# Galaxy Pasteur

Patchwork of experiences and improvements

Olivia Doppelt-Azeroual, Sophie Créno et Fabien Mareuil CIB, Institut Pasteur, Paris



# Summary

Part 0 : Galaxy Pasteur

### Part 1: Adaptations to the Pasteur infrastructure

- Module
- "Libraries" automation
- Galaxy reporting

#### Part 2: Problems and corrections

- I/O Problems
- Purged User Problem

#### Part 3: Future improvements

- Upload submitted for remote execution
- Statistics on Galaxy reporting
- SynBioWatch Project



# **Galaxy Pasteur**

## At Institut Pasteur, Galaxy consists in:

- An instance used by 133 users and administrated by 1.5 fte administrators.
- A ToolShed with 89 repositories containing 289 tools.
- An average of 1783 jobs per month since February 2013.
- Trainings on Galaxy, twice a year.
- Trainings using Galaxy, twice a year.



## Adaptations to the Pasteur infrastructure

#### "Libraries" automation

- Why automate library creation?
  - Private data to deal with,
  - Only 1.5 fte administrators,
  - Big data upload and export.
- New API script scripts/api/automate\_library.py, how it works:
  - Root cron script execution with admin API key (launched every 10 minutes)
  - Retrieves the users list using the API
  - Checks if the exchange directories exist for each user
  - o If not, creates a Galaxy library named "login" using the API and creates 2 directories export/"login" upload/"login" with the right linux permissions
  - Sends an email to admins who modify the library permission (by hand)

#### Clarifications:

- Deals also with linux permissions of exported files.
- User cp/scp the data in upload/"login" and upload in Galaxy through the interface.

- Module provides a way to dynamically modify of a user's environment.
  - Uses modulefiles
  - Allows the management of several packages/software versions on the same instance
- Patches on /lib/galaxy/ directory:

```
o config.py;
o jobs/__init__.py;
o jobs/runners/_init_.py;
```

#### How it works:

A module\_conf.xml file lists tool ids and their associated modules:

```
<tool id="tophat2" version="2.0.7" module="tophat/2.0.7" />
```

- When the tool is launched, Galaxy uses the tool id to retrieve the list of modules
- Then, Galaxy creates a module.sh script to load the modules



## Adaptations to the Pasteur infrastructure

## Galaxy reporting

- Natively in Galaxy
- Setup equivalent to ToolShed
- Provides many interesting metrics
  - Jobs per month
  - Jobs per user
  - Jobs per tool
  - User disk usage
  - o ..

#### **Galaxy Reports** Reports Jobs Today's jobs . Jobs per day this month Jobs in error per day this month All unfinished jobs Jobs per month Jobs in error per month Jobs per user Jobs per tool Sample Tracking · Sequencing requests per month Sequencing requests per user Workflows Workflows per month Workflows per user

Users

System

Registered users
 Date of last login
 User disk usage

Disk space maintenance

## All Jobs for November 2013 Click Total Jobs to see jobs for that day

Day	Date	User Jobs	Monitor Jobs	Total Jobs
Thursday	November 21, 2013	33	0	33
Wednesday	November 20, 2013	29	0	<u>29</u>
Tuesday	November 19, 2013	8	0	8
Monday	November 18, 2013	51	0	<u>51</u>
Thursday	November 14, 2013	82	0	82
Wednesday	November 13, 2013	3	0	<u>3</u>
Tuesday	November 12, 2013	1	0	1
Friday	November 08, 2013	12	0	<u>12</u>
Thursday	November 07, 2013	15	0	<u>15</u>
Wednesday	November 06, 2013	6	0	<u>6</u>
Tuesday	November 05, 2013	12	0	<u>12</u>
Monday	November 04, 2013	15	0	<u>15</u>



## **Status**

Part 0 : Galaxy Pasteur

Part 1: Adaptations to the Pasteur infrastructure

- Module
- "Libraries" automation
- Galaxy reporting

## Part 2: Problems and corrections

- I/O Problems
- Purged User Problem

- Identification of two I/O intensive process
  - Galaxy renaming step for output files (output --> dataset)
  - Execution of set metadata.sh script which collects metadata information

#### Patches on:

- o lib/galaxy/jobs/runners/ init .py
- O set metadata.sh

#### How it works:

- o cp and rm commands are replaced by my command (faster on the same file system)
- set metadata.py script executed on cluster nodes



## Problems and corrections

## Purged User problem

- There and back again at Pasteur (No way to unpurge a user)
  - o A user left the Institut Pasteur (purged) and got back a month later.
  - Impossible to unpurge the user
- Modified API script:
  - o scripts/cleanup datasets/pgcleanup.py
- How it works:
  - New function, operating directly on the Galaxy database
  - Purged and Deleted attributes for that user are changed from true to false

```
update galaxy_user set purged='f', deleted='f' where id in (select id from galaxy user where email='%s');
```



## **Status**

Part 0 : Galaxy Pasteur

## Part 1: Adaptations to the Pasteur infrastructure

- Module
- "Libraries" automation
- Galaxy reporting

#### Part 2: Problems and corrections

- I/O Problems
- Purged User Problem

#### Part 3: Future improvements

- Upload submitted for remote execution
- Statistics on Galaxy reporting
- SynBioWatch Project

# Future improvements

#### Remote execution of big data uploads

Galaxy mainly used for NGS analysis.

- Another I/O intensive process is the upload of big files
  - For the moment, the process is run on the web server (head)
  - Upload is handled like a Galaxy tool, xml + script
- Idea: patch tools/data\_source/upload.py, tools/data\_source/upload.xml
  - We need to differentiate the upload possibilites (http and cp from upload/"login")
  - Identify file system uploads and remotely execute them on the cluster
  - We are testing this solution



#### Other points

- Galaxy reporting
  - More statistics are needed
    - automation of data retrieval from Galaxy reporting
    - graphics generation
  - Project:
    - scripts development to automate it
    - use of Galaxy API to retrieve data
- Tool ID with ToolShed
  - too long name (full path of ToolShed directory)



# Future improvements

## Collaborative project at Institut Pasteur

- The PGP (Pôle de Génotypage des Pathogènes) group is implementing a specific web interface to facilitate the management of their analysis to detect pathogens within NGS sequences samples:
  - It contains a LIMS database and a result exploratory interface
  - It is launched on a web server linked to Institut Pasteur infrastructure.
  - It communicates remotely with Galaxy to execute pre-built analysis workflows.
- Our contribution is to help building the remote communication with Galaxy API.
   They need to:
  - Copy (big) data within Galaxy environment, (ok)
  - Upload those data into Galaxy libraries (ok)
  - Import those libraries content into Galaxy histories (almost ok)
  - Launch the workflows (fixed or tunable options) (not yet)
  - Export the results (not yet)



# Acknowledgments

Galaxy Day team

CIB team

Yes for an unified Galaxy WIKI!!



E&I team

