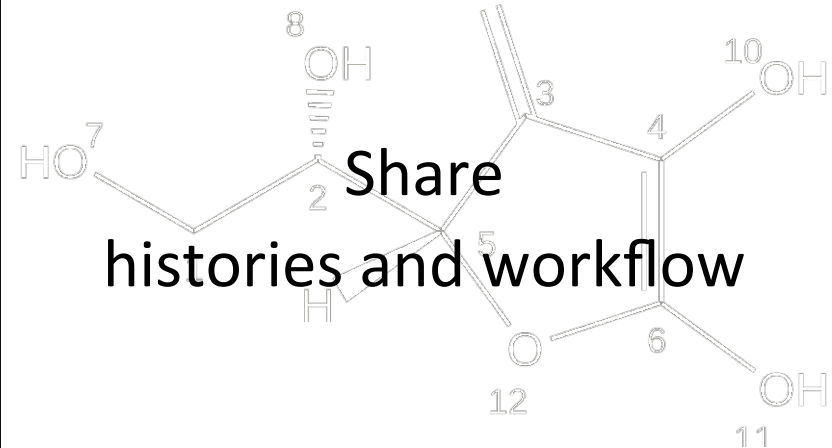


# 4 Wm

Workflow4metabolomics

## HOW TO



30/05/16

v 1.0.0



## Datasets

Galaxy / METABO

Analyze Data Workflow **Shared Data** Visualization Help User

Using 47.0 MB

Tools

search tools

Get Data

WORKFLOW 4 METABOLOMICS

2-Preprocessing

3-Normalisation

4-Quality Control

5-Statistical Analysis

6-Annotation

COMMON TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Statistics

Graph/Display Data

Multiple regression

Workflows

All workflows

### Saved Histories

search history names and tags

Advanced Search

Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated	Status
Preprocessing	8	1	0 Tags	45.6 MB	~18 hours ago	~less than ago	current history
PRC			0 Tags	0 bytes	~2 days ago	~2 minutes ago	
test	1		0 Tags	4.0 KB	Apr 28, 2014	~4 minutes ago	
After_Preprocessing	3		0 Tags	1.4 MB	~37 minutes ago	~7 minutes ago	
Unnamed history			0 Tags	0 bytes	Apr 28, 2014	Apr 28, 2014	

For 0 selected histories: Rename Delete Delete Permanently Undelete

Histories that have been deleted for more than a time period specified by the Galaxy administrator(s) may be permanently deleted.

### History

Preprocessing

45.6 MB

8: [xset.group.retcor.group.fillPeaks.diffreport.tsv.tabular](#)

7: [xset.group.retcor.group.fillPeaks.diffreport.RData.rdata](#)

6: [xset.group.retcor.group.fillPeaks.diffreport.data\\_matrix.tsv.tabular](#)

5: [bio vs blank box/050.png](#)

4: [xset.group.retcor.group.fillPeaks.annotateDiffreport.tsv.tabular](#)

3: [xset.group.retcor.group.fillPeaks.annotateDiffreport.Rdata.rdata](#)

2: [xset.group.retcor.group.fillPeaks.annotateDiffreport.data\\_matrix.tsv.tabular](#)

1: [xset.group.RData.rdata](#)

Galaxy / METABO Analyze Data Workflow Shared Data Visualization Help User Using 4.0 KB

### Your workflows

Create new workflow Upload or import workflow

Name	# of Steps
complete_workflow_RFM	17

Workflow you by others

No workflows ha

Other opt

Configure you

- Edit
- Run
- Share or Publish
- Download or Export
- Copy
- Rename
- View
- Delete

## Share or Publish Workflow 'complete\_workflow\_RFMF'

### Make Workflow Accessible via Link and Publish It

This workflow is currently restricted so that only you and the users listed below can access it. You can:

Make Workflow Accessible via Link



Restricted community

Generates a web link that you can share with other people so that they can view and import the workflow.

Make Workflow Accessible and Publish



All the Galaxy server users

Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's [Published Workflows](#) section, where it is publicly listed and searchable.

### Share Workflow with Individual Users

You have not shared this workflow with any users.

Share with a user



Designated community (login@sb-roscoff.fr)

[Back to Workflows List](#)

**Galaxy / METABO**

Analyze Data Workflow Shared Data Visualization Admin Help User

Using 7.8 MB

Tools

search tools

**Get Data**

WORKFLOW 4 METABOLOMICS

[2-Preprocessing](#)

[3-Normalisation](#)

[4-Quality Control](#)

[5-Statistical Analysis](#)

[6-Annotation](#)

**COMMON TOOLS**

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[Statistics](#)

[Graph/Display Data](#)

[Multiple regression](#)

**Workflows**

[All workflows](#)

**Running workflow "Workflow XCMS"**

Expand All Collapse

**Step 1: xcms.xcmsSet (version 20140507)**

**library directory name**

sacuri

**Method**

matchedFilter

**step**

0.01

**fwhm**

30

**Advanced options**

hide

**Step 2: xcms.group (version 20140507)**

**RData file**

Output dataset 'output' from step 1

**Method**

density

**bw**

30

**minfrac**

0.5

**mzwid**

0.25

**Advanced options**

hide

**Step 3: xcms.retcor (version 20140507)**

**History**

sacuri

0 bytes

This history is empty. You can [load your own data](#) or [get data from an external source](#)

# Share

- Get shared histories

Galaxy / METABO

Analyze Data Workflow Shared Data Visualization Help User

Tools

search tools

Get Data

WORKFLOW 4 METABOLOMICS

2-Preprocessing

3-Normalisation

4-Quality Control

5-Statistical Analysis

## Histories shared with you by others

Name	Datasets	Created	Last Updated	Shared by
mmonsoor	6	Apr 28, 2014	~2 days ago	mmonsoor@sb-roscoff.fr

For 0 selected histories: Copy Unshare

History

- HISTORY LISTS
- Saved Histories
- Histories Shared with Me
- CURRENT HISTORY
- Create New
- Copy History
- Copy Datasets
- Share or Publish

Individual

Galaxy / METABO

Analyze Data Workflow Shared Data Visualization Help User

## Published Histories

search name, annotation, owner, and tags

Advanced Search

Name	Annotation	Owner	Community Tags	Last Updated
Preprocessing		mlandi		~14 seconds ago
TP1 xcms sacuri		mmonsoor	★★★★★	~1 day ago
TP1 xcms sacuri		jfmartin	★★★★★	Apr 28, 2014

Shared Data

- Data Libraries
- Data Libraries Beta
- Published Histories
- Published Workflows
- Published Visualizations
- Published Pages

Public



# Share

- Get shared workflows

Galaxy / METABO Analyze Data **Workflow** Shared Data Visualization Help User Using 216.1 MB

### Your workflows

[Create new workflow](#) [Upload or import workflow](#)

Name	# of Steps
complete_workflow_RFMF	17

**Individual**

**Workflows shared with you by others**

Name	Owner	# of Steps
Workflow mmonsoor	mmonsoor@sb-roscoff.fr	7

Galaxy / METABO Analyze Data Workflow **Shared Data** Visualization Help User Using 111.4 MB

### Published Workflows

[Advanced Search](#)

Name	Annotation	Owner	Rating	Community Tags	Last Updated
complete_workflow_RFMF		mmand			~17 hours ago

**Public**

- Data Libraries
- Data Libraries Beta
- Published Histories
- Published Workflows**
- Published Visualizations
- Published Pages



- Import shared

Galaxy / METABO Analyze Data Workflow **Shared Data** Visualization Help User Using 216.1 MB

Published Histories | mmonsoor | TP1 xcms sacuri **Import history** About this History

## TP1 xcms sacuri

65.4 MB

search datasets

Dataset	Annotation
1: xset.RData	
2: sampleMetadata.tsv	
3: xset.TICs_raw.pdf	
4: xset.ln.txt	

**Author**  
mmonsoor

**Related Histories**  
[All published histories](#)  
[Published histories by mmonsoor](#)

**Rating**  
 Community (0 ratings, 0.0 average) ★★★★★  
 Yours ★★★★★  
**Tags**  
 Community: none

## Histories

Galaxy / METABO Analyze Data **Workflow** Shared Data Visualization Help User Using 216.1 MB

## Your workflows

Create new workflow Upload or import workflow

Name	# of Steps
complete_workflow_RFMF	17

## Workflows shared with you by others

Name	Owner	# of Steps
Workflow mmonsoor	mmonsoor@sb-roscoff.fr	7

**Other**

Configure

- View
- Run
- Copy**
- Remove

## Workflows