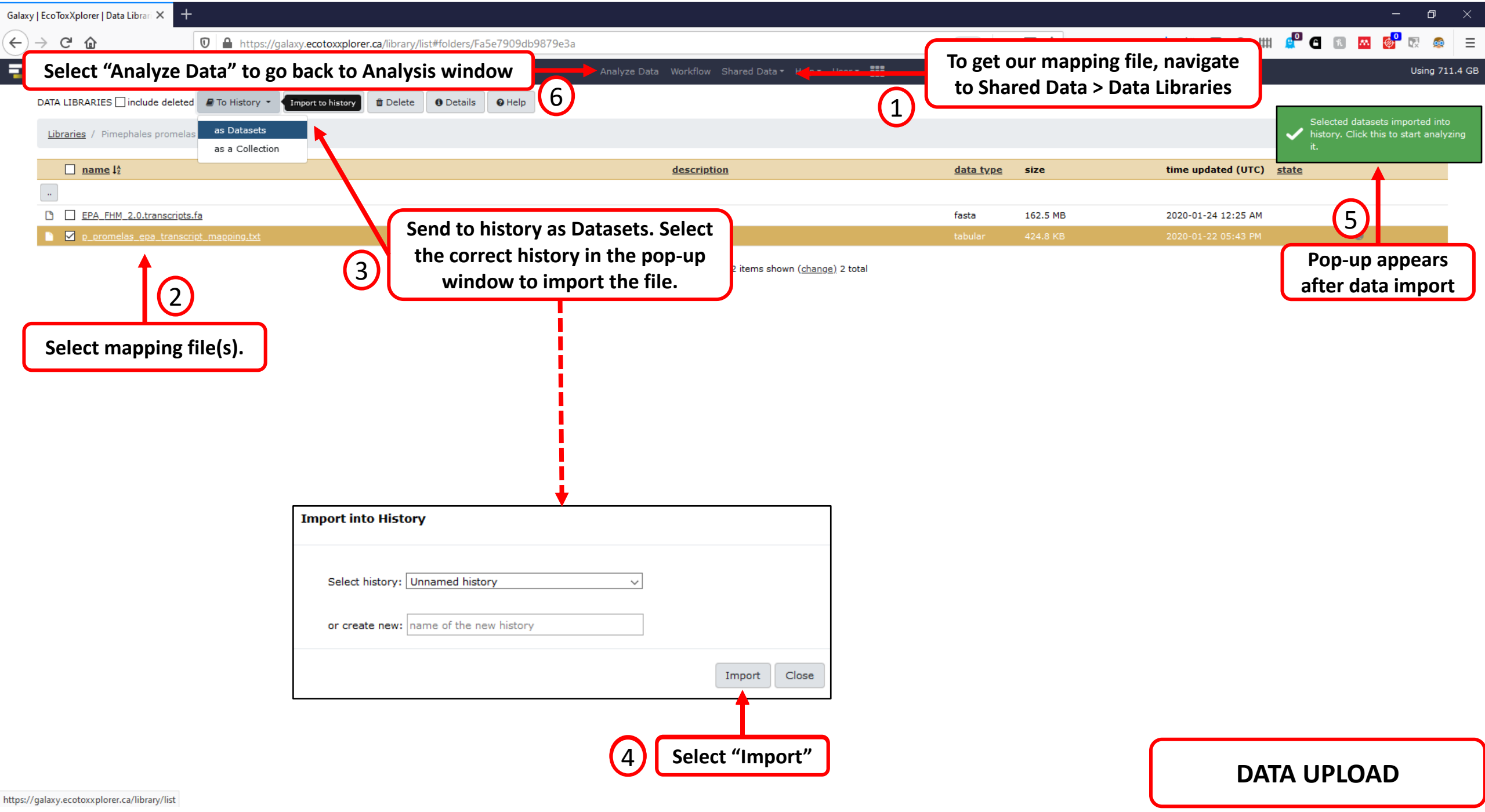
The history pane is the location of all input datasets and datasets produced, as well as operations performed. To learn more about the Galaxy history system, visit the Galaxy Training website.

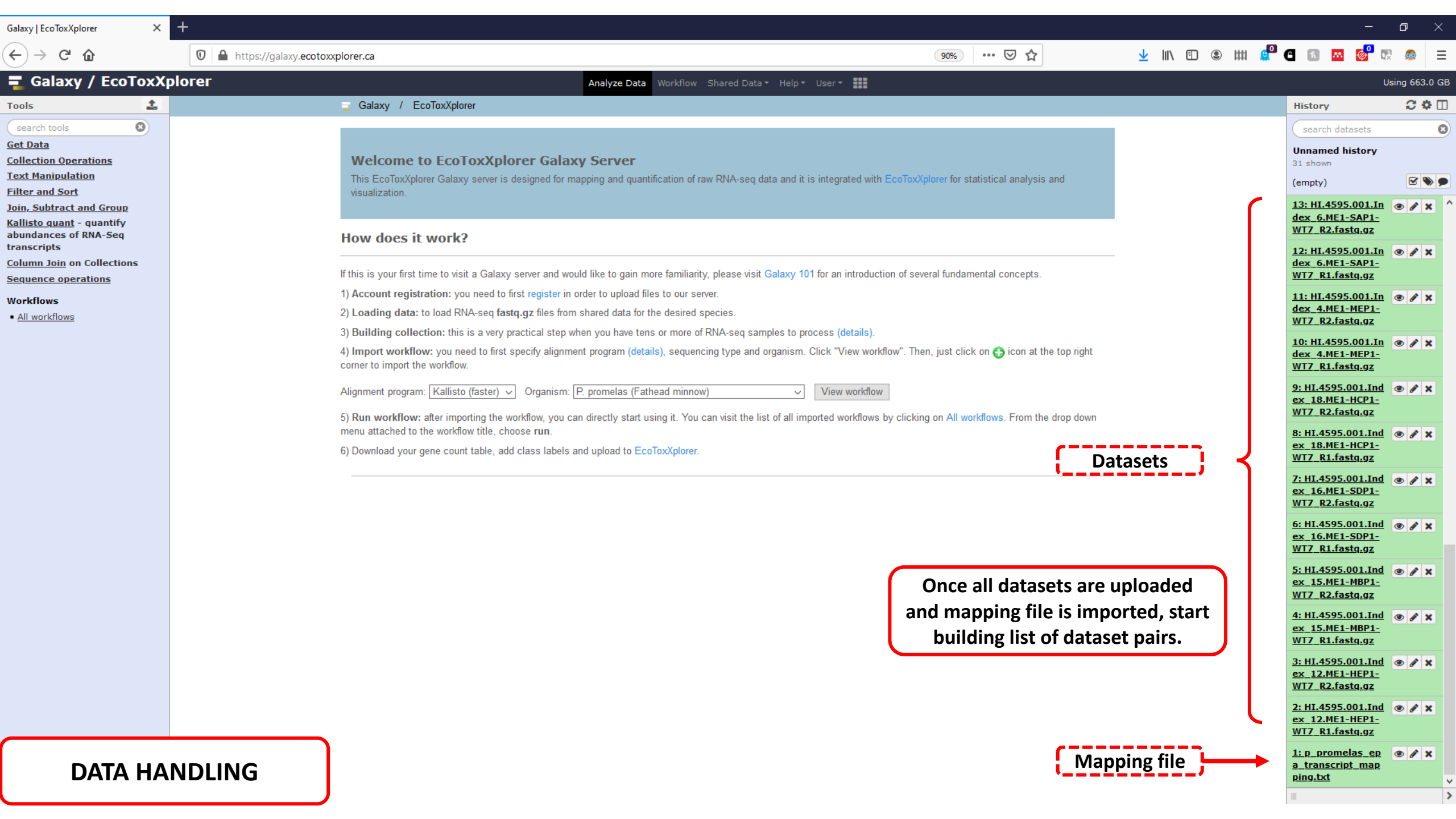
Step-by-step instructions to execute our workflow.

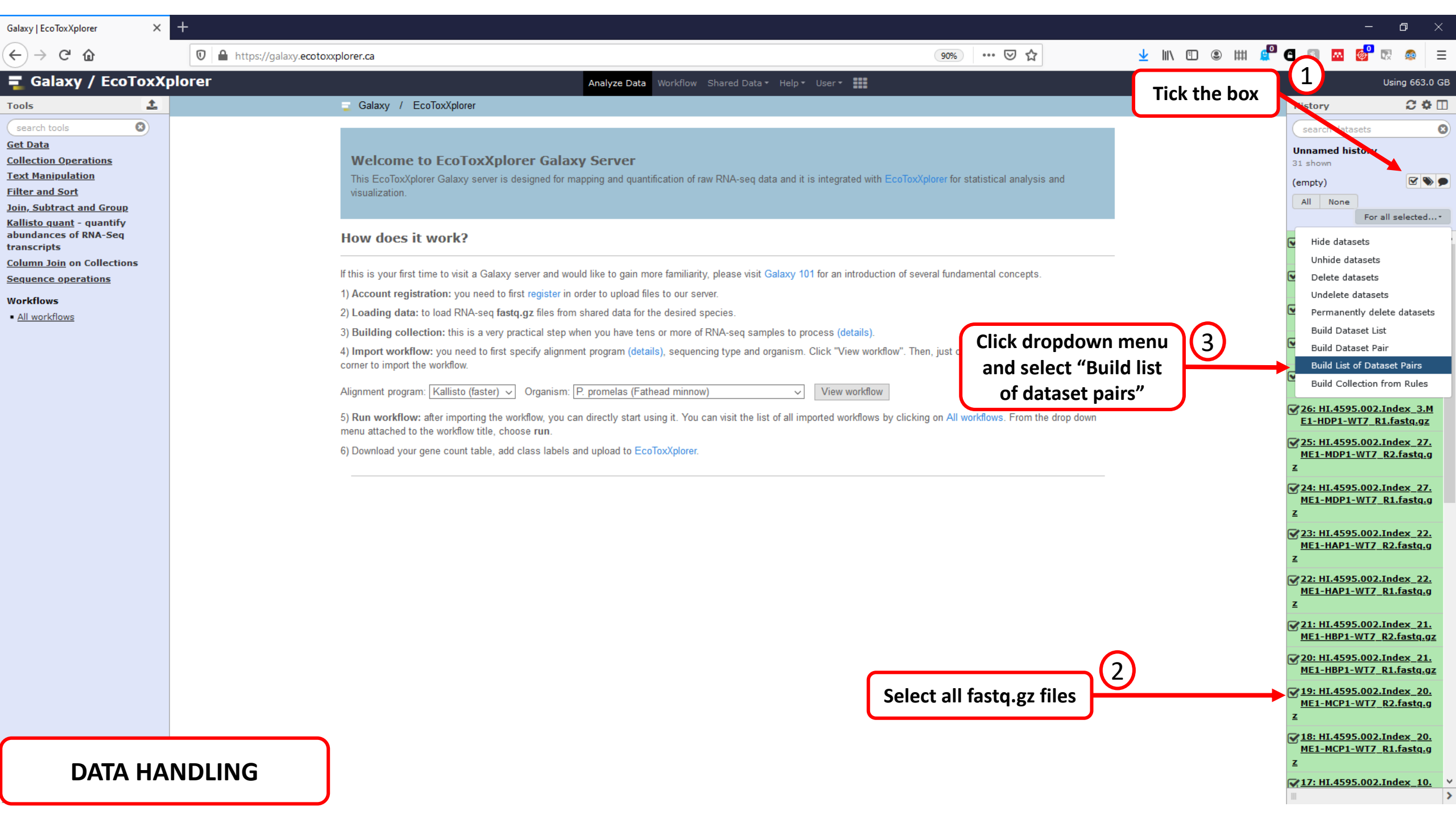

Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
Login or Register
Using 0 bytes
Login
Register
Tools
search tools
Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
Column Join on Collections
Sequence operations
Workflows
All workflows
Create account
Email address:
Password:
Strength
Confirm password:
Public name:
Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes ('.', '_', '-').
Subscribe to mailing list:
See all Galaxy project mailing lists.
Submit
Click here to register or to log-in for subsequent visits.
History
search datasets
Unnamed history
(empty)
This history is empty. You can load your own data or get data from an external source


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
User
Using 663.0 GB
Tools
search tools
Get Data
Upload File from your computer
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
History
search datasets
Unnamed history
(empty)
This history is empty. You can load your own data or get data from an external source
Download from web or upload from disk
Regular
Composite
Collection
Rule-based
Drop files here
Type (set all):
Auto-detect
Genome (set all):
----- Additional Species A...
Choose local file
Paste/Fetch data
Pause
Reset
Start
Close
1
To upload datasets, click Get Data > Upload File or click the Upload icon.
2
To upload datasets, drag-and-drop, select local file, or provide online link of datasets. For larger files, use an FTP Client. For more details on uploading data to Galaxy, visit Galaxy Community Hub tutorial.
DATA UPLOAD


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
User
Using 711.3 GB
Tools
search tools
Get Data
Upload File from your computer
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Column Join on Collections
Sequence operations
Workflows
All workflows
Download from web or upload from disk
Regular
Composite
Collection
Rule-based
Name
Size
Type
Genome
Settings
Status
sub_SD_R1.fastq.gz 6.1 MB Auto-det... ----- Additional S... 100%
sub_SD_R2.fastq.gz 6.4 MB Auto-det... ----- Additional S... 100%
sub_SE_R1.fastq.gz 6.1 MB Auto-det... ----- Additional S... 100%
sub_SE_R2.fastq.gz 6.3 MB Auto-det... ----- Additional S... 100%
Type (set all): Auto-detect
Genome (set all): ----- Additional Specie...
Choose local file
Paste/Fetch data
Pause
Reset
Start
Close
History
search datasets
Unnamed history
4 shown
(empty)
4: sub_SE_R2.fastq.gz
3: sub_SE_R1.fastq.gz
2: sub_SD_R2.fastq.gz
1: sub_SD_R1.fastq.gz
1
Files turn green when uploaded.
2
Once files are selected, it populates the File Upload pop-up menu. Click “Start” to upload.
3
Uploaded files populate history pane
DATA UPLOAD


Galaxy | EcoToxXplorer | Data Libra
https://galaxy.ecotoxxplorer.ca/library/list#folders/Fa5e7909db9879e3a
Select "Analyze Data" to go back to Analysis window
Analyze Data
Workflow
Shared Data
To get our mapping file, navigate to Shared Data > Data Libraries
Using 711.4 GB
DATA LIBRARIES
include deleted
To History
Import to history
Delete
Details
Help
6
1
as Datasets
as a Collection
Libraries / Pimephales promelas
Selected datasets imported into history. Click this to start analyzing it.
name
description
data type
size
time updated (UTC)
state
EPA_FHM_2.0.transcripts.fa
fasta
162.5 MB
2020-01-24 12:25 AM
p_promelas_epa_transcript_mapping.txt
tabular
424.8 KB
2020-01-22 05:43 PM
items shown (change) 2 total
5
Pop-up appears after data import
3
Send to history as Datasets. Select the correct history in the pop-up window to import the file.
2
Select mapping file(s).
Import into History
Select history:
Unnamed history
or create new:
name of the new history
Import
Close
4
Select "Import"
DATA UPLOAD
https://galaxy.ecotoxxplorer.ca/library/list


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
User
Using 663.0 GB
Tools
search tools
Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
Column Join on Collections
Sequence operations
Workflows
All workflows
Galaxy / EcoToxXplorer
Welcome to EcoToxXplorer Galaxy Server
This EcoToxXplorer Galaxy server is designed for mapping and quantification of raw RNA-seq data and it is integrated with EcoToxXplorer for statistical analysis and visualization.
How does it work?
If this is your first time to visit a Galaxy server and would like to gain more familiarity, please visit Galaxy 101 for an introduction of several fundamental concepts.
1) Account registration: you need to first register in order to upload files to our server.
2) Loading data: to load RNA-seq fastq.gz files from shared data for the desired species.
3) Building collection: this is a very practical step when you have tens or more of RNA-seq samples to process (details).
4) Import workflow: you need to first specify alignment program (details), sequencing type and organism. Click "View workflow". Then, just click on icon at the top right corner to import the workflow.
Alignment program: Kallisto (faster)
Organism: P. promelas (Fathead minnow)
View workflow
5) Run workflow: after importing the workflow, you can directly start using it. You can visit the list of all imported workflows by clicking on All workflows. From the drop down menu attached to the workflow title, choose run.
6) Download your gene count table, add class labels and upload to EcoToxXplorer.
History
search datasets
Unnamed history
31 shown
(empty)
13: HI.4595.001.Index_6.ME1-SAP1-WT7_R2.fastq.gz
12: HI.4595.001.Index_6.ME1-SAP1-WT7_R1.fastq.gz
11: HI.4595.001.Index_4.ME1-MEP1-WT7_R2.fastq.gz
10: HI.4595.001.Index_4.ME1-MEP1-WT7_R1.fastq.gz
9: HI.4595.001.Index_18.ME1-HCP1-WT7_R2.fastq.gz
8: HI.4595.001.Index_18.ME1-HCP1-WT7_R1.fastq.gz
7: HI.4595.001.Index_16.ME1-SDP1-WT7_R2.fastq.gz
6: HI.4595.001.Index_16.ME1-SDP1-WT7_R1.fastq.gz
5: HI.4595.001.Index_15.ME1-MBP1-WT7_R2.fastq.gz
4: HI.4595.001.Index_15.ME1-MBP1-WT7_R1.fastq.gz
3: HI.4595.001.Index_12.ME1-HEP1-WT7_R2.fastq.gz
2: HI.4595.001.Index_12.ME1-HEP1-WT7_R1.fastq.gz
1: p_promelas_epa_transcript_mapping.txt
Datasets
Once all datasets are uploaded and mapping file is imported, start building list of dataset pairs.
Mapping file
DATA HANDLING


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
User
Using 663.0 GB
Tools
search tools
Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
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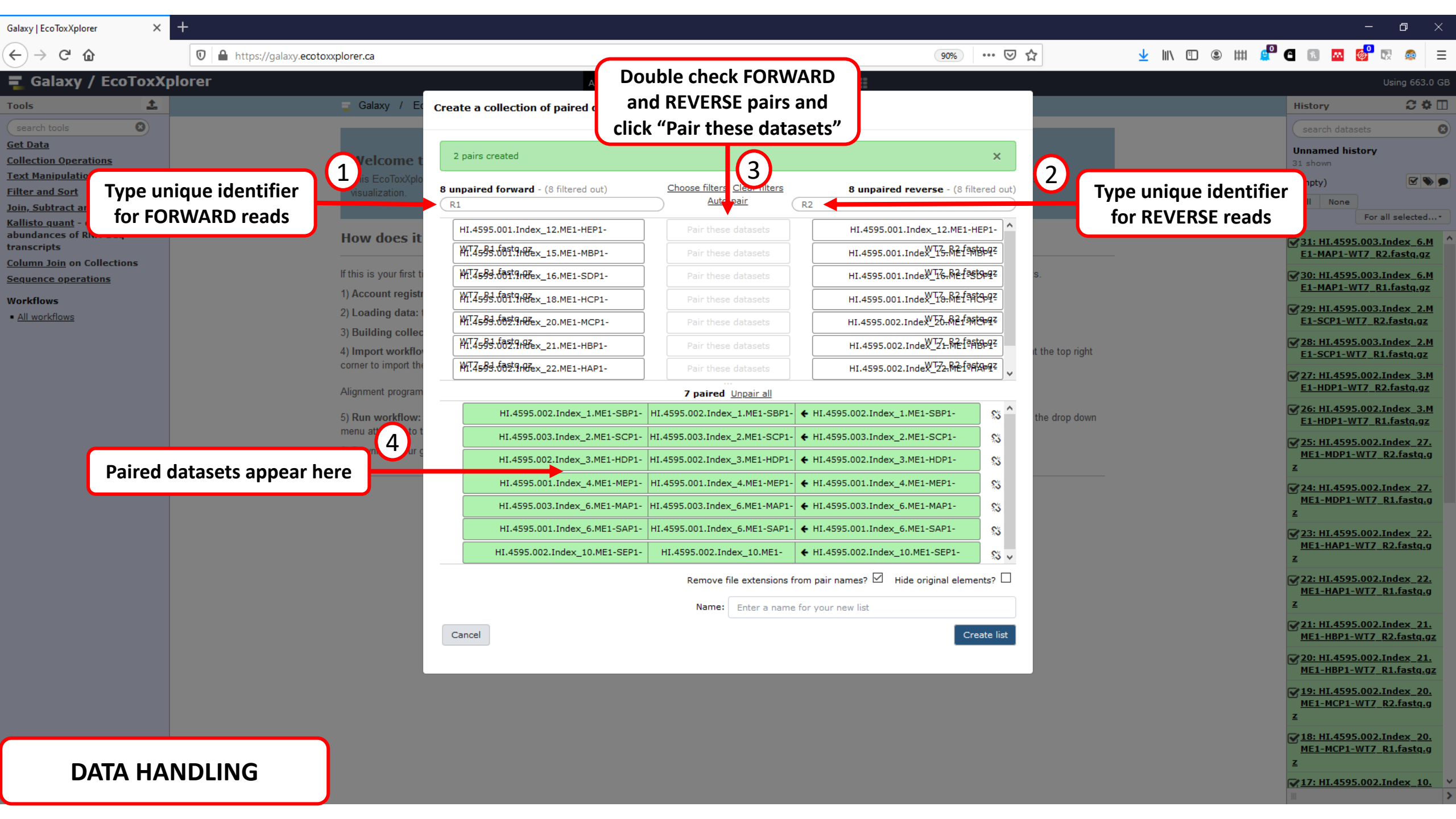
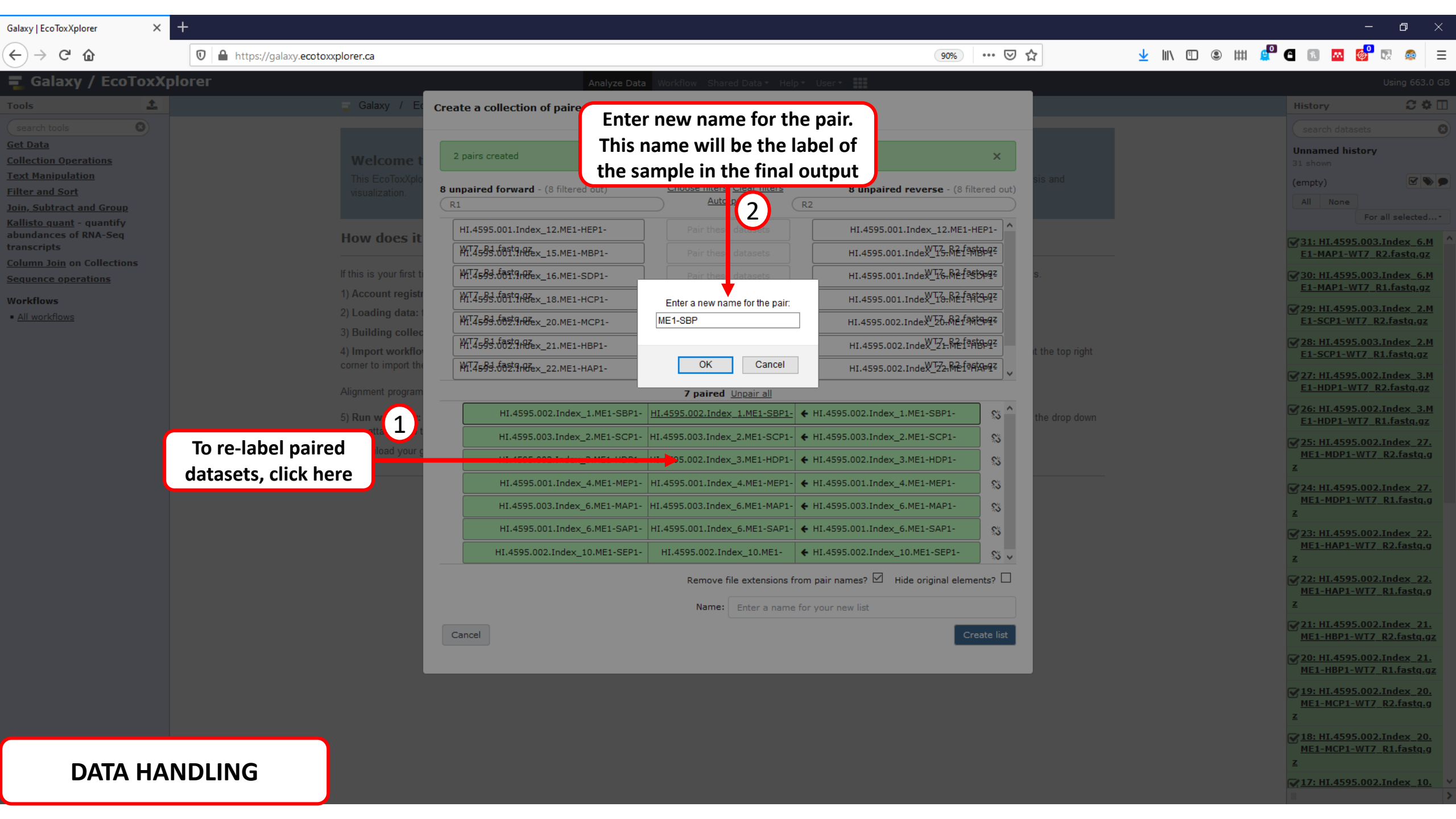
4) Import workflow: you need to first specify alignment program (details), sequencing type and organism. Click "View workflow". Then, just c
corner to import the workflow.
Alignment program: Kallisto (faster)
Organism: P. promelas (Fathead minnow)
View workflow
5) Run workflow: after importing the workflow, you can directly start using it. You can visit the list of all imported workflows by clicking on All workflows. From the drop down menu attached to the workflow title, choose run.
6) Download your gene count table, add class labels and upload to EcoToxXplorer.
Tick the box
1
History
Unnamed histo
31 shown
(empty)
All
None
For all selected...
Hide datasets
Unhide datasets
Delete datasets
Undelete datasets
Permanently delete datasets
Build Dataset List
Build Dataset Pair
Build List of Dataset Pairs
Build Collection from Rules
Click dropdown menu and select “Build list of dataset pairs”
3
26: HI.4595.002.Index_3.ME1-HDP1-WT7_R1.fastq.gz
25: HI.4595.002.Index_27.ME1-MDP1-WT7_R2.fastq.gz
24: HI.4595.002.Index_27.ME1-MDP1-WT7_R1.fastq.gz
23: HI.4595.002.Index_22.ME1-HAP1-WT7_R2.fastq.gz
22: HI.4595.002.Index_22.ME1-HAP1-WT7_R1.fastq.gz
21: HI.4595.002.Index_21.ME1-HBP1-WT7_R2.fastq.gz
20: HI.4595.002.Index_21.ME1-HBP1-WT7_R1.fastq.gz
19: HI.4595.002.Index_20.ME1-MCP1-WT7_R2.fastq.gz
18: HI.4595.002.Index_20.ME1-MCP1-WT7_R1.fastq.gz
17: HI.4595.002.Index_10.
Select all fastq.gz files
2
DATA HANDLING


Double check FORWARD and REVERSE pairs and click “Pair these datasets”
1
Type unique identifier for FORWARD reads
2
Type unique identifier for REVERSE reads
3
4
Paired datasets appear here
DATA HANDLING
Create a collection of paired
2 pairs created
8 unpaired forward - (8 filtered out)
R1
Choose filters
Clear filters
Auto-pair
8 unpaired reverse - (8 filtered out)
R2
Pair these datasets
7 paired
Unpair all
Remove file extensions from pair names?
Hide original elements?
Name:
Enter a name for your new list
Cancel
Create list
Galaxy / EcoToxXplorer
Tools
History
Get Data
Collection Operations
Workflows
All workflows


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca
Galaxy / EcoToxXplorer
Analyze Data
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Using 663.0 GB
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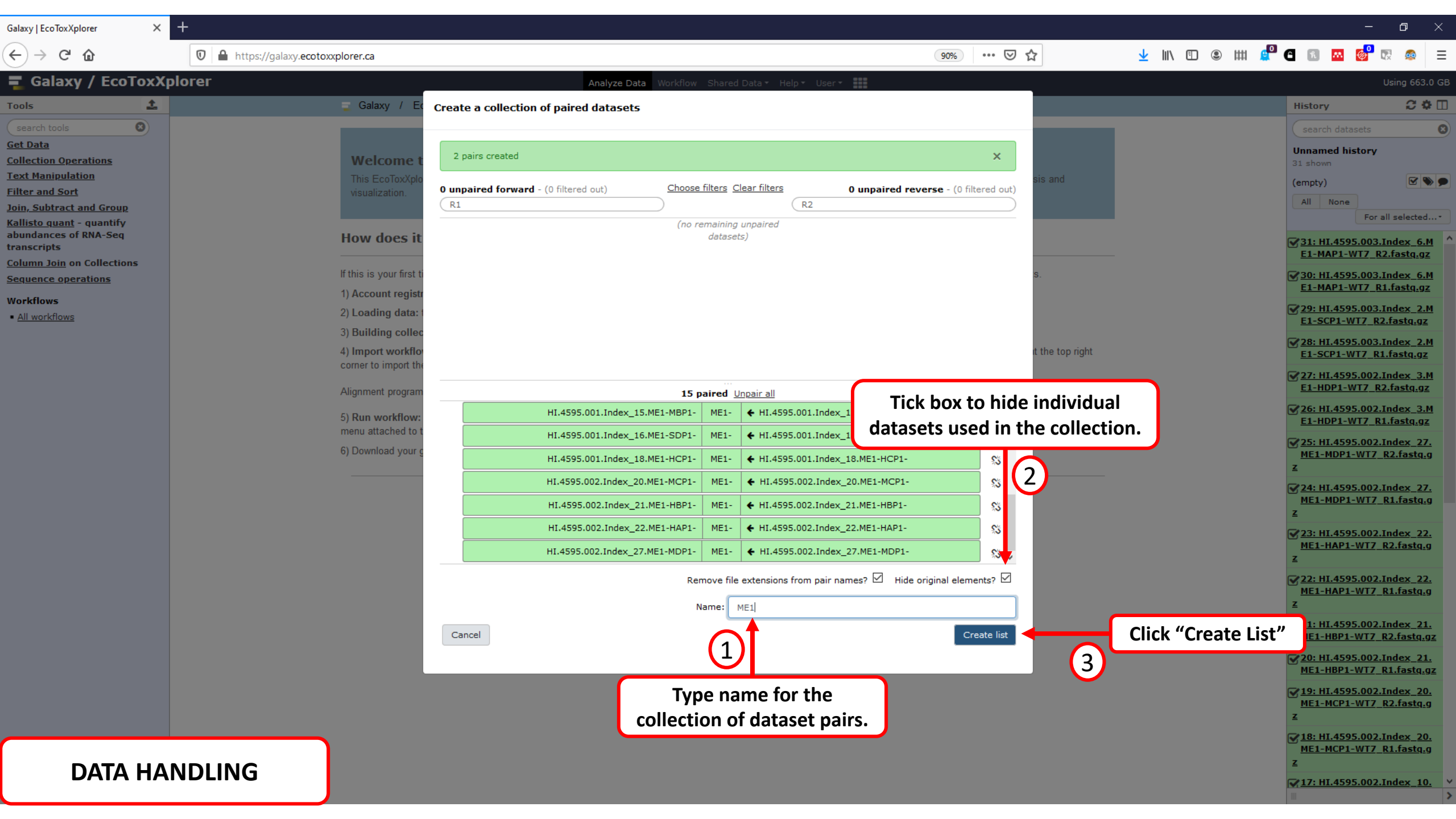
Column Join on Collections
Sequence operations
Workflows
All workflows
Create a collection of paire
2 pairs created
Enter new name for the pair. This name will be the label of the sample in the final output
2
8 unpaired forward - (8 filtered out)
8 unpaired reverse - (8 filtered out)
R1
R2
HI.4595.001.Index_12.ME1-HEP1-
HI.4595.001.Index_15.ME1-MBP1-
HI.4595.001.Index_16.ME1-SDP1-
HI.4595.001.Index_18.ME1-HCP1-
HI.4595.002.Index_20.ME1-MCP1-
HI.4595.002.Index_21.ME1-HBP1-
HI.4595.002.Index_22.ME1-HAP1-
WT7_R1.fastq.gz
WT7_R2.fastq.gz
Enter a new name for the pair:
ME1-SBP
OK
Cancel
7 paired Unpair all
HI.4595.002.Index_1.ME1-SBP1-
HI.4595.003.Index_2.ME1-SCP1-
HI.4595.002.Index_3.ME1-HDP1-
HI.4595.001.Index_4.ME1-MEP1-
HI.4595.003.Index_6.ME1-MAP1-
HI.4595.001.Index_6.ME1-SAP1-
HI.4595.002.Index_10.ME1-SEP1-
HI.4595.002.Index_10.ME1-
1
To re-label paired datasets, click here
Remove file extensions from pair names?
Hide original elements?
Name:
Enter a name for your new list
Cancel
Create list
History
search datasets
Unnamed history
31 shown
(empty)
All
None
For all selected...
31: HI.4595.003.Index_6.ME1-MAP1-WT7_R2.fastq.gz
30: HI.4595.003.Index_6.ME1-MAP1-WT7_R1.fastq.gz
29: HI.4595.003.Index_2.ME1-SCP1-WT7_R2.fastq.gz
28: HI.4595.003.Index_2.ME1-SCP1-WT7_R1.fastq.gz
27: HI.4595.002.Index_3.ME1-HDP1-WT7_R2.fastq.gz
26: HI.4595.002.Index_3.ME1-HDP1-WT7_R1.fastq.gz
25: HI.4595.002.Index_27.ME1-MDP1-WT7_R2.fastq.gz
24: HI.4595.002.Index_27.ME1-MDP1-WT7_R1.fastq.gz
23: HI.4595.002.Index_22.ME1-HAP1-WT7_R2.fastq.gz
22: HI.4595.002.Index_22.ME1-HAP1-WT7_R1.fastq.gz
21: HI.4595.002.Index_21.ME1-HBP1-WT7_R2.fastq.gz
20: HI.4595.002.Index_21.ME1-HBP1-WT7_R1.fastq.gz
19: HI.4595.002.Index_20.ME1-MCP1-WT7_R2.fastq.gz
18: HI.4595.002.Index_20.ME1-MCP1-WT7_R1.fastq.gz
17: HI.4595.002.Index_10.
DATA HANDLING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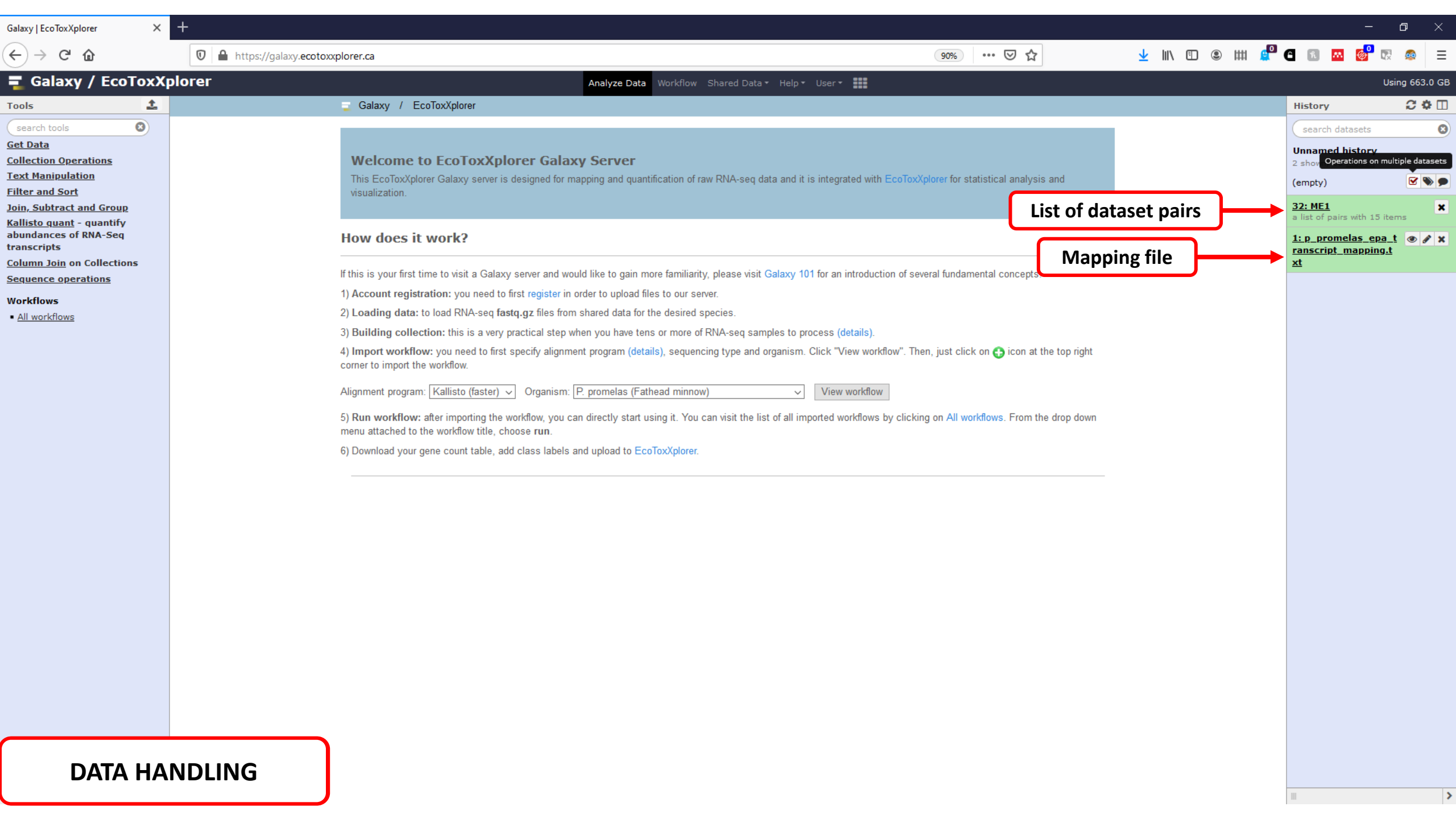
Column Join on Collections
Sequence operations
Workflows
All workflows
History
search datasets
Unnamed history
31 shown
(empty)
All
None
For all selected...
31: HI.4595.003.Index_6.ME1-MAP1-WT7_R2.fastq.gz
30: HI.4595.003.Index_6.ME1-MAP1-WT7_R1.fastq.gz
29: HI.4595.003.Index_2.ME1-SCP1-WT7_R2.fastq.gz
28: HI.4595.003.Index_2.ME1-SCP1-WT7_R1.fastq.gz
27: HI.4595.002.Index_3.ME1-HDP1-WT7_R2.fastq.gz
26: HI.4595.002.Index_3.ME1-HDP1-WT7_R1.fastq.gz
25: HI.4595.002.Index_27.ME1-MDP1-WT7_R2.fastq.gz
24: HI.4595.002.Index_27.ME1-MDP1-WT7_R1.fastq.gz
23: HI.4595.002.Index_22.ME1-HAP1-WT7_R2.fastq.gz
22: HI.4595.002.Index_22.ME1-HAP1-WT7_R1.fastq.gz
21: HI.4595.002.Index_21.ME1-HBP1-WT7_R2.fastq.gz
20: HI.4595.002.Index_21.ME1-HBP1-WT7_R1.fastq.gz
19: HI.4595.002.Index_20.ME1-MCP1-WT7_R2.fastq.gz
18: HI.4595.002.Index_20.ME1-MCP1-WT7_R1.fastq.gz
17: HI.4595.002.Index_10.
Create a collection of paired datasets
2 pairs created
0 unpaired forward - (0 filtered out)
Choose filters
Clear filters
0 unpaired reverse - (0 filtered out)
R1
R2
(no remaining unpaired datasets)
15 paired
Unpair all
HI.4595.001.Index_15.ME1-MBP1- ME1- HI.4595.001.Index_1
HI.4595.001.Index_16.ME1-SDP1- ME1- HI.4595.001.Index_1
HI.4595.001.Index_18.ME1-HCP1- ME1- HI.4595.001.Index_18.ME1-HCP1-
HI.4595.002.Index_20.ME1-MCP1- ME1- HI.4595.002.Index_20.ME1-MCP1-
HI.4595.002.Index_21.ME1-HBP1- ME1- HI.4595.002.Index_21.ME1-HBP1-
HI.4595.002.Index_22.ME1-HAP1- ME1- HI.4595.002.Index_22.ME1-HAP1-
HI.4595.002.Index_27.ME1-MDP1- ME1- HI.4595.002.Index_27.ME1-MDP1-
Remove file extensions from pair names?
Hide original elements?
Name:
ME1
Cancel
Create list
Tick box to hide individual datasets used in the collection.
2
Click “Create List”
3
1
Type name for the collection of dataset pairs.
DATA HANDLING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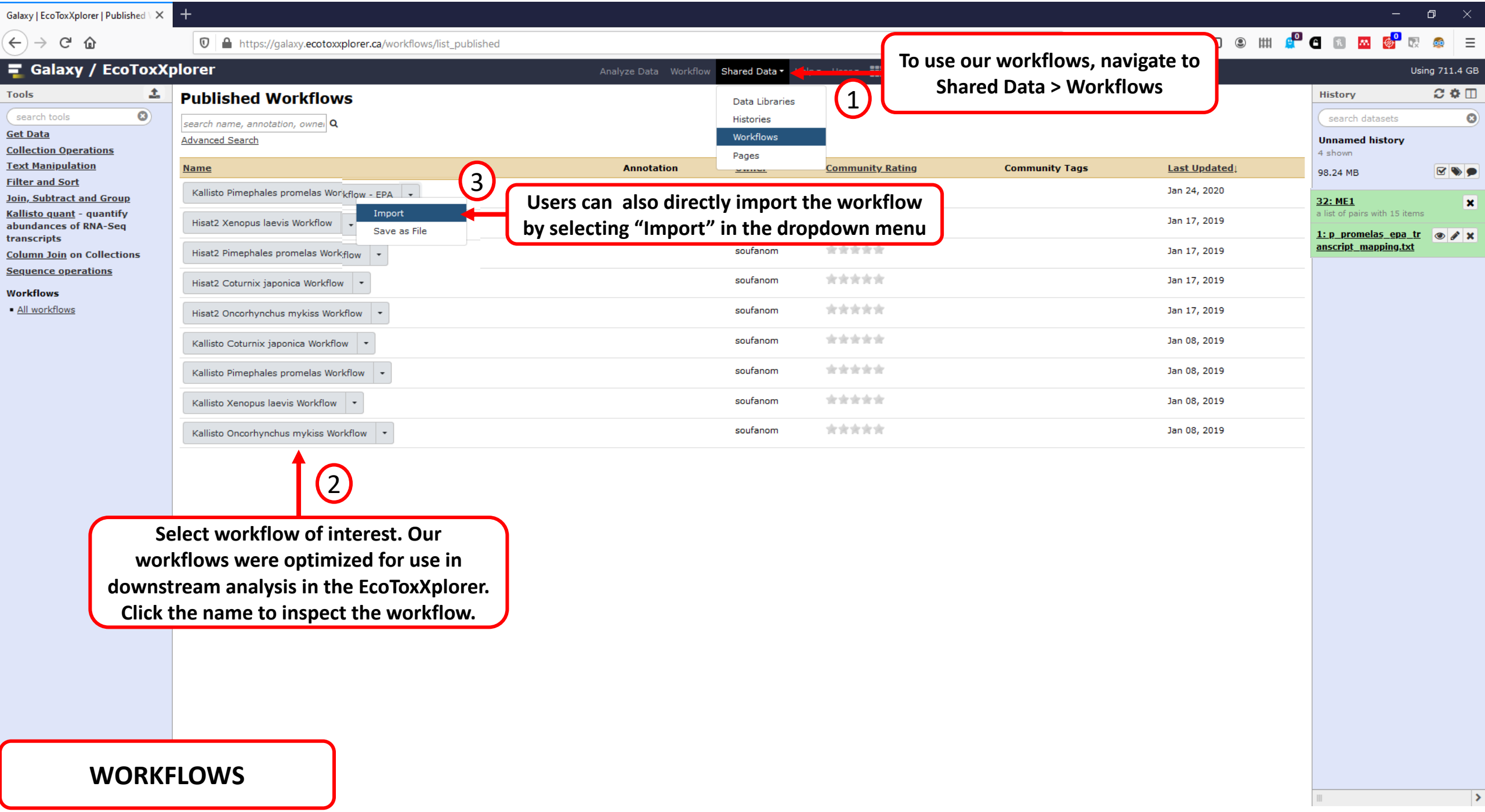
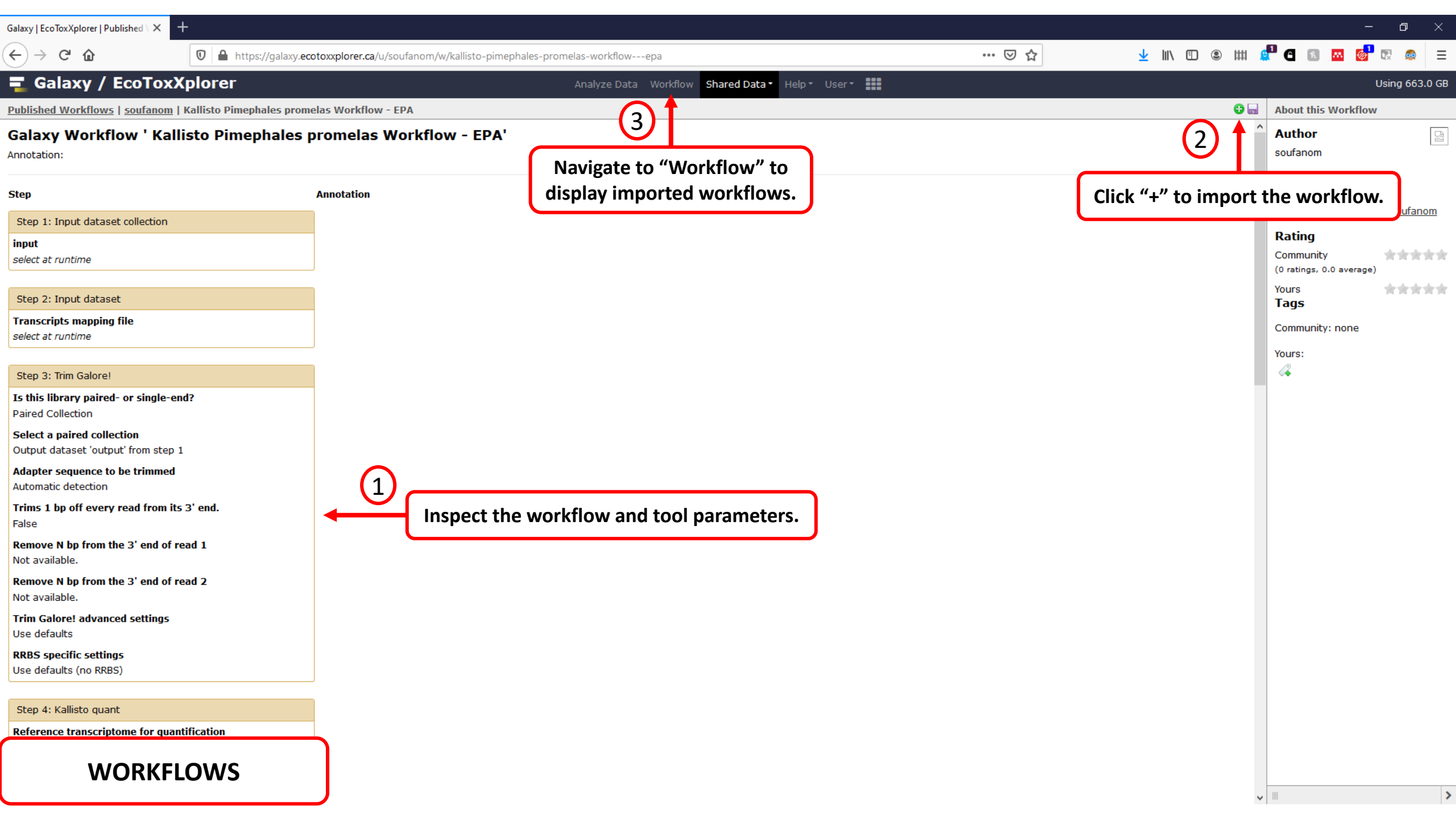
Sequence operations
Workflows
All workflows
Galaxy / EcoToxXplorer
Welcome to EcoToxXplorer Galaxy Server
This EcoToxXplorer Galaxy server is designed for mapping and quantification of raw RNA-seq data and it is integrated with EcoToxXplorer for statistical analysis and visualization.
How does it work?
If this is your first time to visit a Galaxy server and would like to gain more familiarity, please visit Galaxy 101 for an introduction of several fundamental concepts.
1) Account registration: you need to first register in order to upload files to our server.
2) Loading data: to load RNA-seq fastq.gz files from shared data for the desired species.
3) Building collection: this is a very practical step when you have tens or more of RNA-seq samples to process (details).
4) Import workflow: you need to first specify alignment program (details), sequencing type and organism. Click "View workflow". Then, just click on icon at the top right corner to import the workflow.
Alignment program: Kallisto (faster)
Organism: P. promelas (Fathead minnow)
View workflow
5) Run workflow: after importing the workflow, you can directly start using it. You can visit the list of all imported workflows by clicking on All workflows. From the drop down menu attached to the workflow title, choose run.
6) Download your gene count table, add class labels and upload to EcoToxXplorer.
History
search datasets
Unnamed history
Operations on multiple datasets
(empty)
32: ME1
a list of pairs with 15 items
1: p_promelas_epa_transcript_mapping.txt
List of dataset pairs
Mapping file
DATA HANDLING


Galaxy | EcoToxXplorer | Published
https://galaxy.ecotoxxplorer.ca/workflows/list_published
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Using 711.4 GB
Data Libraries
Histories
Workflows
Pages
1
To use our workflows, navigate to Shared Data > Workflows
Tools
search tools
Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
Column Join on Collections
Sequence operations
Workflows
All workflows
Published Workflows
search name, annotation, owner
Advanced Search
Name
Annotation
Owner
Community Rating
Community Tags
Last Updated
Kallisto Pimephales promelas Workflow - EPA
Import
Save as File
3
Users can also directly import the workflow by selecting “Import” in the dropdown menu
Hisat2 Xenopus laevis Workflow
Hisat2 Pimephales promelas Workflow
Hisat2 Coturnix japonica Workflow
Hisat2 Oncorhynchus mykiss Workflow
Kallisto Coturnix japonica Workflow
Kallisto Pimephales promelas Workflow
Kallisto Xenopus laevis Workflow
Kallisto Oncorhynchus mykiss Workflow
Jan 24, 2020
Jan 17, 2019
soufanom
Jan 08, 2019
2
Select workflow of interest. Our workflows were optimized for use in downstream analysis in the EcoToxXplorer. Click the name to inspect the workflow.
History
search datasets
Unnamed history
4 shown
98.24 MB
32: ME1
a list of pairs with 15 items
1: p_promelas_epa_transcript_mapping.txt
WORKFLOWS


Galaxy | EcoToxXplorer | Published
https://galaxy.ecotoxxplorer.ca/u/soufanom/w/kallisto-pimephales-promelas-workflow---epa
Galaxy / EcoToxXplorer
Analyze Data
Workflow
Shared Data
Help
User
Using 663.0 GB
Published Workflows | soufanom | Kallisto Pimephales promelas Workflow - EPA
Galaxy Workflow ' Kallisto Pimephales promelas Workflow - EPA'
Annotation:
Step
Annotation
Step 1: Input dataset collection
input
select at runtime
Step 2: Input dataset
Transcripts mapping file
select at runtime
Step 3: Trim Galore!
Is this library paired- or single-end?
Paired Collection
Select a paired collection
Output dataset 'output' from step 1
Adapter sequence to be trimmed
Automatic detection
Trims 1 bp off every read from its 3' end.
False
Remove N bp from the 3' end of read 1
Not available.
Remove N bp from the 3' end of read 2
Not available.
Trim Galore! advanced settings
Use defaults
RRBS specific settings
Use defaults (no RRBS)
Step 4: Kallisto quant
Reference transcriptome for quantification
About this Workflow
Author
soufanom
Rating
Community
(0 ratings, 0.0 average)
Yours
Tags
Community: none
Yours:
3
Navigate to “Workflow” to display imported workflows.
2
Click “+” to import the workflow.
1
Inspect the workflow and tool parameters.
WORKFLOWS

Galaxy | EcoToxXplorer | Workflows

https://galaxy.ecotoxxplorer.ca/workflows/list

Galaxy / EcoToxXplorer

Analyze Data | Workflow | Shared Data | Help | User | Using 711.4 GB

Tools

search tools

Get Data
Collection Operations
Text Manipulation
Filter and Sort
Join, Subtract and Group
Kallisto quant - quantify abundances of RNA-Seq transcripts
Column Join on Collections
Sequence operations

Workflows
- All workflows

Your workflows

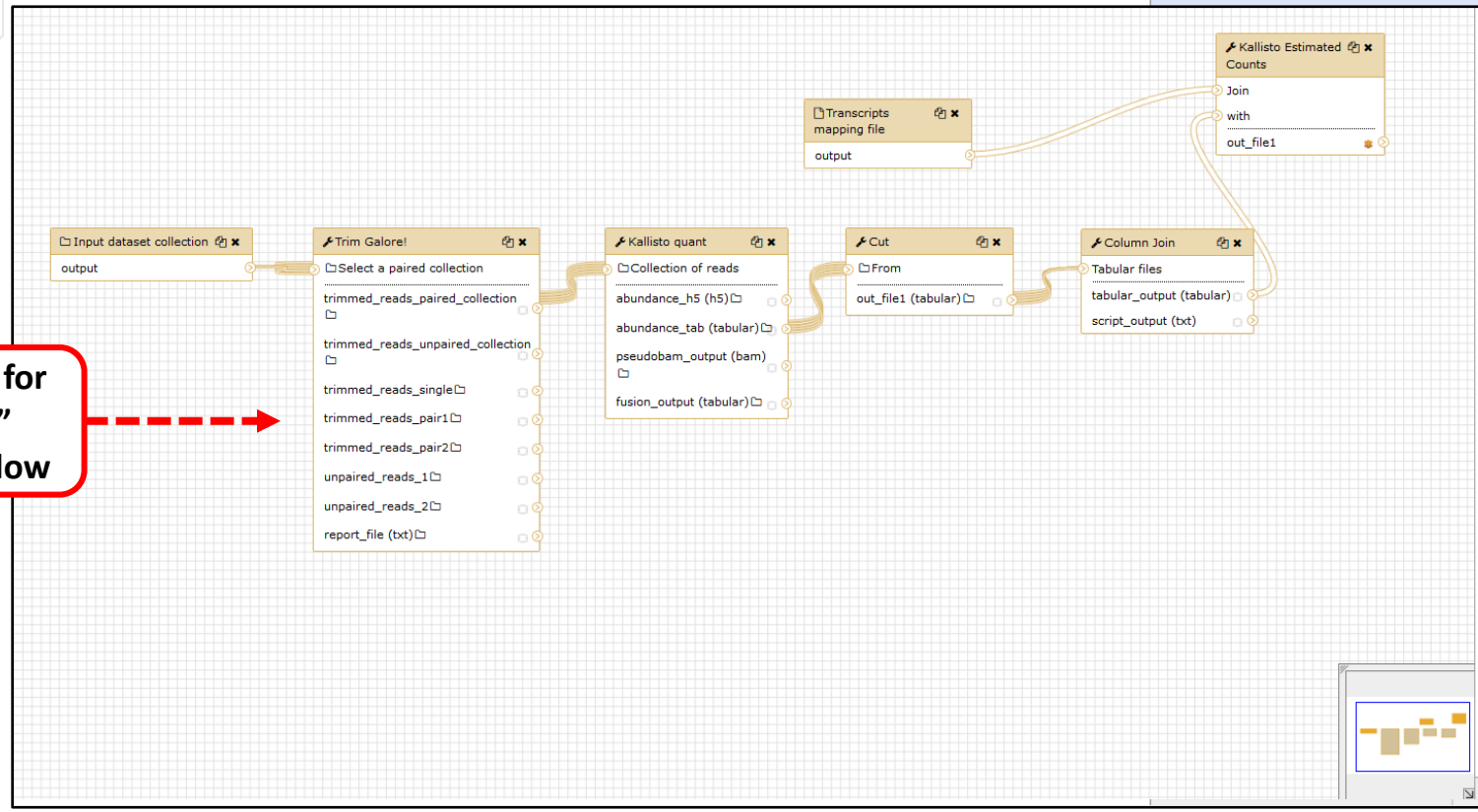
search for workflow...

Name	Tags	Owner	# of Steps	Published	Show in tools panel
imported: Kallisto Pimephales promelas Workflow - EPA		You	7	No	
imported: Kallisto Pimephales promelas Workflow				No	
imported: Kallisto Oncorhynchus mykiss Workflow				No	
imported: Kallisto Pimephales promelas Workflow		You	7	No	
imported: Hisat2 Oncorhynchus mykiss Workflow		You	6	No	

Edit
Run
Share
Download
Copy
Rename
View
Delete

Click "Run" to use selected workflow.

Click dropdown menu for more options. "Edit" displays the full workflow



History

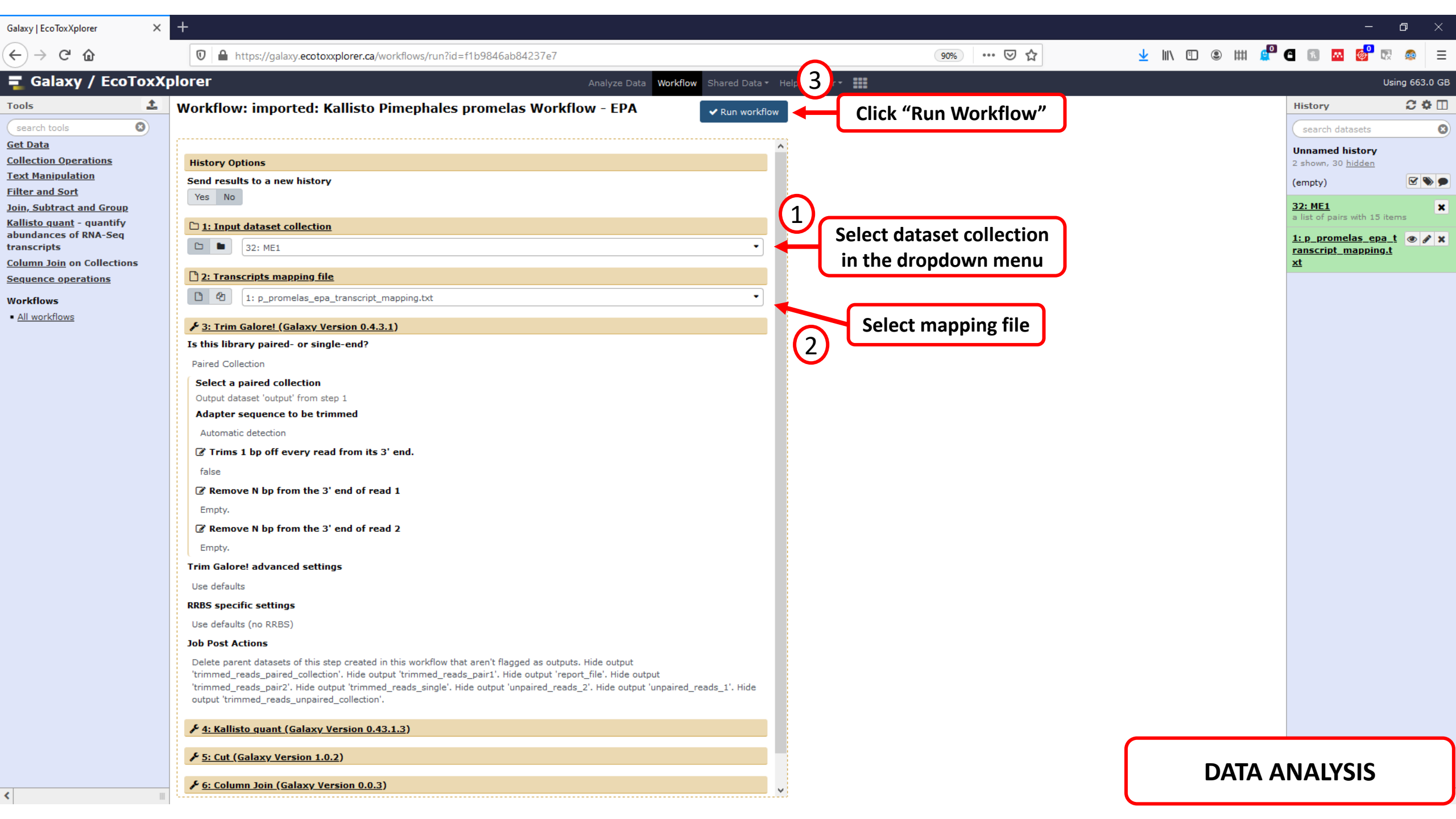
search datasets

Unnamed history
2 shown, 1 deleted, 110 hidden
48.33 GB

32: ME1
a list of pairs with 15 items

1: p_promelas_epa_transcript_mapping.txt

WORKFLOWS


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca/workflows/run?id=f1b9846ab84237e7
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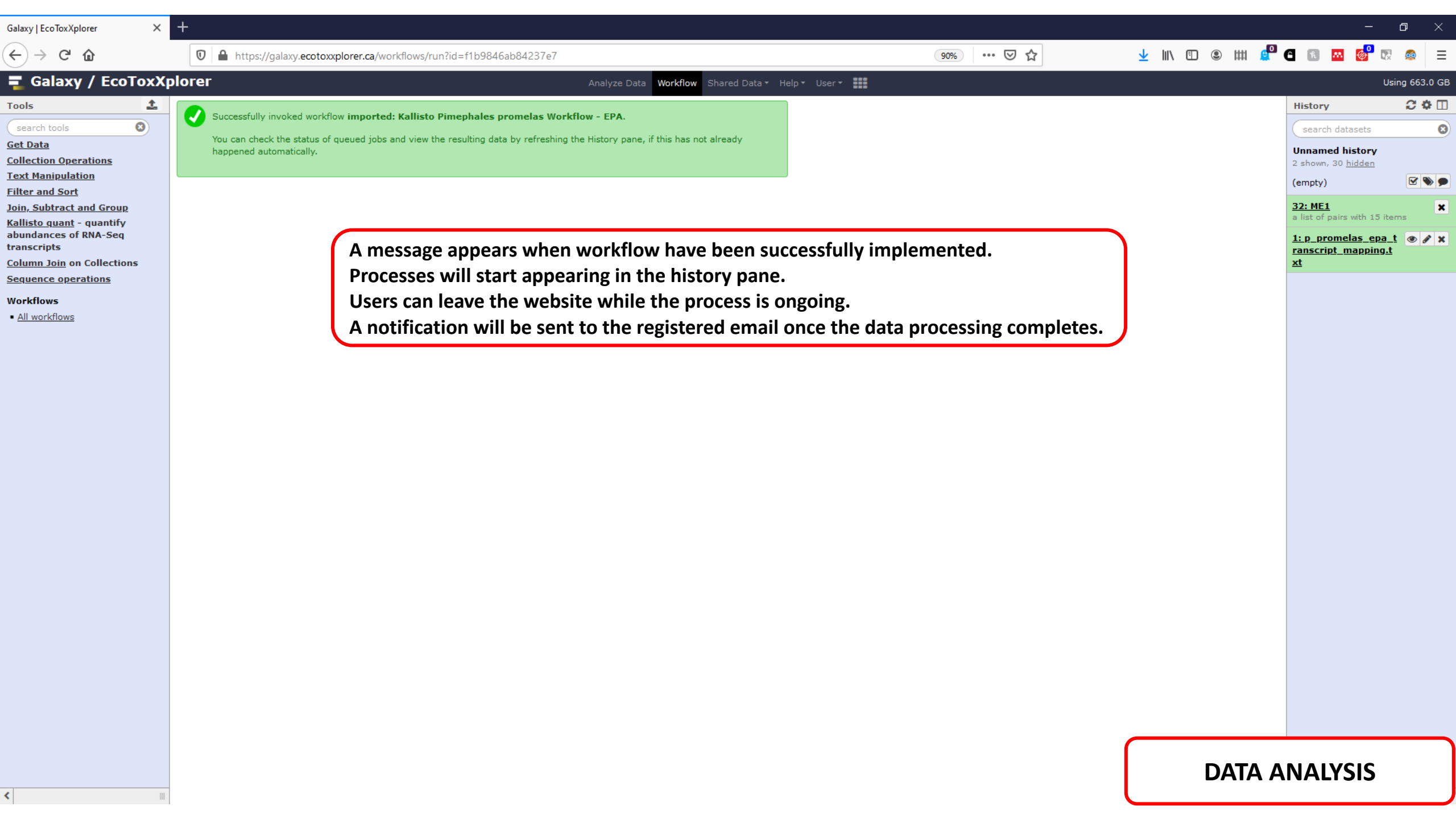
Workflow: imported: Kallisto Pimephales promelas Workflow - EPA
Run workflow
History Options
Send results to a new history
Yes
No
1: Input dataset collection
32: ME1
2: Transcripts mapping file
1: p_promelas_epa_transcript_mapping.txt
3: Trim Galore! (Galaxy Version 0.4.3.1)
Is this library paired- or single-end?
Paired Collection
Select a paired collection
Output dataset 'output' from step 1
Adapter sequence to be trimmed
Automatic detection
Trims 1 bp off every read from its 3' end.
false
Remove N bp from the 3' end of read 1
Empty.
Remove N bp from the 3' end of read 2
Empty.
Trim Galore! advanced settings
Use defaults
RRBS specific settings
Use defaults (no RRBS)
Job Post Actions
Delete parent datasets of this step created in this workflow that aren't flagged as outputs. Hide output 'trimmed_reads_paired_collection'. Hide output 'trimmed_reads_pair1'. Hide output 'report_file'. Hide output 'trimmed_reads_pair2'. Hide output 'trimmed_reads_single'. Hide output 'unpaired_reads_2'. Hide output 'unpaired_reads_1'. Hide output 'trimmed_reads_unpaired_collection'.
4: Kallisto quant (Galaxy Version 0.43.1.3)
5: Cut (Galaxy Version 1.0.2)
6: Column Join (Galaxy Version 0.0.3)
History
search datasets
Unnamed history
2 shown, 30 hidden
(empty)
32: ME1
a list of pairs with 15 items
1: p_promelas_epa_transcript_mapping.txt
3
Click “Run Workflow”
1
Select dataset collection in the dropdown menu
2
Select mapping file
DATA ANALYSIS


Galaxy | EcoToxXplorer
https://galaxy.ecotoxxplorer.ca/workflows/run?id=f1b9846ab84237e7
Galaxy / EcoToxXplorer
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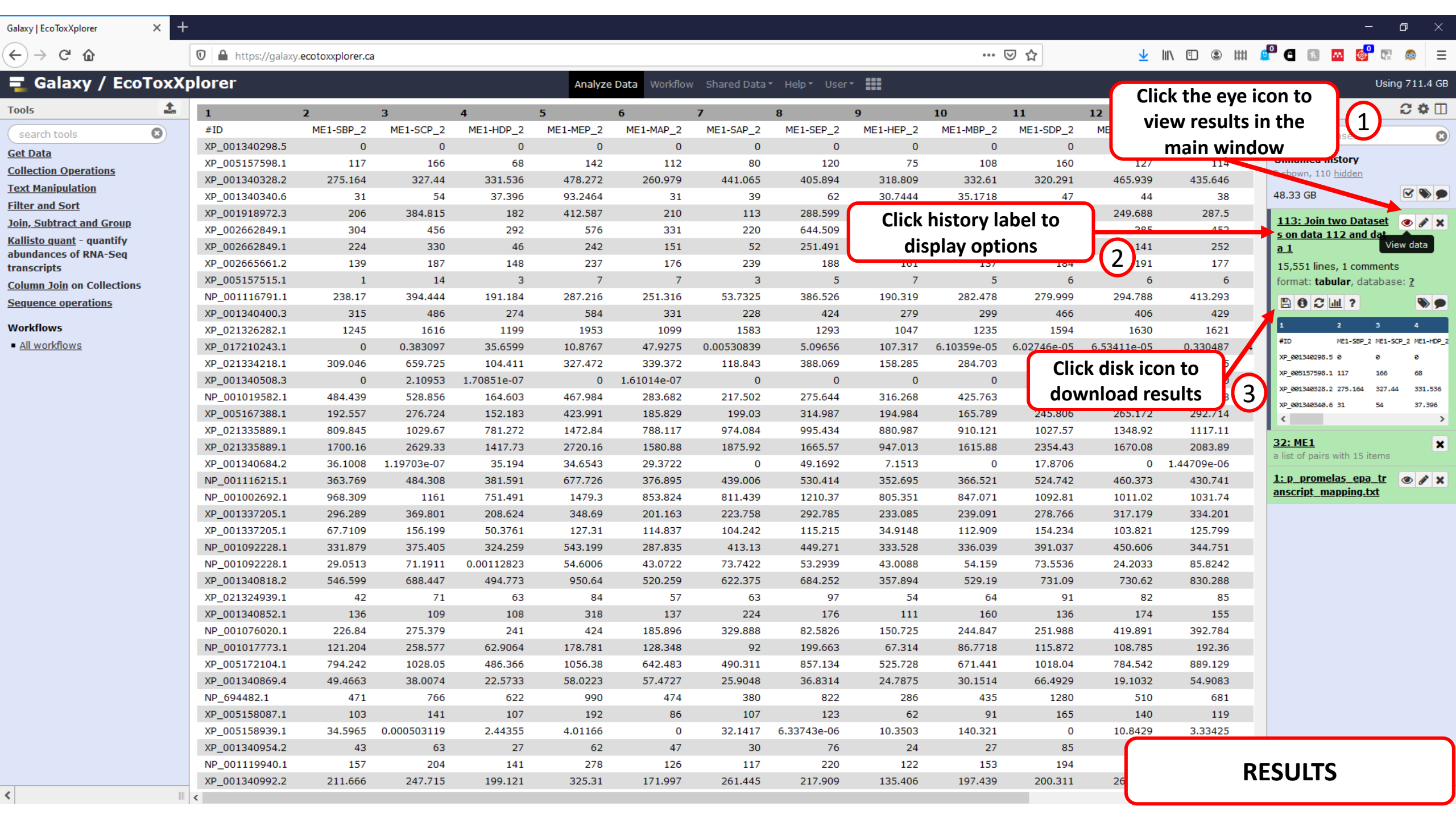
Workflows
All workflows
Successfully invoked workflow imported: Kallisto Pimephales promelas Workflow - EPA.
You can check the status of queued jobs and view the resulting data by refreshing the History pane, if this has not already happened automatically.
History
search datasets
Unnamed history
2 shown, 30 hidden
(empty)
32: ME1
a list of pairs with 15 items
1: p_promelas_epa_transcript_mapping.txt
A message appears when workflow have been successfully implemented.
Processes will start appearing in the history pane.
Users can leave the website while the process is ongoing.
A notification will be sent to the registered email once the data processing completes.
DATA ANALYSIS



1	2	3	4	5	6	7	8	9	10	11	12	
#ID	ME1-SBP_2	ME1-SCP_2	ME1-HDP_2	ME1-MEP_2	ME1-MAP_2	ME1-SAP_2	ME1-SEP_2	ME1-HEP_2	ME1-MBP_2	ME1-SDP_2	ME	
XP_001340298.5	0	0	0	0	0	0	0	0	0	0		
XP_005157598.1	117	166	68	142	112	80	120	75	108	160	127	114
XP_001340328.2	275.164	327.44	331.536	478.272	260.979	441.065	405.894	318.809	332.61	320.291	465.939	435.646
XP_001340340.6	31	54	37.396	93.2464	31	39	62	30.7444	35.1718	47	44	38
XP_001918972.3	206	384.815	182	412.587	210	113	288.599				249.688	287.5
XP_002662849.1	304	456	292	576	331	220	644.509					
XP_002662849.1	224	330	46	242	151	52	251.491				141	252
XP_002665661.2	139	187	148	237	176	239	188	161	137	184	191	177
XP_005157515.1	1	14	3	7	7	3	5	7	5	6	6	6
NP_001116791.1	238.17	394.444	191.184	287.216	251.316	53.7325	386.526	190.319	282.478	279.999	294.788	413.293
XP_001340400.3	315	486	274	584	331	228	424	279	299	466	406	429
XP_021326282.1	1245	1616	1199	1953	1099	1583	1293	1047	1235	1594	1630	1621
XP_017210243.1	0	0.383097	35.6599	10.8767	47.9275	0.00530839	5.09656	107.317	6.10359e-05	6.02746e-05	6.53411e-05	0.330487
XP_021334218.1	309.046	659.725	104.411	327.472	339.372	118.843	388.069	158.285	284.703			
XP_001340508.3	0	2.10953	1.70851e-07	0	1.61014e-07	0	0	0	0			
NP_001019582.1	484.439	528.856	164.603	467.984	283.682	217.502	275.644	316.268	425.763			
XP_005167388.1	192.557	276.724	152.183	423.991	185.829	199.03	314.987	194.984	165.789	245.806	265.172	292.714
XP_021335889.1	809.845	1029.67	781.272	1472.84	788.117	974.084	995.434	880.987	910.121	1027.57	1348.92	1117.11
XP_021335889.1	1700.16	2629.33	1417.73	2720.16	1580.88	1875.92	1665.57	947.013	1615.88	2354.43	1670.08	2083.89
XP_001340684.2	36.1008	1.19703e-07	35.194	34.6543	29.3722	0	49.1692	7.1513	0	17.8706	0	1.44709e-06
NP_001116215.1	363.769	484.308	381.591	677.726	376.895	439.006	530.414	352.695	366.521	524.742	460.373	430.741
NP_001002692.1	968.309	1161	751.491	1479.3	853.824	811.439	1210.37	805.351	847.071	1092.81	1011.02	1031.74
XP_001337205.1	296.289	369.801	208.624	348.69	201.163	223.758	292.785	233.085	239.091	278.766	317.179	334.201
XP_001337205.1	67.7109	156.199	50.3761	127.31	114.837	104.242	115.215	34.9148	112.909	154.234	103.821	125.799
NP_001092228.1	331.879	375.405	324.259	543.199	287.835	413.13	449.271	333.528	336.039	391.037	450.606	344.751
NP_001092228.1	29.0513	71.1911	0.00112823	54.6006	43.0722	73.7422	53.2939	43.0088	54.159	73.5536	24.2033	85.8242
XP_001340818.2	546.599	688.447	494.773	950.64	520.259	622.375	684.252	357.894	529.19	731.09	730.62	830.288
XP_021324939.1	42	71	63	84	57	63	97	54	64	91	82	85
XP_001340852.1	136	109	108	318	137	224	176	111	160	136	174	155
NP_001076020.1	226.84	275.379	241	424	185.896	329.888	82.5826	150.725	244.847	251.988	419.891	392.784
NP_001017773.1	121.204	258.577	62.9064	178.781	128.348	92	199.663	67.314	86.7718	115.872	108.785	192.36
XP_005172104.1	794.242	1028.05	486.366	1056.38	642.483	490.311	857.134	525.728	671.441	1018.04	784.542	889.129
XP_001340869.4	49.4663	38.0074	22.5733	58.0223	57.4727	25.9048	36.8314	24.7875	30.1514	66.4929	19.1032	54.9083
NP_694482.1	471	766	622	990	474	380	822	286	435	1280	510	681
XP_005158087.1	103	141	107	192	86	107	123	62	91	165	140	119
XP_005158939.1	34.5965	0.000503119	2.44355	4.01166	0	32.1417	6.33743e-06	10.3503	140.321	0	10.8429	3.33425
XP_001340954.2	43	63	27	62	47	30	76	24	27	85		
NP_001119940.1	157	204	141	278	126	117	220	122	153	194		
XP_001340992.2	211.666	247.715	199.121	325.31	171.997	261.445	217.909	135.406	197.439	200.311	26	

Questions?

Contact us at

https://www.ecotoxxplorer.ca/doc/ContactView.xhtml