# **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
  - 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.



# Adaptations to the Pasteur infrastructure



- 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

- <u>Today's jobs</u>
- Jobs per day this month
- Jobs in error per day this month
- <u>All unfinished jobs</u>
- 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

- Registered users
- Date of last login
- User disk usage

#### System

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	<u>33</u>
Wednesday	November 20, 2013	29	0	<u>29</u>
Tuesday	November 19, 2013	8	0	<u>8</u>
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>



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# **Problems and corrections**

#### I/O Problems

### 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:

- 0 lib/galaxy/jobs/runners/\_\_init\_\_.py
- o set\_metadata.sh

### • How it works:

- cp and rm commands are replaced by mv 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)
  - 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');
```



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### **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



# **Future improvements**

#### 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)

galaxy.web.pasteur.fr/toolshed-pasteur/repos/fmareuil/gatk2/gatk2\_base\_recalibrator/0.0.4



# **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

