INTRODUCTION / PROBLEMATIC
Introduction

- Graphical interface click-button tools within windows
  + very ergonomic
  - too ergonomic → lack of flexibility
  - don’t count on it! Have you ever seen a PhD student having the time to make beautiful green buttons?
  - paying for it!

- Tools available on the internet
  + very ergonomic
  - too ergonomic → lack of flexibility
  - A small part of the available tools
  - distributed on different universities locations
  - the submission size is often limited
  - must not be paranoid
Introduction

- Command line tools + represent almost the majority of scientific tools + good parameters completeness + can be executed on high performance computers + g33ks love it, since automatable, workflowsable, ...

- minimum Linux knowledge is required
- cruel lack of ergonomics
INTRODUCTION / GALAXY
Introduction / Galaxy

• Galaxy it’s ...
  – No need to execute a command line through a terminal
  – Programming or scripting skills are not required
  – Submission of jobs is transparent through a high performance computer cluster
  – Secure histories and data manager
  – A data and protocols sharing system
  – Tool-boxes of several bioinformatics fields
    – NGS
    – Metabolomics
    – Statistics
    – Chemistry
    – Image analysis
    – Etc ...
  – A web-based interface
Introduction / Galaxy

RNA-Seq Analysis Tools

COST

DIFFICULTY OF USE/LEARNING CURVE

Size of dot indicates flexibility/power

CLC Bio
Geneious
Galaxy
iPlant DE
Command Line
R
Why Galaxy?

- Accessibility
- Reproductibility
- Transparency
Introduction / Galaxy

```bash
[login@n0 ~]$ cdprojet
[login@n0 login]$ cd 13-07-29-panda/tmp/mapping
[login@n0 mapping]$ cat tophat.qsub
#!/bin/bash
#$ -S /bin/bash
#$ -M login@sb-roscoff.fr
#$ -m bea
#$ -V
#$ -cwd
#$ -o qsub.out
#$ -e qsub.err
tophat2 panda_v121029 ../input/I1R1-1.fq ../input/I1R1-2.fq 
--bowtie2-sensitive --r 100
--num-threads 8
[login@n0 mapping]$ qsub -q long.q -pe thread 8 tophat.qsub
Your job 533869 ("tophat.qsub") has been submitted
```
**Introduction / Galaxy**

**xcmsSet.matchedFilter(object, fwhm = 30, sigma = f)**

### Arguments
- **object**: xcmsRaw object
- **fwhm**: full width at half maximum of matched filtration gaussian model peak
- **sigma**: standard deviation (width) of matched filtration model peak
- **max**: maximum number of peaks per extracted ion chromatogram
- **snthresh**: signal to noise ratio cutoff
- **step**: step size to use for profile generation
- **steps**: number of steps to merge prior to filtration
- **mzdiff**: minimum difference in m/z for peaks with overlapping retention times
- **index**: return indicies instead of values for m/z and retention times
- **sleep**: number of seconds to pause between plotting peak finding cycles
- **scanrange**: scan range to process

---

**Choose your inputs method**

Zip file from your history containing your chromatograms

**Zip file**

No no_unzip.zip dataset available.

**Extraction method for peaks detection**

matchedFilter

**[method]** See the help section below

**Step size to use for profile generation**

0.01

**[step]** The peak detection algorithm creates extracted ion base peak chromatograms (EIBPC) on a fine mesh.

**Full width at half maximum of matched filtration gaussian model peak**

30

**[fwhm]** Only used to calculate the actual sigma

**Advanced options**

**Maximum number of peaks per extracted ion chromatogram**

5

**[max]**

**Signal to noise ratio cutoff**

10

**[snthresh]**

**Number of steps to merge prior to filtration**

2

**[steps]** The peak identification algorithm combines a given number of EIBPCs prior to filtration and uses that steps argument
Introduction / Connection

http://workflow4metabolomics.org

STEP 4
Make reproducible science
### Galaxy interface

#### Batch_correction (version 2.0.0)

**Data Matrix file**: 
17: xset.group.rector.group.fillPeaks.annotate.dataMatrix.tsv

**Sample metadata file**: 
3: sampleMetadata.tsv

must contain at least the three following columns: 'batch' + 'injectionOrder' + 'sampleType'

**Variable metadata file**: 
16: xset.group.rector.group.fillPeaks.annotate.variableMetadata.tsv

**Type of regression model**: 
- linear

To select between linear or non-linear (lowess or loess) methods to be used in Van der Koot algorithm; when using loess, you can choose to use pools or samples to model batch effect.

**Factor of interest**: 
- batch

column name of factor of interest (often a biological factor); if none, leave 'batch'

**Level of details for plots**: 
- basic

Amount of plots in the pdf file output. See Help section for more details.

### Authors
- Jean-François Martin - PF MetaToul-AXIOM ; INRA ; MetaboHUB (for original version of this tool and overall development of the R script)

### Contributors
- Melanie Petera - PFEM ; INRA ; MetaboHUB (for R wrapper and R script improvement)
- Etienne Thevenot - LIST/LADIS ; CEA ; MetaboHUB (for R script and wrapper concerning "all loess pool" and "all loess sample" methods)
GET HELP
Get help

Workflow4metabolomics

**Main menu**
- Home
- Events
- History
  - Introduction
    - The Galaxy environment
    - The LC-MS workflow
    - The GC-MS workflow
    - The NMR workflow
    - References
  - HowTo
    - Download
      - Datasets and histories
    - Developer resources
      - Virtual environments
    - People
    - Publications

**W4M HowTo**

<table>
<thead>
<tr>
<th>Description</th>
<th>PDF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Import datasets &lt; 2Go</td>
<td>Download</td>
</tr>
<tr>
<td>Import datasets &gt; 2Go</td>
<td>Download</td>
</tr>
<tr>
<td>Build And Configure A Workflow</td>
<td>Download</td>
</tr>
<tr>
<td>Share Histories And Workflows</td>
<td>Download</td>
</tr>
<tr>
<td>Format Data For Postprocessing</td>
<td>Download</td>
</tr>
<tr>
<td>Perform Xcms Preprocessing</td>
<td>Download</td>
</tr>
<tr>
<td>Perform Ddrift And Batch Correction</td>
<td>Download</td>
</tr>
<tr>
<td>Perform Univariate Analyzes</td>
<td>Download</td>
</tr>
<tr>
<td>Perform Multivariate Analyzes</td>
<td>Download</td>
</tr>
<tr>
<td>Perform LCMS Annotations</td>
<td>Download</td>
</tr>
<tr>
<td>Use NIST</td>
<td>Download</td>
</tr>
</tbody>
</table>

For requests, please fill in the webform here

**workflow4metabolimcs.org**
DATA IMPORT
DATA IMPORT

< 2 GO
Welcome to workflow4metabolomics.org v2.0


Help and support: support@workflow4metabolomics.org

Latest news

01/06/2015 - Workflow4Metabolomics v2.0 starts today - Check the changelog section below

01/06/2015 - The W4M 2.0 release is presented in the June 2015 MetaboNews Spotlight [link]


19/12/2014 - W4M publication in Bioinformatics is now available - Workflow4Metabolomics: A collaborative research infrastructure for computational metabolomics
Data import < 2 Go

Copy / Paste data

Download data directly from web or upload files from your disk

1. Choose local file
2. Paste/Fetch data
3. Upload configuration
   - Convert spaces to tabs
   - Use POSIX standard

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.
Data import < 2 Go

From local files
Data import < 2 Go

From local files
Data import < 2 Go

From local files
Data import < 2 Go

From local files
Step 1: Choose a FTP Client

DATA IMPORT

> 2 GO
STEP 1: CHOOSE A FTP CLIENT

Avoid:
Malwares inside

FileZilla
Cyberduck
WinSCP
Step 2: Easy!

DATA IMPORT

< 2 GO
Welcome to workflow4metabolomics.org v2.0


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- Changelog
- Tutorials
- Past events

LC/MS

MS

Common
Data import > 2 Go
Data import > 2 Go
Data import > 2 Go
Data import > 2 Go
Data import > 2 Go

Download data directly from web or upload files from your disk

<table>
<thead>
<tr>
<th>Name</th>
<th>Size</th>
<th>Type</th>
<th>Genome</th>
<th>Settings</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>securi.zip</td>
<td>0.2 GB</td>
<td>Auto-det.</td>
<td>unspecified (?)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

FTP files

This Galaxy server allows you to upload files via FTP. To upload some files, log in to the FTP server at ftp.workflow4metabolomics.org using your Galaxy credentials (email address and password).

Available files:

<table>
<thead>
<tr>
<th>Name</th>
<th>Size</th>
<th>Created</th>
</tr>
</thead>
<tbody>
<tr>
<td>securi.zip</td>
<td>0.2 GB</td>
<td>06/04/2015 06:13:33 PM</td>
</tr>
</tbody>
</table>
Data import > 2 Go
Data import > 2 Go

Welcome to workflow4metabolomics.org v2.0


Help and support: support@workflow4metabolomics.org

Latest news

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Changelog
Tutorials
Past events

LC/MS
MS
Common
Exercise
DATA IMPORT
Data import

• Exercise

1. Fetch those files

   goo.gl/KWIEjL
   goo.gl/Yyqmnh

2. Unzip the zip file sacuri.zip

3. Upload the individual files within Galaxy
   • For this Exercise, consider that it is >2 Go
   • So use a FTP client
TOOLS
Tools - panel

Workflow4metabolomics

version 2.1


Help and support: support@workflow4metabolomics.org
Tools - form

**xcms.xcmsSet** version 2.0.1

Choose your inputs method:
Zip file from your history containing your chromatograms:

Zip file:
1: sacuri.zip

Extraction method for peaks detection:
matchedFilter:
[method] See the help section below

Step size to use for profile generation:
0.01
[step] The peak detection algorithm creates extracted ion base peak chromatograms (EIBPC) on a fixed step size

Full width at half maximum of matched filtration gaussian model peak:
30
[w/hm] Only used to calculate the actual sigma

Advanced options:
hide:

Execute

---

**Authors** Colin A. Smith csmith@scripps.edu, Ralf Tautenhahn rtautenh@gmail.com, Steffen Neumann sneumann@ipb-halle.de, Paul Benton paul.benton08@imperial.ac.uk and Christopher Conley cconley@ucdavis.edu


**Galaxy Integration** ABIMS TEAM, Station biologique de Roscoff.

Contact support@workflow4metabolomics.org for any questions or concerns about the Galaxy implementation of this tool.
Tools can have some advanced options
Tools can have some advanced options

A job has been successfully added to the queue - resulting in the following datasets:

- 2: xset.RData
- 3: sampleMetadata.tsv
- 4: xset.TICs_raw.pdf
- 5: xset.BPCs_raw.pdf
- 6: xset.log.txt

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from ‘running’ to ‘finished’ if completed successfully or ‘error’ if problems were encountered.
Tools - Job status

- Status

Job is waiting to run

= the job is in the scheduler « queue »

Duration time of this status depends on the amount of actual queued jobs or on the requested number of processors
Tools - Job status

- Status

Job is currently running

= the job is being executed on the computing cluster

Duration time of this status depends completely on the job’s attributes and the computing resources allocated.

Some programs are executed with several processors

(using 4, 8 or 16 Gb of RAM).

And others are mono-threaded 😞
Tools - Job status

- Status

Job is finished

It’s status is OK

but warnings or errors can be hidden behind. Ah hum!
Tools - Job status

- Status

**16: xset.RData**

Job is finished but with an error status

= the program sends an error

The error is often explained by the program and sometimes … not.

Error causes:

- The user :P
  - Bad usage: input file, format or option
  - Wrong porting of the program through Galaxy … sorry :/
  - Non anticipated crash of the program
Exercise

TOOLS
• Aim of this Exercise
  – Import data into Galaxy into a new history
  – Execute and chain example of little Galaxy friendly tools together.
Tools - Exercise

• Create a New history

• Fetch these two tabular files (<2Go)
  – Link1: http://tinyurl.com/w4mddata2
  – Link2: http://tinyurl.com/w4mddata3

  – Tabular files (data separated by tab delimiters)
    • VariableMetadata.tsv
    • DataMatrix.tsv

• Check their contents and datatypes through Galaxy.
Tools - Exercise

• First tool:
  – Search for the tool « Compute an expression on every row » in the toolbar)
  – Calculate the average for each metabolite by sample:

  • Set the parameters
    – Add expression:
      \[(c2+c3+c4+c5+c6+c7)/6\]
    – as a new column to: Choose the DataMatrix.tsv
Tools - Exercise

• Second tool:
  – Search for the tool « Cut columns from a table » in the toolbar
  – Keep only columns 1 and 8:

• Set the parameters
  – Cut columns: c1,c8
  – Delimited by: Tab
  – From?: compute on Data 1
• Third tool:
  – Search for the tool « Join two Datasets side by side on a specified field » in the toolbar)
  – Join the two tab files by the metabolite name:

• Set the parameters
  – Join: **Cut on Data 3**
  – Using column: **column 1**
  – with: **variableMetadata.tsv**
  – And column: **column 1**
Part II

TOOLS
Tools – Handle errors

Sent to the support team

Report this error to the Galaxy Team

The Galaxy team regularly reviews errors that occur in the application. However, if you would like to provide additional information (such as what you were trying to do when the error occurred) and a contact e-mail address, we will be better able to investigate your problem and get back to you.

Error Report

Your email
leorguille@sb-roscoff.fr

Message

[Blank field for message]

[Report button]
HISTORY
Both inputs and outputs

History panel

Authors
Jean-Francois Martin - PF MetaToul-AXIOM ; INRA ; MetaboHUB (for original version of this tool and overall development of the R script)

Contributors
Melanie Petera - PFEM : INRA ; MetaboHUB (for R wrapper and R script improvement)
Etienne Thevenot - LIST/LADIS ; CEA ; MetaboHUB (for R script and wrapper concerning "all loess pool" and "all loess sample" methods)
History panel

renaming and annotation
## History panel

Saved histories: Rename, Delete, **Delete Permanently**

### Saved Histories

<table>
<thead>
<tr>
<th>Name</th>
<th>Datasets</th>
<th>Tags</th>
<th>Size on Disk</th>
<th>Created</th>
<th>Last Updated</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sacuri</td>
<td>19</td>
<td>2 Tags</td>
<td>289.7 MB</td>
<td>Sep 02, 2015</td>
<td>~3 days ago</td>
<td>current history</td>
</tr>
<tr>
<td>Sacuri Lib</td>
<td>30</td>
<td>0 Tags</td>
<td>17.3 MB</td>
<td>May 14, 2014</td>
<td>Sep 02, 2015</td>
<td></td>
</tr>
<tr>
<td>Cooper Stress Lib</td>
<td>19</td>
<td>0 Tags</td>
<td>7.8 MB</td>
<td>May 13, 2014</td>
<td>Sep 02, 2015</td>
<td></td>
</tr>
</tbody>
</table>

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 panel

Saved histories: Switch histories

<table>
<thead>
<tr>
<th>Name</th>
<th>Datasets</th>
<th>Tags</th>
<th>Sharing</th>
<th>Size on Disk</th>
<th>Created</th>
<th>Last Updated</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Saeuri</td>
<td>19</td>
<td>2 Tags</td>
<td></td>
<td>289.7 MB</td>
<td>Sep 02, 2015</td>
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<td>7.8 MB</td>
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<td></td>
</tr>
</tbody>
</table>

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.
DATASET
Both inputs and outputs

### Dataset

#### Batch_correction (version 2.0.0)

<table>
<thead>
<tr>
<th>Data Matrix file</th>
<th>Sample metadata file</th>
<th>Variable metadata file</th>
</tr>
</thead>
<tbody>
<tr>
<td>xset.group.retcor.group.fillPeaks.annotate.dataMatrix.tsv</td>
<td>sampleMetadata.tsv</td>
<td>xset.group.retcor.group.fillPeaks.annotate.variableMetadata.tsv</td>
</tr>
</tbody>
</table>

**Type of regression model:**
- **Linear**

To select between linear or non-linear (lowess or loess) methods to be used in Van der Kloot algorithm; when using loess, you can choose to use pools or samples to model batch effect.

**Factor of interest:**
- **batch**

Column name of factor of interest (often a biological factor); if none, leave 'batch'

**Level of details for plots:**
- **basic**

Amount of plots in the pdf file output. See Help section for more details.

#### Authors
- Jean-François Martin - PF MetaToul-AXIOM; INRA; MetaboHUB (for original version of this tool and overall development of the R script)

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Dataset Informations

**Tool: xcms.group**

- **Name:** xset.group.recor.group.RData
- **Created:** Wed Sep 2 09:11:48 2015 (UTC)
- **Filesize:** 5.2 MB
- **Dokey:** ?
- **Format:** rdata.xcms.group
- **Galaxy Tool ID:** tools.he.inefn.fr/bioinformatique/ti/repos/entregale/xcms_group/xams.xcms_group/2.0.1
- **Galaxy Tool Version:** 2.0.1
- **Tool Standard:** stdin
- **Input Parameter**
  - **RData file**
  - **Method to use for grouping**
    - Bandwidth: 5
    - Minimum fraction of samples necessary: 0.3
    - Width of overlapping m/z slices: 0.01
    - Advanced options: show
  - **Maximum number of groups to identify in a single m/z slice:** 50

**Inheritance Chain**

```r
xset.group.recor.group.RData
```
Dataset

Dataset display: text, tabular, pdf, picture, html...

Galaxy / 4 / Metabolomics

Dataset display: text, tabular, pdf, picture, html...
Dataset

Renaming and annotation
Change the Datatype of the Dataset

Select the 'Datatype' tab to change the data type of the dataset. You can choose from various options such as 'txt', 'rgb', 'sam', 'scf', 'sff', 'sif', 'svg', 'tabix', and 'tabular'. Choose the appropriate type to ensure Galaxy correctly interprets your dataset's content.
Dataset

Graphics

Visualize charts

name: Black

Scatterplot

C1_011 HU_neg_184 HU_neg_185

Provide a chart title:

New Chart

How many data points would you like to analyze?

- Few (<500)
- Some (<10k)
- Many (>10k)

- Bar diagrams
  - Regular (NVD3)
  - Stacked (NVD3)
  - Horizontal (NVD3)
  - Stacked horizontal (NVD3)

- Others
  - Line with focus (NVD3)
  - Line chart (NVD3)
  - Scatter plot (NVD3)
  - Heatmap (Custom)

- Area charts
  - Regular (NVD3)
  - Expanded (NVD3)
  - Stream (NVD3)

- Data processing (requires 'charts' tool from Toolshed)
Dataset  Graphics
Dataset

Re-run a job
Cleanup

DATASET
Delete a dataset

Dataset / Cleanup

Delete xset.group.recor.group.fillPeaks.RData
The dataset isn’t really deleted
It’s in the Trash
“Empty Trash” : to free up disk space
WORKFLOW
Workflow

• A workflow is a sequence of tool operations and parameters

• Can match the experiment protocol

• A workflow is built to be replayed (more or less strict)
Workflow

- Our workflow
Our workflow with Galaxy
From a history
### Workflow manager

#### Your workflows

<table>
<thead>
<tr>
<th>Name</th>
<th># of Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>LS-MS</td>
<td>7</td>
</tr>
<tr>
<td>Copy of 'gigaXml'</td>
<td>13</td>
</tr>
<tr>
<td>'gigaXml' shared by '<a href="mailto:etevenot@sb-roscoff.fr">etevenot@sb-roscoff.fr</a>'</td>
<td>13</td>
</tr>
<tr>
<td>Workflow LC/MS</td>
<td>6</td>
</tr>
<tr>
<td>Community</td>
<td>10</td>
</tr>
<tr>
<td>Full_workflow</td>
<td>19</td>
</tr>
<tr>
<td>Workflow XCMS</td>
<td>8</td>
</tr>
</tbody>
</table>

#### Workflows shared with you by others

<table>
<thead>
<tr>
<th>Name</th>
<th>Owner</th>
<th># of Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>demo_workflow_06_annotation</td>
<td><a href="mailto:mlandi@sb-roscoff.fr">mlandi@sb-roscoff.fr</a></td>
<td>6</td>
</tr>
<tr>
<td>cohort</td>
<td><a href="mailto:etevenot@sb-roscoff.fr">etevenot@sb-roscoff.fr</a></td>
<td>15</td>
</tr>
<tr>
<td>gigaRaw-convert</td>
<td><a href="mailto:etevenot@sb-roscoff.fr">etevenot@sb-roscoff.fr</a></td>
<td>1</td>
</tr>
</tbody>
</table>

### Other options

- Configure your workflow menu
### Your workflows

<table>
<thead>
<tr>
<th>Name</th>
<th># of Steps</th>
</tr>
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<tbody>
<tr>
<td>S.A.S.</td>
<td>7</td>
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<td>1</td>
</tr>
</tbody>
</table>

### Other options

Configure your workflow menu
Edit a workflow: drag and drop
Workflow

Edit a workflow: drag and drop
Edit a workflow: delete a noodle
Edit a workflow: add a tool
Edit a workflow: add a tool

Add the tool
Select random lines from a file
Workflow

Edit a workflow: add a noodle
Edit a workflow: set or release a parameter

1 - Select **Select random lines from a file**
2 - Set **Randomly select as 100**
Run a workflow
Successfully ran workflow "Workflow XCMS". The following datasets have been added to the queue:

1: xset.RData
2: sampleMetadata.tsv
3: xset.TICs_raw.pdf
4: xset.log.txt
5: xset.group.RData
6: xset.group.Rplots.pdf
7: xset.group.log.txt
8: xset.group.recor.RData
9: xset.group.recor.TICs_corrected.pdf
10: xset.group.recor.log.txt
11: xset.group.recor.group.RData
12: xset.group.recor.group.Rplots.pdf
13: xset.group.recor.group.log.txt
14: xset.group.recor.group.recor.RData
15: xset.group.recor.group.recor.TICs_corrected.pdf
16: xset.group.recor.group.recor.log.txt
17: xset.group.recor.group.recor.RData
18: xset.group.recor.group.recor.Rplots.pdf
19: xset.group.recor.group.recor.log.txt
20: xset.group.recor.group.recor.group.fillPeaks.RData
21: xset.group.recor.group.recor.group.fillpeaks.log.txt
22: xset.group.recor.group.recor.group.fillPeaks.annotateDiffreport.variableMetadata.tsv
23: xset.group.recor.group.recor.group.fillPeaks.annotateDiffreport.dataMatrix.tsv
24: xset.group.recor.group.recor.group.fillPeaks.annotateDiffreport.zip
25: xset.group.recor.group.recor.group.fillPeaks.annotateDiffreport.log.txt
• Possible

• Impossible (until now)
SHARE
biologist ↔ biologist

- Sharing histories or datasets
  - With or without linked workflow
bioanalyst ↔ biologist

• Sharing workflows
  – Pre-configured parameters
  – With or without release parameters (set at runtime)

• According to the user-end knowledge
bioinformatician ↔ bioinformatician

- Sharing tools, scripts and wrappers
  - Toolshed
Datasets

Saved Histories

<table>
<thead>
<tr>
<th>Name</th>
<th>Datasets</th>
<th>Tags</th>
<th>Sharing</th>
<th>Size on Disk</th>
<th>Created</th>
<th>Last Updated</th>
<th>Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Preprocessing</td>
<td>8</td>
<td>1</td>
<td></td>
<td>45.6 MB</td>
<td>~18 hours ago</td>
<td>~less than ago</td>
<td>current history</td>
</tr>
<tr>
<td>Switch</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>View</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Share or Publish</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Name</td>
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<tr>
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<td></td>
<td>1.4 MB</td>
<td>~37 minutes ago</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Name</td>
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<td></td>
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<td></td>
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</table>

Histories that have been deleted for more than a time period specified by the Galaxy administrator(s) may be permanently deleted.
<table>
<thead>
<tr>
<th>Name</th>
<th># of Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>complete_workflow_RFME</td>
<td>17</td>
</tr>
</tbody>
</table>

Workflow

- **Your workflows**

  - No workflows have been shared by others.

Workflow

- **Workflow options**

  - 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**
  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**
  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**

**Mode**

- **Restricted community**
- **All the Galaxy server users**
- **Designated community** (login@workflow4metabolomics.org)
• Get shared histories
Share

- Get shared workflows
- Import shared

### Histories

<table>
<thead>
<tr>
<th>Annotation</th>
<th>Dataset</th>
</tr>
</thead>
<tbody>
<tr>
<td>xset.RData</td>
<td>1</td>
</tr>
<tr>
<td>sampleMetadata.tsv</td>
<td>2</td>
</tr>
<tr>
<td>xset.TICs_raw.pdf</td>
<td>3</td>
</tr>
<tr>
<td>xset.log.txt</td>
<td>4</td>
</tr>
</tbody>
</table>

### Workflows

#### Your workflows

<table>
<thead>
<tr>
<th>Name</th>
<th># of Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>complete_workflow_RFMF</td>
<td>17</td>
</tr>
</tbody>
</table>

#### Workflows shared with you by others

<table>
<thead>
<tr>
<th>Name</th>
<th>Owner</th>
<th># of Steps</th>
</tr>
</thead>
<tbody>
<tr>
<td>Workflow-mmnsoor</td>
<td><a href="mailto:mmnsoor@sb-roscoff.fr">mmnsoor@sb-roscoff.fr</a></td>
<td>7</td>
</tr>
</tbody>
</table>
Share

Level 5
- Share of tools and descriptions in the ToolShed

Level 4
- Launch autonomously tools
- Use advanced parameters
- Use the Galaxy API
- Provide workflow for colleagues Level 1-3

Level 3
- Launch autonomously tools
- Use workflow more or less presetted

Level 2
- Use presetted workflow

Level 1
- Share his data to colleagues Level 2-5
END