

## Tools

Options ▾

Your user name: smaman

Your file path : /work/smaman/

## 1 - UPLOAD YOUR DATA

Get Data

## 2 - FILES MANIPULATION

Text ManipulationFilter and SortJoin, Subtract and GroupConvert Formats3 - SEQUENCES  
MANIPULATIONFASTA manipulationFASTQ manipulationSAM/BAM manipulation : Picard  
(beta)SAM/BAM manipulation : SAM  
Tools

## 4 - MAPPING

BWA - Bowtie

## 5 - INDEL ET SNP

Indel AnalysisRNA-SeqGATK Tools (beta)

## 6 - SRNASEQ

Analyse des miRNAAnnotationsAlignement sur reference**WELCOME ON SIGENAE GALAXY WORKBENCH**

Galaxy is a workbench available for biologists from Sigenae Platform. Galaxy objectives are:

- Make bioinfo Linux tools accessible to biogists.
  - Hide the complexity of the infrastructure.
- Allow creation, execution and sharing of workflows.

## History

Options ▾



TP FastQC

54.0 Mb

**8: FastQC\_data 5.html** **6: GM.fastqsanger** **5: h1.fastqsanger** **4: FastQC\_data  
18.html** **3: FASTQ Summary  
Statistics on data 18** **2: FASTQ Summary  
Statistics on data 18**

76 lines, 1 comments  
format: tabular, database: ?  
Info: 99115 fastq reads were processed.  
Based upon quality values and sequence characters, the input data is valid for: sanger  
Input ASCII range: '#'(35) - 'C'(67)  
Input decimal range: 2 - 34  
Epilog : job finished at ven mai 11 10:36:43 CEST 2012



1	2	3	4	5	6
#column	count	min	max	sum	mean
1	99115	2	33	3194703	32.2
2	99115	2	34	3156652	31.8
3	99115	2	34	3145060	31.7
4	99115	2	34	3120431	31.4
5	99115	2	34	3096075	31.2

**Durée / Programme** : 2journées ½.

Galaxy : First step.

Galaxy : Reads alignment and SNP calling.

**Public** : Personnes souhaitant traiter des données (bio)informatiques sans connaissances spécifiques en informatique (sans avoir à connaître Linux et la ligne de commande).

**Liste des sessions disponibles** : <http://bioinfo.genotoul.fr>

**Les formateurs** :

Jour 1 « Initiation » : Sarah Maman, Sabrina Legoueix-Rodriguez.

Jour 2 + 3 « SNP » : Philippe Bardou, Sabrina Legoueix-Rodriguez, Sarah Maman.

# Vos traitements bioinformatiques avec GALAXY

Philippe Bardou – Sarah Maman – Sabrina Legoueix-Rodriguez  
Novembre 2015

<http://galaxy-workbench.toulouse.inra.fr>



Vidéo disponible  
sur « sig-learning »

**Présentation de la plateforme Galaxy.**

**Premiers pas dans l'instance.**

**Notions d'outils, d'historique et de workflow.**

**Lancement de traitements bioinformatiques.**

**Quelques statistiques.**

**Auto-formations disponibles en ligne.**

Equipe “Galaxy project” :

- Le Center for Comparative Genomics and Bioinformatics - Penn State,
- Des départements “Biology” et “Mathematics and Computer Science” de l’Université d’Emory.

Une communauté active autour de cet outil.

**Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences**

Jeremy Goecks<sup>1</sup>, Anton Nekrutenko<sup>2,3</sup>, James Taylor<sup>1,3</sup> and The Galaxy Team



EMORY  
UNIVERSITY



Anton Nekrutenko  
Penn State



Nate Coraor  
Penn State



James Taylor  
Emory

## Groupe de travail Galaxy IFB

- ✓ Documentation collaborative (wiki)
- ✓ Formations (mise en commun agenda PF)
- ✓ Architecture
- ✓ Intégration d'outils (Tool Shed)

<http://www.ifb-galaxy.org>



Afficher [Galaxy IFB France](#) sur une carte plus grande

### Liste des instances

<b>ABIMS Roscoff</b>	Initiation, NGS Cleaning, RNASeq Differential Expression	<a href="http://galaxy.sb-roscoff.fr/">http://galaxy.sb-roscoff.fr/</a>	Christophe Caron - Alexandre Cormier - Gildas Lecorguille - Pierre Pericard
<b>Institut Curie</b>	ChIP-Seq Analysis	<a href="http://nebula.curie.fr/">http://nebula.curie.fr/</a>	Alban Lermine
<b>Genotoul / Siginae</b>	Initiation to Galaxy, SNP calling, RNASeq, sRNASeq	<a href="http://galaxy-workbench.toulouse.inra.fr/">http://galaxy-workbench.toulouse.inra.fr/</a>	Sarah Maman
<b>INRA URGI</b>	Differential expression analysis, Variant detection	<a href="http://urgi.versailles.inra.fr/galaxy2">http://urgi.versailles.inra.fr/galaxy2</a>	Olivier Inizan
<b>INRA MIGALE</b>	Initiation to Galaxy, NGS Galaxy	<a href="http://migale.jouy.inra.fr/galaxy/">http://migale.jouy.inra.fr/galaxy/</a>	Sandra Derozier - Franck Samson
<b>Southgreen</b>	Generalist platform, and crop breeding	<a href="http://gohelle.cirad.fr/galaxy/root/">gohelle.cirad.fr/galaxy/root/</a>	Jean-Francois Dufayard
<b>INRA PFEM / MetaboHUB</b>	Metabolomics data analysis	<a href="https://pfem-galaxy/">https://pfem-galaxy/</a>	Franck Giacomoni



**Serveur public** (<https://main.g2.bx.psu.edu/>) :

- Gratuit & "open source",
- Quota limité, petits jeux de données,
- Impossible d'ajouter des banques, génomes, outils.
- Données non protégées.

**Une communauté nationale et internationale très active :**

- Listes de diffusion (US, FR)
- Wiki
- Twitter
- "Galaxy tour de France"



**L'instance locale Sigenae de Galaxy :**

- Maintenu par Sigenae.
  - Intégration possible de nouveaux outils / scripts / génomes ...
- **Présentation des particularités de l'instance Sigenae.**



Inutile de savoir :

- ✓ Lancer une ligne de commande, un script
- ✓ Programmer en perl, python, shell ...

Inutile de s'inquiéter pour son disque dur:

- ✓ Jobs lancés sur un cluster de calculs.
- ✓ Pas d'archivage de fichiers sur votre PC.

Inutile d'attendre la fin d'un traitement:

- ✓ Possibilité de lancer plusieurs jobs en parallèle
- ✓ Partir prendre un café ..fermer votre navigateur! puis voir les résultats le lendemain matin.
- ✓

Vous pouvez :

- ✓ Lancer des traitements depuis votre navigateur,
- ✓ Dupliquer des traitements,
- ✓ Partager des analyses complètes,

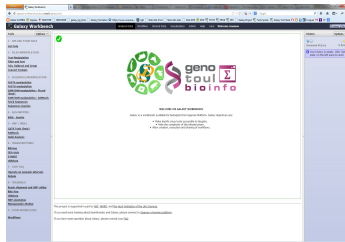
•

**et ceci de manière très intuitive !**



- ✓ Complémentaire au « **cahier de laboratoire** »  
→ Retrouver les données, les outils, les références pour la **publication** ....
  
- ✓ Manipuler **facilement et rapidement** les informations de votre fichier.
  
- ✓ Utiliser des outils bioinformatiques.
  
- ✓ Construction de **chaînes de traitement**.
  
- ✓ Intégration de **vos propres outils**.
  
- Galaxy devient **VOTRE BOITE A OUTILS**.

Galaxy est installée sur une machine virtuelle qui envoie les calculs à un cluster.



Utilisateur de Galaxy

Envoie de données

Récupération des résultats



Serveur Web  
Galaxy

Envoie des jobs



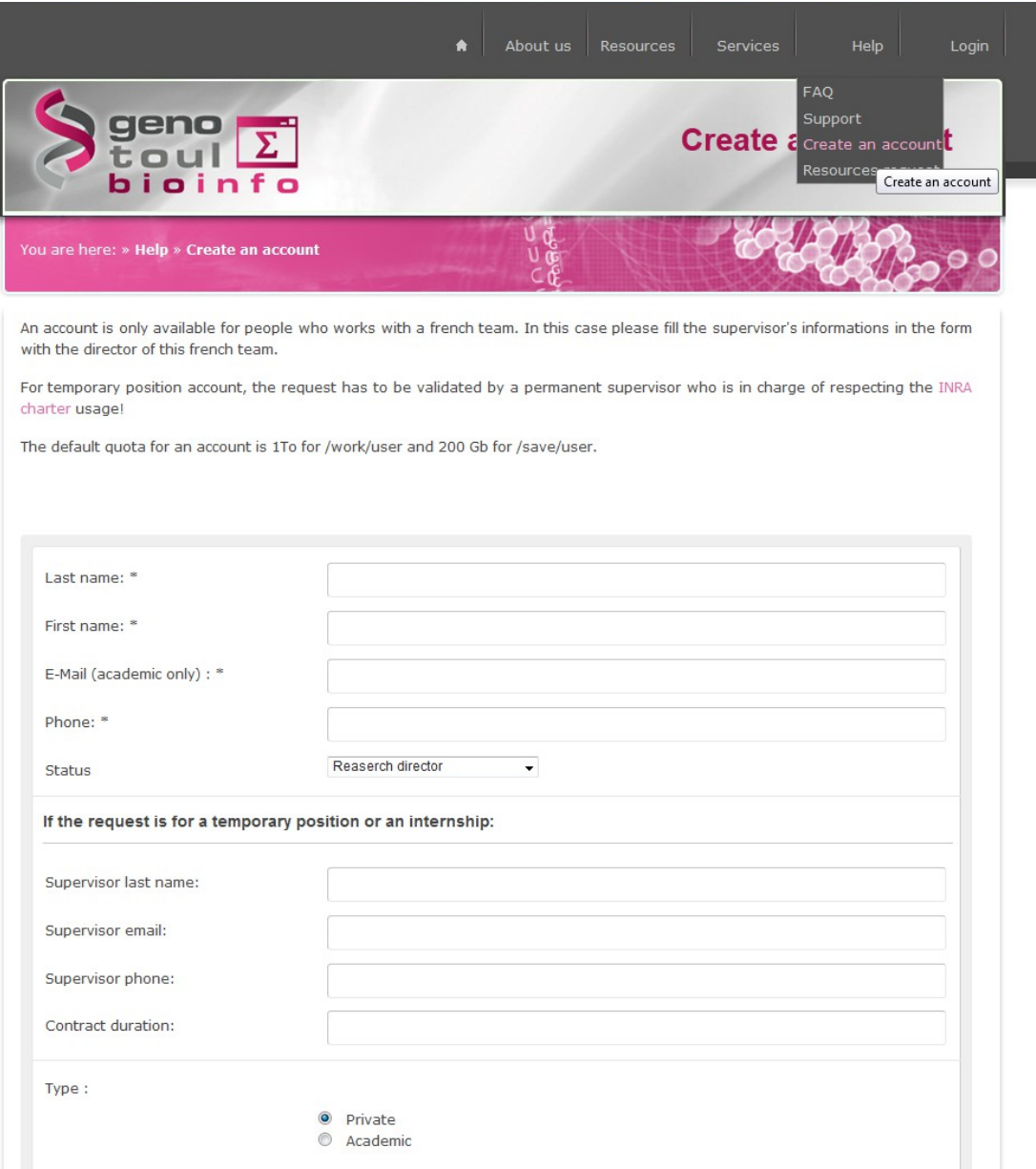
Gère la file d'attente

Gestionnaire de  
tâches

Cluster de calculs



Exécute



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[FAQ](#) | [Support](#) | [Create an account](#) | [Resources](#)

[Create an account](#)

You are here: [» Help](#) [» Create an account](#)

An account is only available for people who works with a french team. In this case please fill the supervisor's informations in the form with the director of this french team.

For temporary position account, the request has to be validated by a permanent supervisor who is in charge of respecting the [INRA charter](#) usage!

The default quota for an account is 1To for /work/user and 200 Gb for /save/user.

Last name: \*

First name: \*

E-Mail (academic only) : \*

Phone: \*

Status

**If the request is for a temporary position or an internship:**

Supervisor last name:

Supervisor email:

Supervisor phone:

Contract duration:

Type :

Private

Academic

## 1 – Ouvrir un compte sur Genotoul :

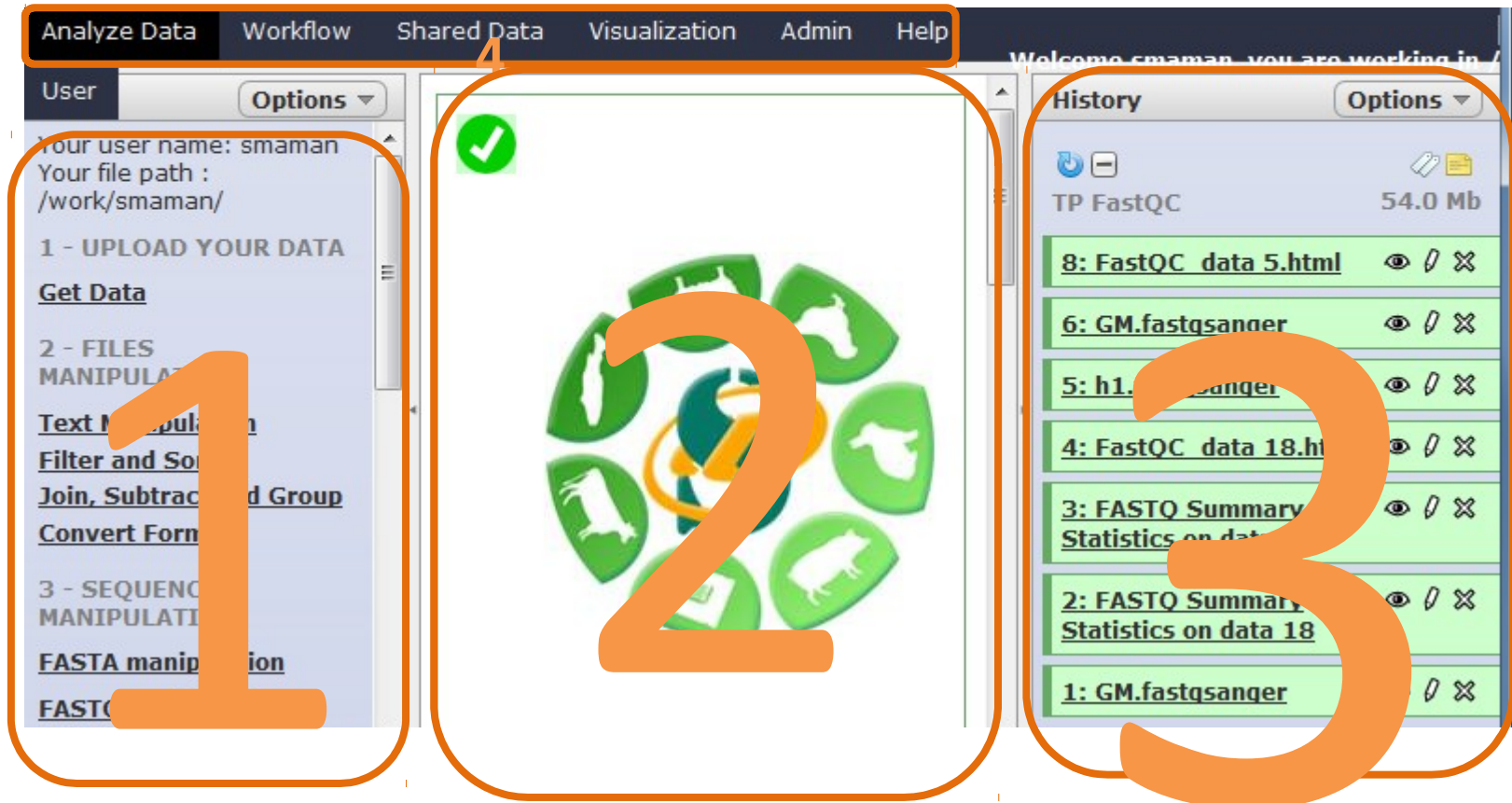
Formulaire de demande de compte:  
<http://bioinfo.genotoul.fr>  
 (Menu / Help/ Create an account )

## 2 – Accéder à Galaxy à l'aide du login/mot de passe obtenus :

<http://sigenae-workbench.toulouse.inra.fr/>

Interface divisée en 4 parties :

- 1 - Liste des outils disponibles.
- 2 - Visualisation de l'outil utilisé, historique, dataset ou workflow.
- 3 - Historique ou workflow détaillé.
- 4 - Menu .



Analyze Data   Workflow   Shared Data   Visualization   Admin   Help   Using 13%

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Your user name: smaman  
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Get Data

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Text Manipulation  
Filter and Sort  
Join, Subtract and Group  
Convert Formats

**3 - SEQUENCES MANIPULATION**



FASTA manipulation  
FASTQ manipulation  
SAM/BAM manipulation : Picard (beta)  
SAM/BAM manipulation : SAM Tools

**4 - MAPPING**

BWA - Bowtie

**5 - INDEL ET SNP**

Indel Analysis  
RNA-Seq  
GATK Tools (beta)

**WELCOME ON SIGENAE GALAXY WORKBENCH**

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**History**   Options ▾

Unnamed history   0 bytes

**i** Your history is empty. Click 'Get Data' on the left pane to start

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**\* Upload local file from filesystem path (version 1.0.0)**

**File Name:**

**File type:**

**Path to file:**

**History** Options

Unnamed history 0 bytes

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File Name:

File type:

Path to file:

History Options

Galaxy sensibilisation - TP12.1 Mb  
2 - BWA and FastQC

**14:**  
**phiX174 reads.fastqsanger**  
1.0 Mb  
format: fastqsanger, database: ?

```
@080917-and-080922:5:1:185:82  
GATGTTATTTCTTCATTTGGAGGTAACCTCTTAT  
+  
IIIIIIIIIIIIIIIIII<III@FI8A/I0II4I  
@080917-and-080922:5:1:1366:223  
GTTTTCTTCTGCGTCAGTAAGAACGTCAGTGTTC
```



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**NGS: Mapping**

- [Lastz map short reads](#) against reference sequence
- [Lastz paired reads](#) map short paired reads against reference sequence
- [Map with Bowtie for Illumina](#)
- [Map with Bowtie for SOLiD](#)
- [Map with BWA for Illumina](#)

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**BWA - Bowtie**

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**Indel Analysis**

**RNA-Seq**

**GATK Tools (beta)**

### Map with BWA for Illumina (version 1.2.2)

Will you select a reference genome from your I

Use one from the history ▾

Select a reference from history:

11: phiX174\_genome.fa ▾

Is this library mate-paired?:

Single-end ▾

FASTQ file:

14: phiX174\_reads.fastqsanger ▾

FASTQ with either Sanger-scaled quality values (f

History   Options

Unnamed history   0 bytes

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14: phiX174\_reads.fastqsanger ▾

FASTQ with either Sanger-scaled quality values (f

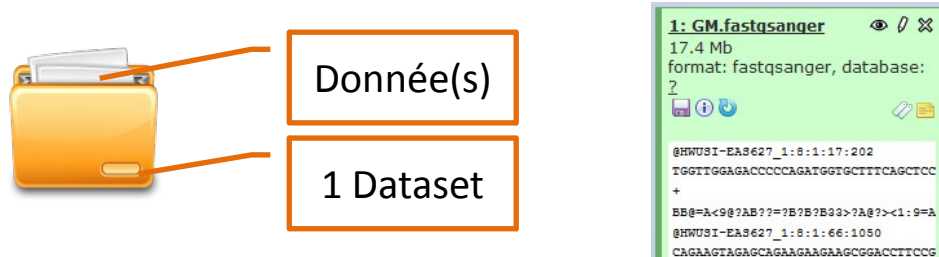
History   Options

Unnamed history   0 bytes

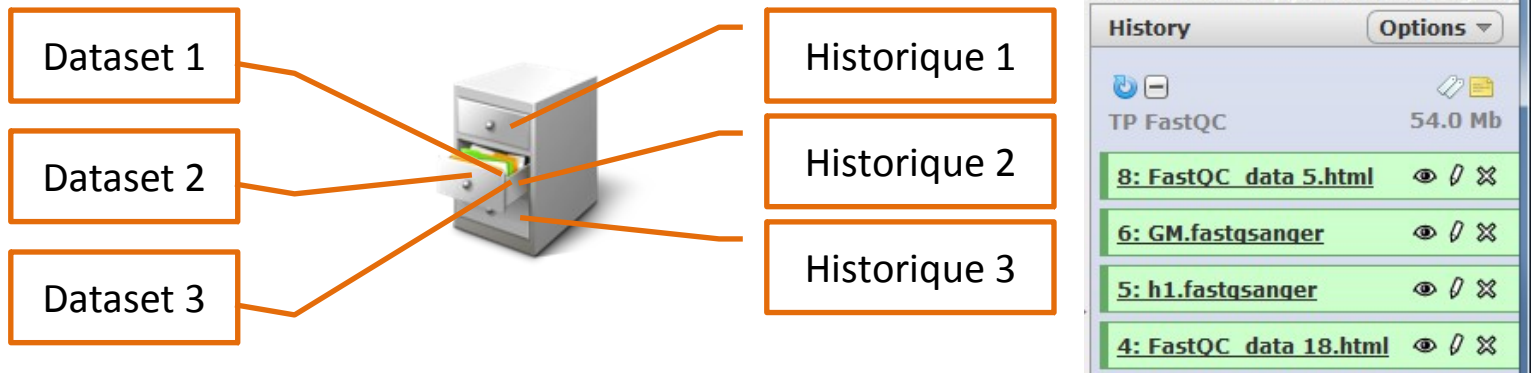
15: Map with BWA for Illumina on data 14 and data 11: mapped reads

Job is waiting to run

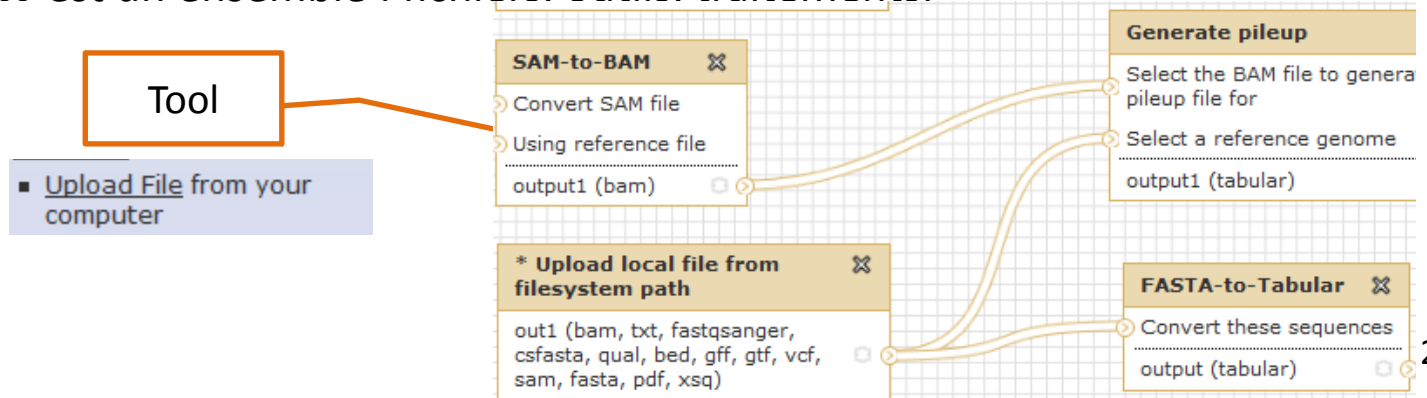
Un **DATASET** est un fichier de données (fichiers d'entrée, fichiers résultats) :



Votre **HISTORIQUE** est un « répertoire » qui « liste » l'ensemble de vos fichiers de données (fichiers d'entrée, fichier résultat) utilisés ou générés par un **TOOL** :



Votre **WORKFLOW** est un ensemble : fichiers. outils. traitements.



- **ANALYSE DATA** : Page d'accueil de Galaxy.
- **WORFLOW** : Liste des workflows .
- **SHARED DATA** : Liste des datasets, historiques et workflows partagés.
- **VISUALIZATION** : Outil de visualisation de vos fichiers résultats.
- **USER** : Accès à vos historiques et datasets sauvegardés.

The screenshot shows the Galaxy web interface. At the top is a dark navigation bar with the following tabs: **Analyze Data**, **Workflow**, **Shared Data**, **Visualization**, **Help**, and **User**. Below this, three orange arrows point from the navigation bar to specific sections of the interface:

- The first arrow points from the **Analyze Data** tab to the **Your workflows** section, which displays a list of workflows:

Name
Workflow constructed from history 'Test BWA fichiers Gnome' ▾
Workflow / 'TP : NGS - Polymorphisme' (imported from uploaded file) ▾
Workflow / 'FastQC' (imported from uploaded file) ▾
Workflow / 'IGV bai' (imported from uploaded file) ▾
Workflow 'Get flanks / region promoters' ▾
Workflow 'RNA seq statistics' et FastQC ▾

The second arrow points from the **User** tab to the **Saved Histories** section, which shows a search bar and a table of saved histories:

Name	Datasets
<input type="checkbox"/> <u>Unnamed history</u> ▾	
<input type="checkbox"/> <u>Unnamed history</u> ▾	
<input type="checkbox"/> <u>Unnamed history</u> ▾	
<input type="checkbox"/> <u>TP FastQC</u> ▾	7

The third arrow points from the **Workflow** tab to the **Workflows shared with you by others** section, which currently displays the message: "No workflows have been shared with you."

Présentation de la plateforme Galaxy.

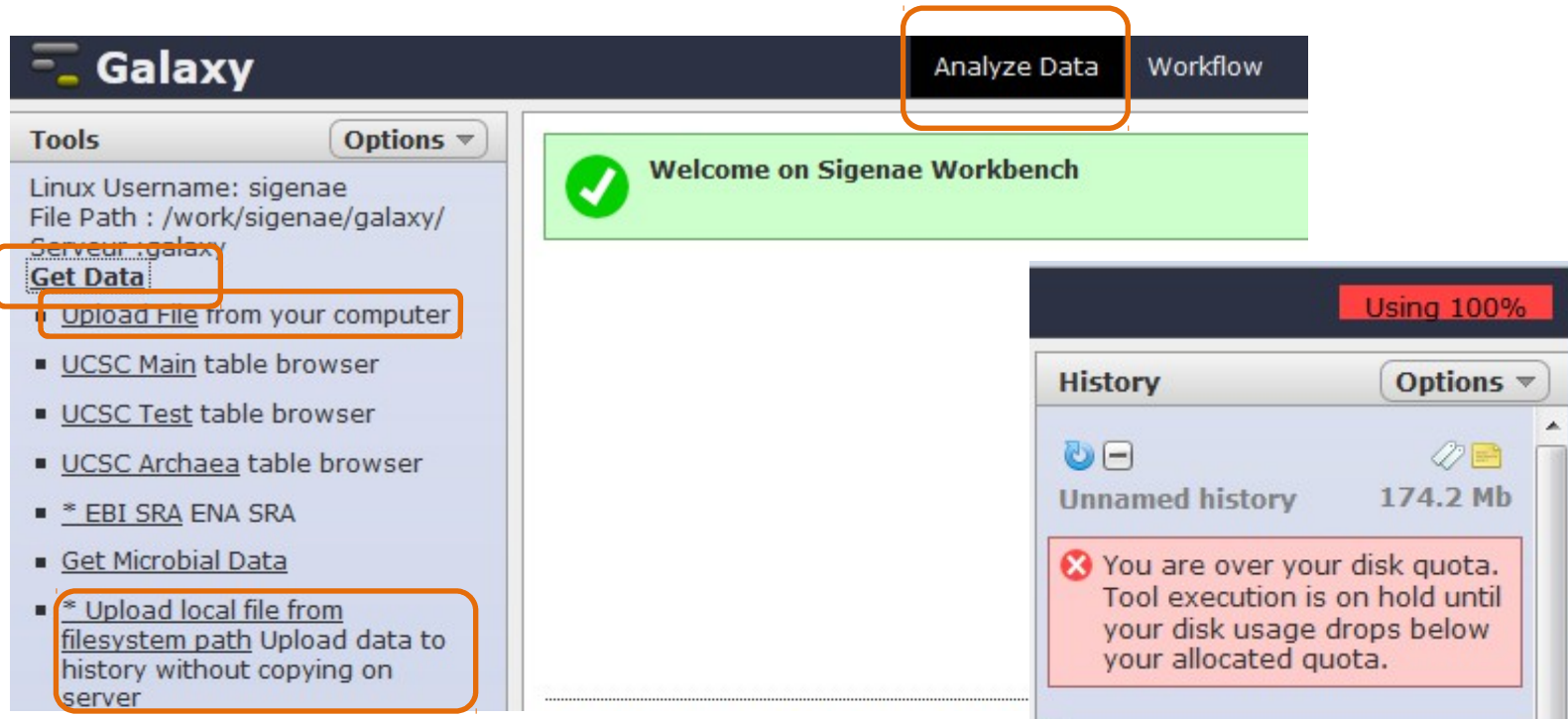
**Premiers pas dans l'instance.**

Notions d'outils, d'historique et de workflow.

Lancement de traitements bioinformatiques.

Quelques statistiques.

Auto-formations disponibles en ligne.



**Solution 1 (recommandée si vos fichiers sont sur Genotoul) :**

« Upload local file from filesystem path ».

**Solution 2 :**

« Upload file from your computer, with a copy on server ».



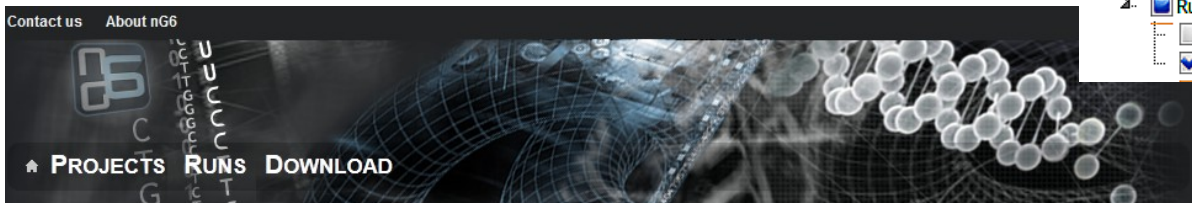
L'espace disque utilisé n'est pas celui de votre PC.

Vos traitements ne sont pas limités par la capacité de votre PC.

NG6 (Next Generation Sequencing Information System) :

- Environnement de stockage et de mise à disposition des données issues des nouvelles technologies de séquençage.
- Organisé autour des notions de projet et de run, permet un accès sécurisé aux données brutes, aux statistiques de traitements ainsi qu'aux assemblages et annotations produites.

<http://ng6.toulouse.inra.fr>



- Project Demonstration
- Project Demonstration2
- Project Galaxy training
- Run Galaxy - First steps (Sample) - (25-10-13) produced 10000 reads
- Raw data
- Analyse Data files

### User login

Enter your username and password here in order to log in on the website:

**Login**

Username:

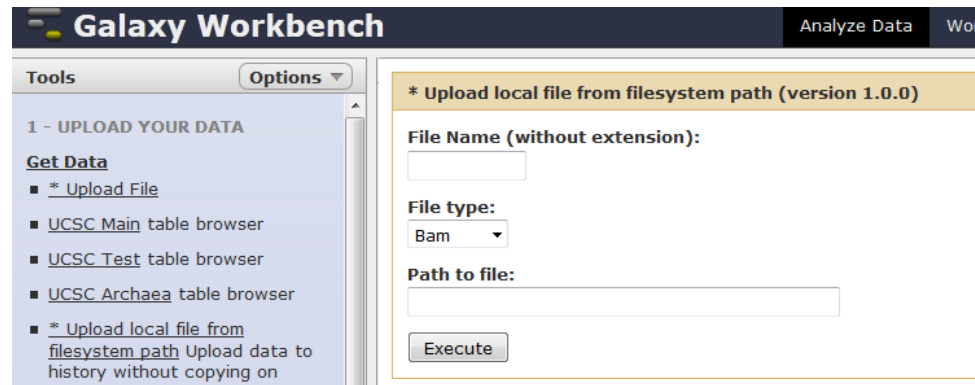
Password:

### Keep up with news

- June 17 2013** NG6 v2.0 is now available. This new version is based upon the jflow workflow engine instead of ergatis. This version is coming with several new features for runs administrators.
- November 27 2012** NG6 is now only available in english.
- September 14 2012** New user management system. 3 rights levels: administrator (in charge to run workflows), manager (in charge to manage project access) and member (browsing projects/runs/analyses).
- September 9 2012** Publication of NG6 in [BMC Genomics](#).
- August 7 2012** NG6 is available in french and in english.
- June 4 2012** Fix a bug in the generation of cigarline graphs produced by the AlignmentStats analysis.
- November 23 2011** Since the 3rd of october 2011 the HiSeq quality encoding is in Sanger format, no longer in illumina format.
- August 2nd 2011** New functionalities are available to browse your projects/runs /analyses. A hierarchical display is now available for analysis. For project administrators new functionalities are also available.



-Soit fichier par fichier (repris en TP) :



**Galaxy Workbench** Analyze Data Wor

**Tools** Options

1 - UPLOAD YOUR DATA

**Get Data**

- \* Upload File
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- \* Upload local file from filesystem path Upload data to history without copying on

**\* Upload local file from filesystem path (version 1.0.0)**

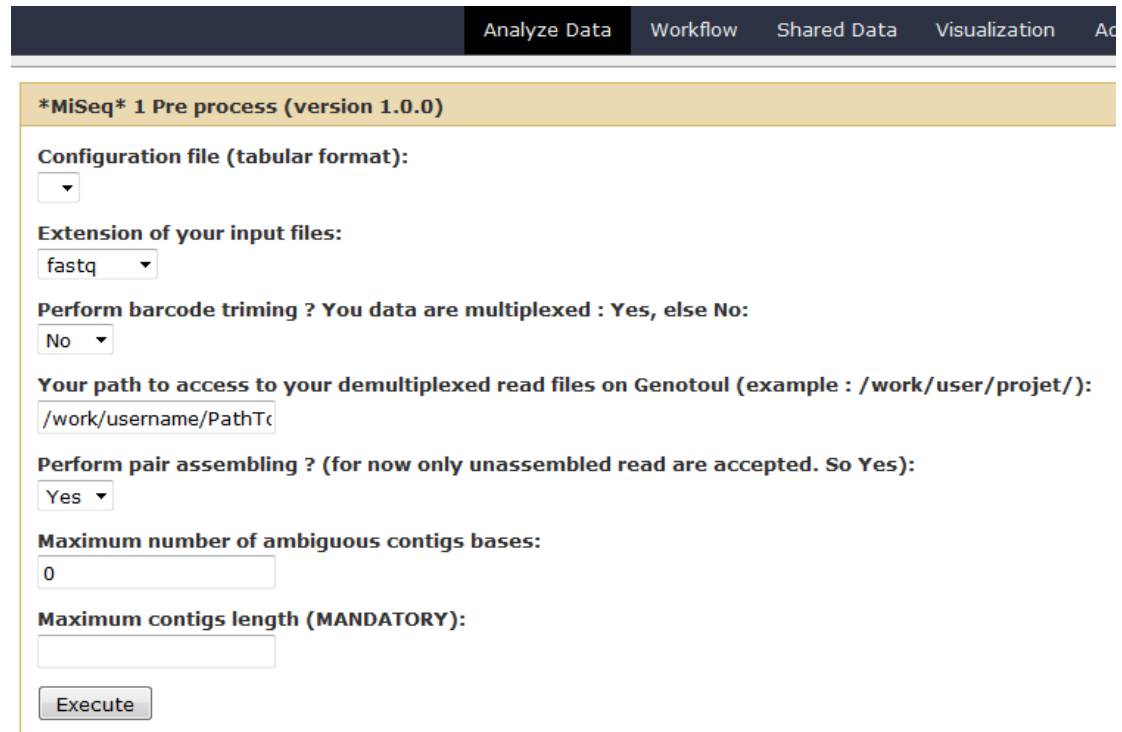
**File Name (without extension):**

**File type:**  
 Bam

**Path to file:**

Execute

-Soit un répertoire de fichiers :



Analyze Data Workflow Shared Data Visualization Ac

**\*MiSeq\* 1 Pre process (version 1.0.0)**

**Configuration file (tabular format):**

**Extension of your input files:**  
 fastq

**Perform barcode trimming ? You data are multiplexed : Yes, else No:**  
 No

**Your path to access to your demultiplexed read files on Genotoul (example : /work/user/projet/):**  
 /work/username/PathTc

**Perform pair assembling ? (for now only unassembled read are accepted. So Yes):**  
 Yes

**Maximum number of ambiguous contigs bases:**

**Maximum contigs length (MANDATORY):**

Execute



Données UCSC, Ensembl, BIOMART :

## Exercice 1 :

Connexion à Galaxy, exploration de l'interface, téléchargement de datasets

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Conserver toutes les étapes de vos analyses.

Partager vos analyses.

A chaque (re)run d'un outil, un nouveau dataset est créé. Les données ne sont pas écrasées.

Répéter, autant de fois que nécessaire, une analyse en modifiant vos paramètres pour explorer les différences de résultats.

<input type="checkbox"/>	SwanPorc ▾	18	0	0 Tags	Shared	0 bytes
<input type="checkbox"/>	FastQC ▾	6	0	0 Tags	Shared	17.4 Mb
<input type="checkbox"/>	TP : NGS - Polymorphisme ▾	8	2	0 Tags	Shared	6.6 Gb
<input type="checkbox"/>	TP FastQC ▾	12	16	0 Tags		54.0 Mb
<input type="checkbox"/>	indexation genome ▾	1	0	0 Tags		46 bytes
For 0 selected histories: <span style="margin-left: 20px;">Rename</span> <span style="margin-left: 20px;">Delete</span> <span style="margin-left: 20px;">Delete Permanently</span>						

The screenshot shows the Galaxy Sig interface. At the top, there are navigation tabs: 'Analyze Data', 'Workflow', 'Shared Data', and 'Visualizations'. The 'Shared Data' tab is active. Below the navigation, there is a search bar for 'Published Histories' with the placeholder text 'search name, annotation, owner, and tags'. Below the search bar, there is a table with columns 'Name' and 'Annotation'. The table contains two entries: 'RNAseq' and 'TP 1 suite : region promotrices'. To the right, there is a sidebar menu with options like 'Data Libraries', 'Published Histories', 'Published Workflow', 'Published Visualizations', 'History Lists', 'Saved Histories', 'Histories Shared with Me', 'Current History', and 'Create New'. The user 'smaman' is logged in.

Vos historiques sont automatiquement sauvegardés.

Pour partager ou publier un historique :

User / Saved histories / Cliquer sur le nom de l'historique / Share ou Publish

The screenshot shows the user menu for 'smaman' in the Galaxy Sig interface. The menu is open, showing options: 'Logged in as smaman@toulouse.inra.fr', 'Logout', 'Saved Histories', 'Saved Datasets', and 'Public Name'. The user is logged in as 'smaman'.

Vos historiques publiés sont accessibles à l'ensemble des utilisateurs loggés sur Galaxy (Shared Data / Published Histories).

Les historiques partagés sont accessibles uniquement à un utilisateur spécifique (History / Option / Histories Shared With Me).

## 1 – Télécharger vos données :

\* Upload local file from filesystem path (version 1.0.0)

File Name:

File type:

Path to file:

Galaxy sensibilisation - TP 12.1 Mb  
 2 - BWA and FastQC

**14:**  
**phiX174\_reads.fastqsanger**  
 1.0 Mb  
 format: fastqsanger, database: ?

```
@080917-and-080922:5:1:185:82
GATGTTATTTCTTCATTGGAGGTAACCTCTTAT
+
IIIIIIIIIIIIIIIIIIII<III@FI8A/I0II4I
@080917-and-080922:5:1:1366:223
GTTTCTTCTGCGTCAGTAAGAACGTCAGTGTTC
```

**11: phiX174\_genome.fa**  
 1 sequences  
 format: fasta, database: ?  
 Info: uploaded fasta file sur :  
 ftp://ftp.gmod.org/pub/gmod  
 /Courses  
 /2010/SummerSchoolAmericas  
 /Galaxy/phiX174\_genome.fa

```
>phix
GAGTTTTATCGCTCCATGACGCAGAAGTTAACCTI
AAATTATCTTGATAAAGCAGGAATTACTACTGCTTG
TGCTGGCGGAAAATGAGAAAATTCGACCTATCCTTGC
GCGACCTTTCGCCATCACTAACGATTCTGTCAAAA
TGGCTTAATATGCTTGGCAGCTTCGTCAAGGACTGGT
```

## 2 – Choisir un outil dans « Tools » :

**NGS: Mapping**

- [Lastz map short reads](#) against reference sequence
- [Lastz paired reads](#) map short paired reads against reference sequence
- [Map with Bowtie for Illumina](#)
- [Map with Bowtie for SOLiD](#)
- [Map with BWA for Illumina](#)

**Map with BWA for Illumina (version 1.2.2)**

Will you select a reference genome from your I

Select a reference from history:

Is this library mate-paired?:

FASTQ file:

FASTQ with either Sanger-scaled quality values (f

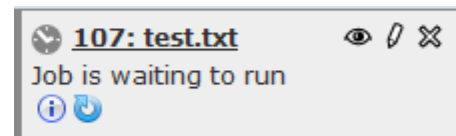
## 3 – Lancer le job en cliquant sur « Executer ».

L'execution du job en cours est visible dans votre historique.

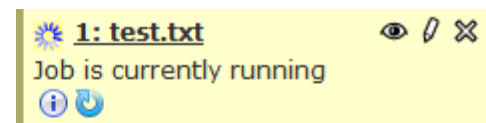
Finis les lignes de commande !

**15: Map with BWA for**  
**Illumina on data 14 and data 11:**  
**mapped reads**  
 Job is waiting to run

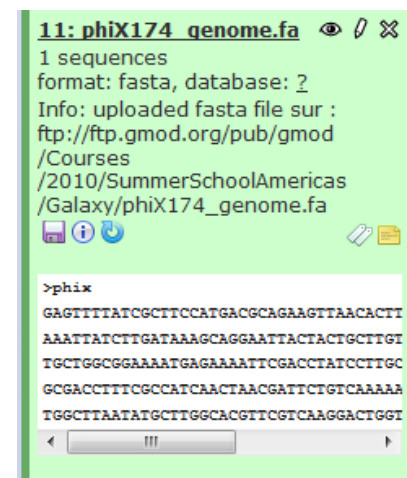
Etat 1 – GRIS : Votre job est en file d'attente.



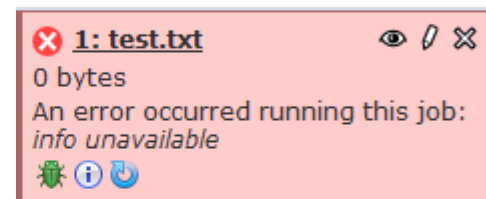
Etat 2 – JAUNE : Votre job est en cours d'exécution



Etat 3 – VERT : Votre job est fini.

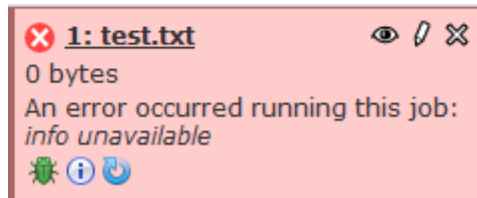


Bug - ROUGE : Votre job est planté !





Bug - **ROUGE** : Votre job est planté !



Voici les informations à transmettre par mail à [sigenae-support@listes.inra.fr](mailto:sigenae-support@listes.inra.fr) :  
 Le contenu (copier/coller) du bug ou/et (i)/stderr  
 Un share de votre historique.

## Dataset generation errors

Dataset 3: ContigLengthG1000ProfG8.res

Tool execution generated the following error message:

```

Traceback (most recent call last):
  File "/usr/local/bioinfo/src/galaxy/galaxy-dist/tools/sm_clones/scripts_module2/ace_statistics.py", line 98, in <module>
    plt.clf()
  File "/usr/local/bioinfo/src/python/current/lib/python2.7/site-packages/matplotlib/pyplot.py", line 443, in clf
    gcf().clf()
  File "/usr/local/bioinfo/src/python/current/lib/python2.7/site-packages/matplotlib/pyplot.py", line 369, in gcf
    return figure()
  File "/usr/local/bioinfo/src/python/current/lib/python2.7/site-packages/matplotlib/pyplot.py", line 343, in figure
    **kwargs)
  File "/usr/local/bioinfo/src/python/current/lib/python2.7/site-packages/matplotlib/backends/backend_tkagg.py", line 80, in new_figure_manager
    window = Tk.Tk()
  File "/usr/local/bioinfo/src/python/current/lib/python2.7/lib-tk/Tkinter.py", line 1685, in __init__
    self.tk = tkinter.create(screenName, baseName, className, interactive, wantobjects, useTk, sync, use)
tkinter.TclError: no display name and no $DISPLAY environment variable
    
```

The tool produced the following additional output:

```

Votre repertoire de travail : /work/galaxy/database/files/workspace/38401
Epilog : job finished at mar. avril 1 15:47:29 CEST 2014
    
```

## Report this error to Sigeneae Team

Please create a ticket in [Redmine](#) or send a mail to [Galaxy administrator](#).

### Tool: Clone metagenomic

Name:	ContigLengthG1000ProfG8.res
Created:	Apr 01, 2014
Filesize:	134 bytes
Dbkey:	?
Format:	txt
Tool Version:	
Tool Standard Output:	<a href="#">stderr</a>
Tool Standard Error:	<a href="#">stderr</a>

### Input Parameter

Other ace files  
 Other ace files

### Inheritance Chain

ContigLengthG1000ProfG8.res

Vous pouvez aussi créer un ticket sous Redmine.



**Galaxy Sig** Analyze Data Workflow Shared Data Visualization Admin Help User Welcome smaman Using 30%

**Saved Histories**

search history names and tags

Advanced Search

Name	Datasets	Tags	Sharing
TP Galaxy project	2	1	0 Tags
miRNA tests	59	21	0 Tags
TP SNPs calling	84	9	0 Tags
TP RNAseq	88	1	0 Tags, Shared, Accessible
test TP miRNA	36	1	0 Tags
Unnamed history			0 Tags

**Analyse OK**

**Analyse en attente**

**Analyse en erreur**

**Analyse en cours**

2: UCSC Main on Human: snp137Common (chr22:1-51304566) ~180,000 regions format: bed, database: hg19 view in GeneTrack display at Ensembl Current



Rapidement, beaucoup de données sont générées

→ D'où l'importance de bien nommer ses historiques / datasets / workflows pour les trier et les organiser au mieux.

Galaxy Workbench
Using 37%

Analyze Data
Workflow
Shared Data
Visualization
Admin
Help
User
Welcome smaman

**Tools**

FASTA manipulation

FASTQ manipulation

SAM/BAM manipulation : Picard (beta)

SAM/BAM manipulation : SAMtools

Fetch Sequences

Sequences Queries

4 - SGS MAPPING

BWA - Bowtie

5 - SNP / INDEL

GATK Tools (beta)

SAMtools

Indel Analysis

6 - TRANSCRIPTOMIC

**RNAseq**

RNASEQ ALIGNEMENT

- **Tophat for Illumina** Find splice junctions using RNA-seq data
- htseq count
- Merge Htseq count output file into a global counting file
- Slicufflinks to obtain raw count of reads
- Merge slicufflinks count file

RNASEQ RAW EXPRESSION

7 - CHIP-SEQ

Operate on Genomic Intervals

Nebula

8 - TRAININGS

Galaxy Initiation

Reads alignment and SNP calling

RNA-Seq

sRNAseq

SNP annotation

**\* EN COURS DE TEST \* Tophat for Illumina (version 1.0.0)**

Your RNA-Seq FASTQ file (read 1):  
2: M\_Pf\_2\_ACAGTG\_L00..fastqsanger

Your RNA-Seq FASTQ file (read 2):  
2: M\_Pf\_2\_ACAGTG\_L00..fastqsanger

Your RNA-seq FASTQ file are zipped:  
 Yes  
Please check this option if your files are zipped.

Choose your reference genome:  
Select a reference genome  
Please choose either use a bank available on your BioInfo Genotoul Plateform or use your own FASTA reference file (this FASTA file will automatically be indexed by Galaxy)

Select a reference genome:  
Danio rerio Zv9 62 chr 22

Number of threads used to align reads:  
16

Maximum intron length:  
5000

Expected (mean) inner distance between mate pairs:  
200

More options ?:  
No more option  
Please choose Show if you want to see more options.

What is Tophat?

reads to a genome in order to identify exon-exon splice junctions. It is built on the ultrafast short read mapping program Bowtie. TopHat was designed to work with reads produced by the Illumina Genome Analyzer, although users have been successful in using TopHat with reads from other technologies. In 1.1.0, we began supporting Applied Biosystems' Colospace format. The software is optimized for reads 75bp or longer.

Mixing paired- and single- end reads together is not supported.

*How does TopHat find junctions?*

TopHat can find splice junctions without a reference annotation. By first mapping RNA-Seq reads to the genome, TopHat identifies potential exons, since many RNA-Seq reads will contiguously align to the genome. Using this initial mapping information, TopHat builds a database of possible splice junctions and then maps the reads against these junctions to them.

Short read sequencing machines can currently produce reads 100bp or longer but many exons are shorter than this so they would be missed in the initial mapping. TopHat solves this problem mainly by splitting all input reads into smaller segments which are then mapped independently. The segment alignments are put back together in a final step of the program to produce the end-to-end read alignments.

TopHat generates its database of possible splice junctions from two sources of evidence. The first and strongest source of evidence for a splice junction is when two segments from the same read (for reads of at least 45bp) are mapped at a certain distance on the same genomic sequence or when an internal segment fails to map - again suggesting that such reads are spanning multiple exons. With this approach, "GT-AG", "GC-AG" and "AT-AC" introns will be found ab initio. The second source is pairings of "coverage islands", which are distinct regions of

**History**

Test / Phylofish 3.9 Gb

15:  
{(M\_Pf\_2\_ACAGTG\_L007\_R2.fastqsanger)-BWA.bam}-head.txt  
100 lines  
format: txt, database: 2  
Info: Epilog : job finished at mar. juil. 16 11:35:24 CEST 2013

ENSD	ENSDART00000112983	2064	0	0
ENSD	ENSDART00000122537	579	0	0
ENSD	ENSDART00000129800	810	0	0
ENSD	ENSDART00000099219	2553	0	0
ENSD	ENSDART00000079354	1245	0	0
ENSD	ENSDART0000024841	1405	0	0

14:  
{(M\_Pf\_2\_ACAGTG\_L007\_R2.fastqsanger)-BWA.bam}-BWA.bam  
9.9 Mb  
format: bam, database: 2  
Info: Etape 1  
Indexation : /usr/local/bioinfo/bin/bwa index -a is /work/galaxy/database/files/011/dataset\_11741.dat >> ./bwaindex.log 2>&1

Etape 2  
Alignement du premier fastq : /usr/local/bioinfo/bin/bwa aln /work/galaxy/database/files/011/dataset\_11741.d

ENSDART00000112983	2064	0	0
ENSDART00000122537	579	0	0
ENSDART00000129800	810	0	0
ENSDART00000099219	2553	0	0
ENSDART00000079354	1245	0	0
ENSDART0000024841	1405	0	0

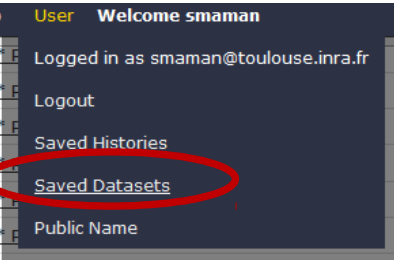
(\*) Outils Sigenae

Accès à plus d'options de l'outil

Affichage de la ligne de commande et des étapes de traitement

# Pour sauver vos datasets Galaxy dans votre /work

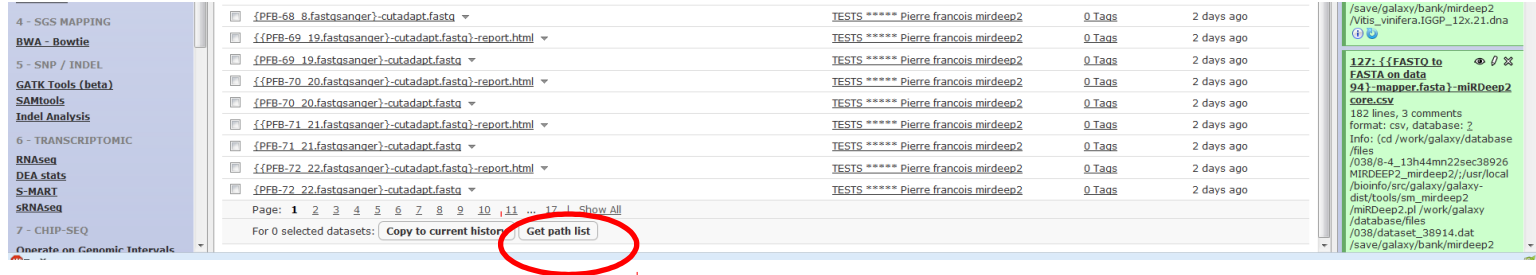
1



User Welcome smaman

- Logged in as smaman@toulouse.inra.fr
- Logout
- Saved Histories
- Saved Datasets**
- Public Name

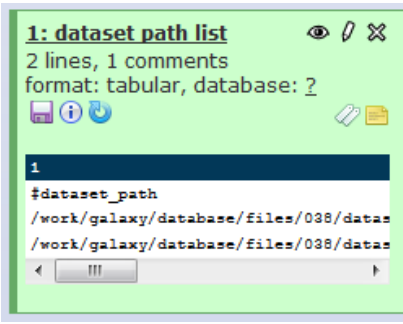
2



Dataset Name	Tags	Created
{PFB-68_8.fastqsanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-69_19.fastqsanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-69_19.fastqsanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-70_20.fastqsanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-70_20.fastqsanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-71_21.fastqsanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-71_21.fastqsanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-72_22.fastqsanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago
{PFB-72_22.fastqsanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags 2 days ago

For 0 selected datasets: [Copy to current history](#) **Get path list**

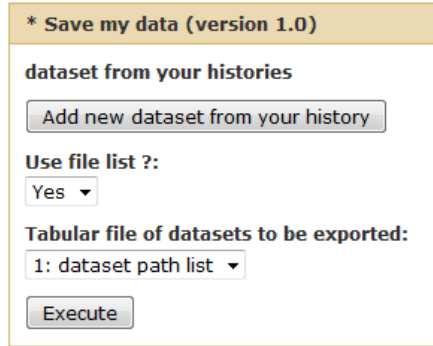
3



1: dataset path list  
2 lines, 1 comments  
format: tabular, database: ?

```
#dataset_path
/work/galaxy/database/files/038/datas
/work/galaxy/database/files/038/datas
```

4



\* Save my data (version 1.0)

dataset from your histories

Add new dataset from your history

Use file list?: Yes

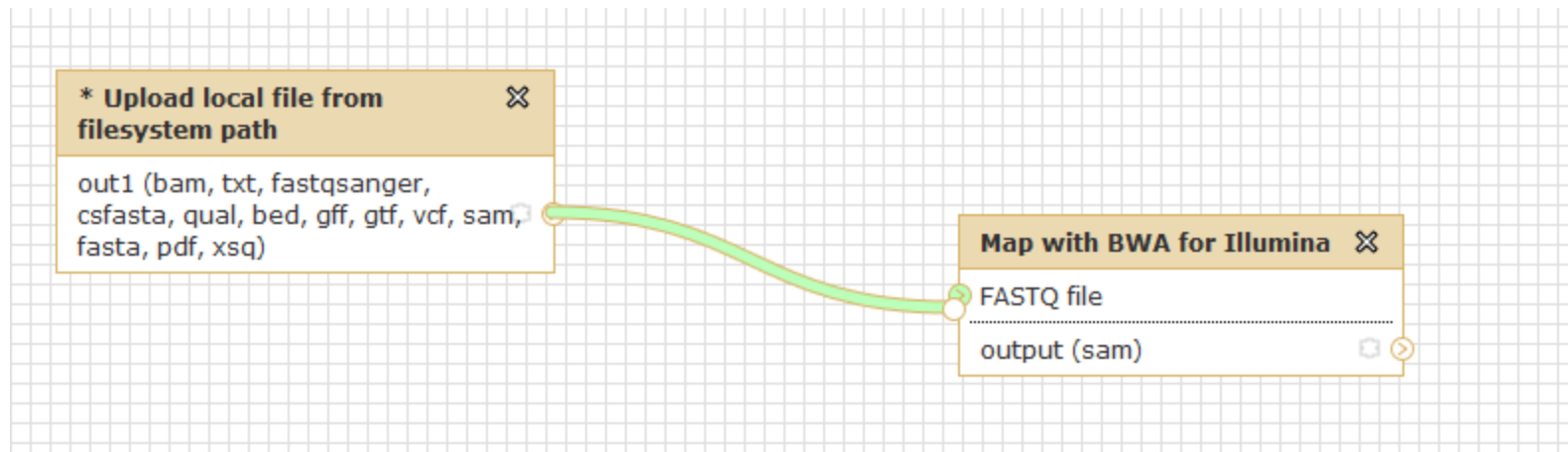
Tabular file of datasets to be exported: 1: dataset path list

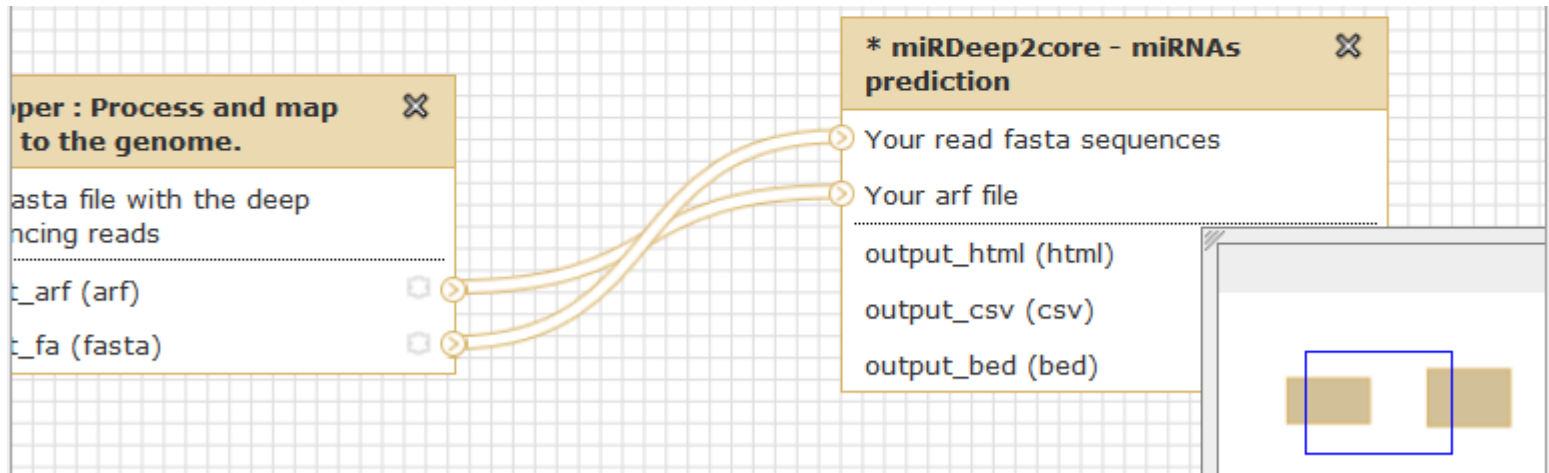
Execute

Mise en pratique prévue lors du TP.

Depuis une page blanche, vous pouvez concevoir un workflow.

Aide : les résultats produits sont typés, il n'est donc pas possible de brancher un dataset sur un mauvais tool !





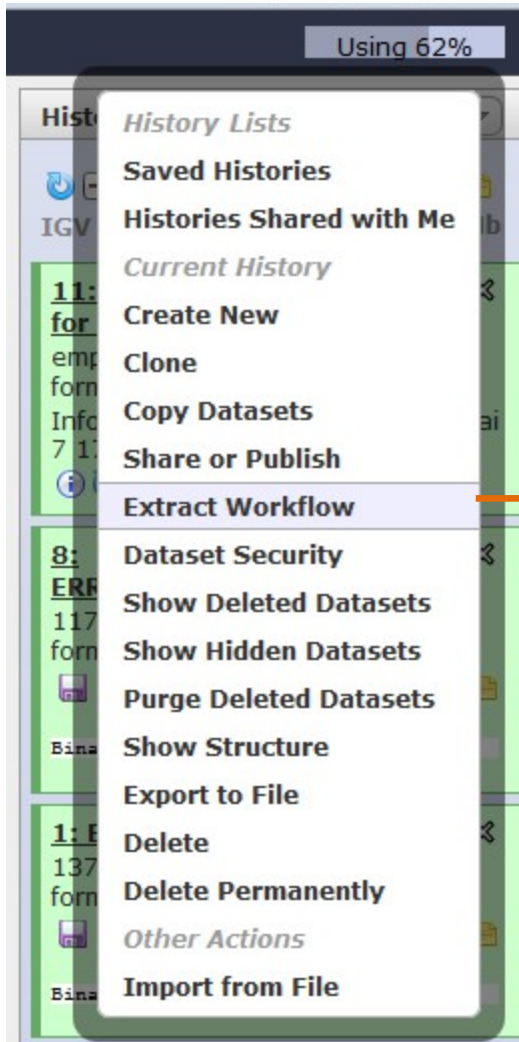
Si tout est coché, alors tout se passe comme si rien est coché.

Si le dataset n'est pas coché, alors qu'au moins un autre est coché, alors le dataset non coché ne sera pas visible dans l'historique. Sauf si l'utilisateur choisi d'afficher les fichiers cachés, alors, dans cette config uniquement, il pourra le voir.

Si un 2ieme (ou plus) dataset est coché , alors il sera visible dans l'historique après analyse.



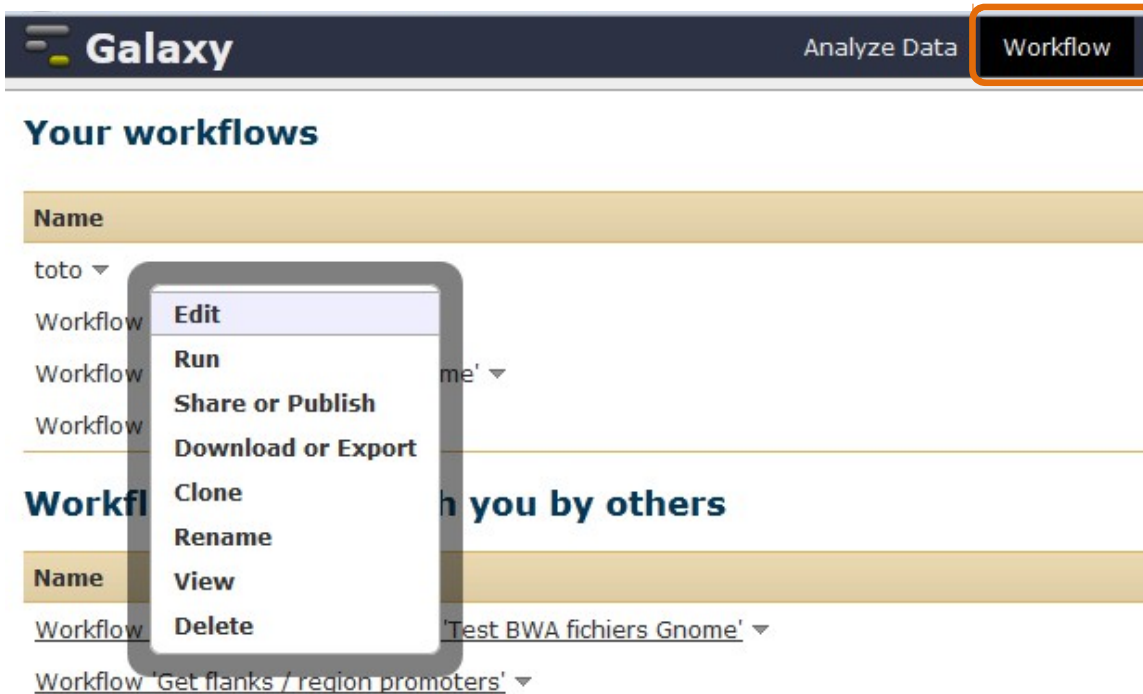
Depuis votre fenêtre « History », vous pouvez extraire un workflow.



**Workflow name**  
 Workflow constructed from history 'IGV bai'

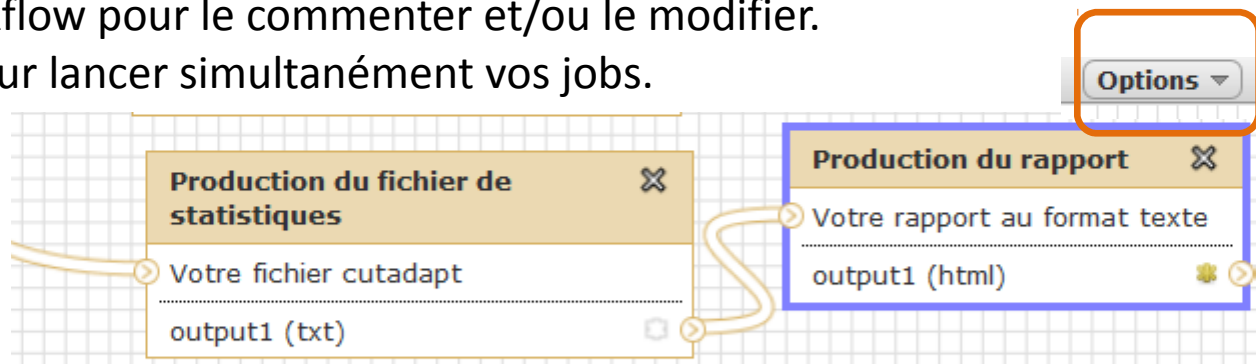
Tool	History items created
* Upload local file from filesystem path <input checked="" type="checkbox"/> Include "*" Upload local file from filesystem path" in workflow	▶ 1: ERR000017.bam
* Upload local file from filesystem path <input checked="" type="checkbox"/> Include "*" Upload local file from filesystem path" in workflow	▶ 8: ERR000017.sorte
* BAM sorted to BAI for IGV <input checked="" type="checkbox"/> Include "*" BAM sorted to BAI for IGV" in workflow	▶ 11: * BAM sorted to

Cliquer sur le menu « Workflow » pour lister vos workflows :



Vous pouvez ensuite, depuis le menu « Options », soit :

- Editer votre workflow pour le commenter et/ou le modifier.
- Run workflow pour lancer simultanément vos jobs.





Présentation de la plateforme Galaxy.

Premiers pas dans l'instance.

Notions d'outils, d'historique et de workflow.

**Lancement de traitements bioinformatiques.**

Quelques statistiques.

Auto-formations disponibles en ligne.

## 1 - UPLOAD YOUR DATA

### Get Data

## 2 - FILES MANIPULATION

### Text Manipulation

### Filter and Sort

### Join, Subtract and Group

### Convert Formats

## 3 - SEQUENCES MANIPULATION

### FASTA manipulation

### FASTQ manipulation

### SAM/BAM manipulation : Picard (beta)

### SAM/BAM manipulation : SAM Tools

## 4 - MAPPING

### BWA - Bowtie

## 5 - INDEL ET SNP

### Indel Analysis

Menu évolutif et organisé par thématique

Ajout d'outils sur demande :

- Tool Shed
- Wrapper à façon (scripts maison, outils bioinfos)

-> Envoyer vos demandes à :  
[sigenae-support@listes.inra.fr](mailto:sigenae-support@listes.inra.fr)

Ces outils sont nombreux et constituent une bonne alternative à la ligne de commande.

Voici les principaux outils « non bioinfo » proposés :

- Join (ex : fichiers lourds), Substract and Group
- Text Manipulation
- Filter and sort
- Convert Formats

**Select first (version 1.0.0)**

**Select first:**  
  
 lines

**from:**

### What it does

This tool outputs specified number of lines from the **beginning** of a dataset

### Example

Selecting 2 lines from this:

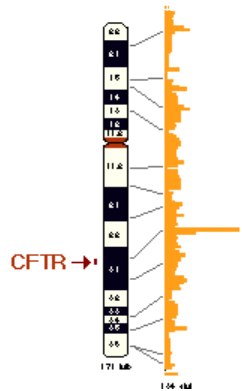
```
chr7 56632 56652 D17003_CTCF_R6 310 +
chr7 56736 56756 D17003_CTCF_R7 354 +
chr7 56761 56781 D17003_CTCF_R4 220 +
chr7 56772 56792 D17003_CTCF_R7 372 +
chr7 56775 56795 D17003_CTCF_R4 207 +
```

will produce:

```
chr7 56632 56652 D17003_CTCF_R6 310 +
chr7 56736 56756 D17003_CTCF_R7 354 +
```

Mapper un FASTQ sur une référence avec BWA.

The CFTR gene maps to chromosome 7



### NGS: Mapping

- Lastz map short reads against reference sequence
- Lastz paired reads map short paired reads against reference sequence
- Map with Bowtie for Illumina
- Map with Bowtie for SOLiD
- Map with BWA for Illumina

**Map with BWA for Illumina (version 0.7.17)**

Will you select a reference genome?

Select a reference from history:

Is this library mate-paired?:

FASTQ file:

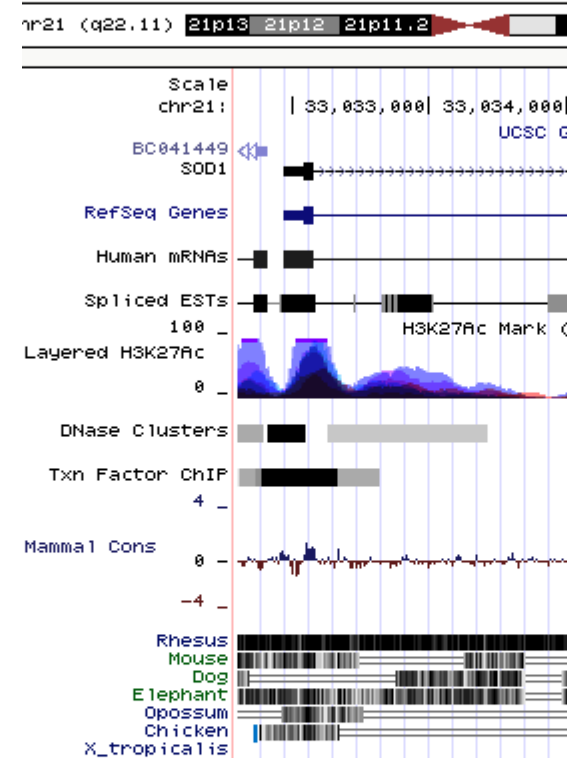
FASTQ with either Sanger-scaled quality

BWA settings to use:

For most mapping needs use Commonly Used

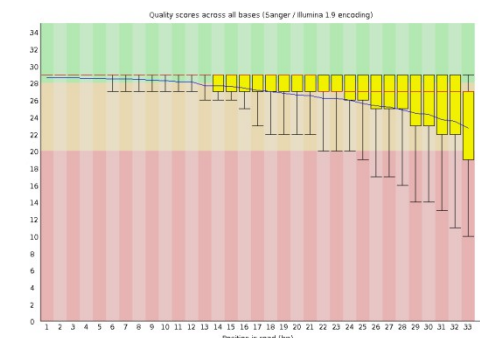
Suppress the header in the output

BWA produces SAM with several lines



Visualiser la qualité des données avec FASTQC Report.

Visualiser un génome avec UCSC .



## **Exercice 2 & 3 :**

Utilisation d'outils de traitements (bio-)informatiques.

Création et partage d'historiques et de workflows.

Suppression des datasets, historiques et workflows inutiles.  
 Suppression temporaire ≠ Suppression permanente (purge)  
 Organiser son espace de travail pour maîtriser son quota.

The screenshot shows the Galaxy web interface with a list of workflows and a context menu open. The workflow list includes columns for name, number of datasets, number of deleted datasets, tags, and size. The context menu is open over a workflow, and the option 'Purge Deleted Datasets' is circled in red.

Workflow	Shared Data	Visualization	Admin	Help	User	Using
cripmunk	1	3	0 Tags		328.0	
: fichiers abs du	4		0 Tags		3.6 G	
ation SNP	17		0 Tags		2.4 M	
rted: anTargetCreator	6	10	0 Tags		3.6 G	
Mirdeep2 sans ination de la ndance intra ni inter	51		0 Tags	Accessible	12.8	
ry_archive	4		0 Tags	Shared	0 byt	
rted: Unnamed ry	6		0 Tags		742.0	
iere session ation Galaxy	21		0 Tags		1.4 G	
- GALAXY	16		0 Tags		1.6 G	
VGS - norphisme	14	6	0 Tags	Shared	0 byt	
NGS RNA Analysis	4	2	0 Tags		41.1	

selected histories: **Rename** **Delete** **Delete Permanently** **Undelet**


**History Lists**

- Saved Histories
- Histories Shared with Me
- Current History
- Create New
- Clone
- Copy Datasets
- Share or Publish
- Extract Workflow
- Dataset Security
- Show Deleted Datasets
- Show Hidden Datasets
- Purge Deleted Datasets**
- Show Structure
- Export to File
- Delete
- Delete Permanently
- Other Actions
- Import from File

## Saved Histories

[Close Advanced Search](#)

name:  

tags:  

sharing: [private](#) | [shared](#) | [accessible](#) | [published](#) | **all**

status: **active** | [deleted](#) | [all](#)

<input type="checkbox"/> <u>Name</u>	<u>Datasets</u>		<u>Tags</u>
<input type="checkbox"/> <a href="#">TP Galaxy project</a> ▼	2	1	<a href="#">0 Tags</a>
<input type="checkbox"/> <a href="#">miRNA tests</a> ▼	59		21 <a href="#">0 Tags</a>
<input type="checkbox"/> <a href="#">TP SNPs calling</a> ▼	84		9 <a href="#">0 Tags</a>
<input type="checkbox"/> <a href="#">TP RNAseq</a> ▼	88		1 <a href="#">0 Tags</a>
<input type="checkbox"/> <a href="#">test TP miRNA</a> ▼	36	1	1 <a href="#">0 Tags</a>

Pour vos publications, citer:

- ✓ Les outils utilisés (nom, version).
- ✓ Le workflow généré.
- ✓ Les références Sigenae et « Galaxy project ».



## How to cite Galaxy workbench ?

Depending on the help provided you can cite us in acknowledgements, references or both.

Examples :

Acknowledgements

We wish to thank the SIGENAE group for ....

References

X. SIGENAE [<http://www.sigenae.org/>]

## Primary Publications

If you use or extend Galaxy in your published work, please cite **each** of the following publications:

1. Goecks, J, Nekrutenko, A, Taylor, J and The Galaxy Team. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome Biol.* 2010 Aug 25;11(8):R86.
2. Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. "Galaxy: a web-based genome analysis tool for experimentalists". *Current Protocols in Molecular Biology.* 2010 Jan; Chapter 19:Unit 19.10.1-21.
3. Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, "Galaxy: a platform for interactive large-scale genome analysis." *Genome Research.* 2005 Oct; 15(:



Présentation de la plateforme Galaxy.

Premiers pas dans l'instance.

Notions d'outils, d'historique et de workflow.

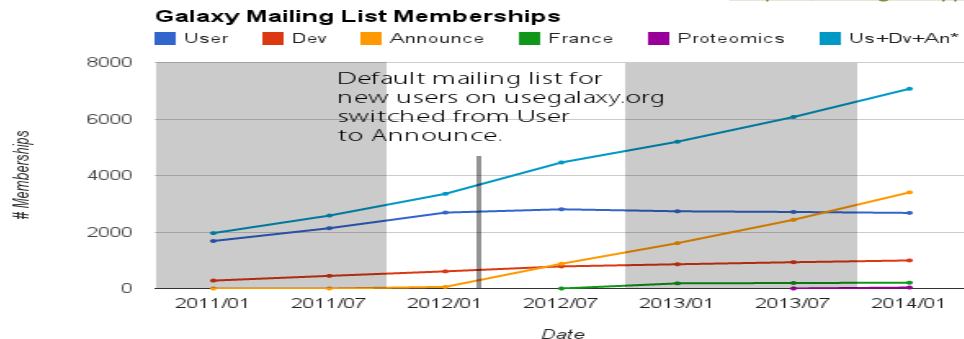
Lancement de traitements bioinformatiques.

**Quelques statistiques.**

Auto-formations disponibles en ligne.

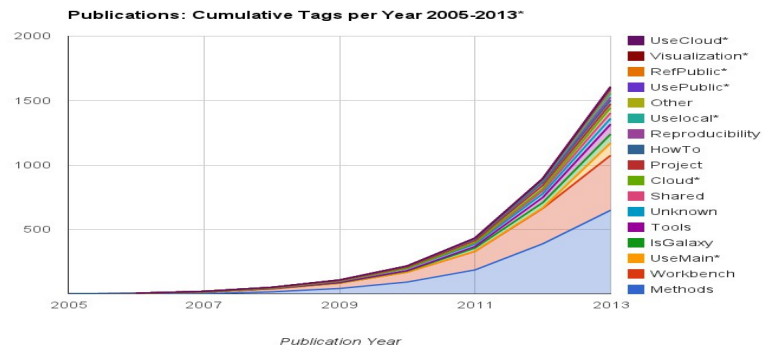
## Statistiques du Galaxy Project

<https://wiki.galaxyproject.org>



Une communauté internationale vivante.

Une communauté française grandissante.



Belle augmentation des citations Galaxy dans les publications

## Statistiques de l'instance Galaxy Sigeneae / BioInfo Genotoul

<http://galaxy-workbench.toulouse.inra.fr>

### Historique mensuel des visites



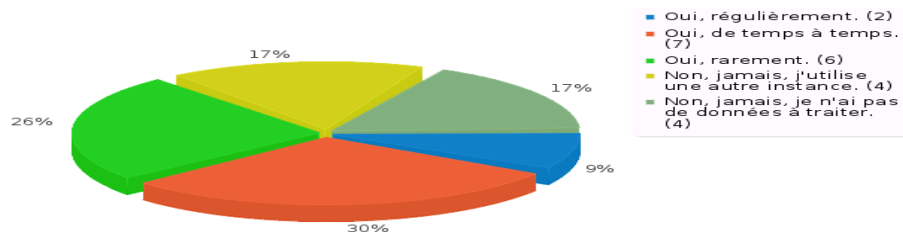
23 réponses sur ~40 utilisateurs

~40 utilisateurs

Les 10 plus gros utilisateurs (hors tests Sigeneae) utilisent Galaxy dans le cadre de leur projet.

65% des utilisateurs Galaxy ayant répondu à l'enquête utilisent l'instance Sigeneae

### Utilisez-vous l'instance Sigeneae de Galaxy ?



Présentation de la plateforme Galaxy.

Premiers pas dans l'instance.

Notions d'outils, d'historique et de workflow.

Lancement de traitements bioinformatiques.

Quelques statistiques.

**Auto-formations disponibles en ligne.**

Une FAQ et le lien vers « sig-learning » sont disponibles depuis la page d'accueil.

Shared Data Lab Visualization Admin Help User User **Welcome smaman,**



## FAQ on your Galaxy tool

### ▼ Dataset, history and workflow ?

#### **Step 1 : Import your datasets**

First of all, you have to import your data files thanks to "Data Analysis / Get Data" tool. Then your downloaded datasets are automatically archived in "User / Saved Datasets".

#### **Step 2 : Select tools and create your history**

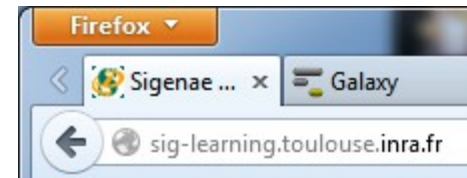
Then you select relevant tool in "Data Analysis", on the left side of Galaxy interface.

Vos supports sont disponibles depuis : <http://sig-learning.toulouse.inra.fr>




"If you need more training about bioinformatic and Galaxy, please connect to [Sigenae e-learning platform](http://sig-learning.toulouse.inra.fr)."

- 1 Taper l'adresse de « sig-learning » :  
**<http://sig-learning.toulouse.inra.fr/>**  
**Ou directement depuis Galaxy**



## Sigena e-learning platform

If you need more training about bioinformatic and Galaxy, please connect to [Sigena e-learning platform](#)

Some of the tools have a direct access to the e-learning platform of sigena. Those tools will have this  in the help section. Click on this icon to be redirected to the e-learning platform.


Sigena support : [sigena-support@listes.inra.fr](mailto:sigena-support@listes.inra.fr)

If you have some question about Galaxy, please consult your [FAQ](#)

- 2 **Authentication**

Login

Pass

 Enter

- 3 Onglet « Trainings » pour accéder à vos e-formations :

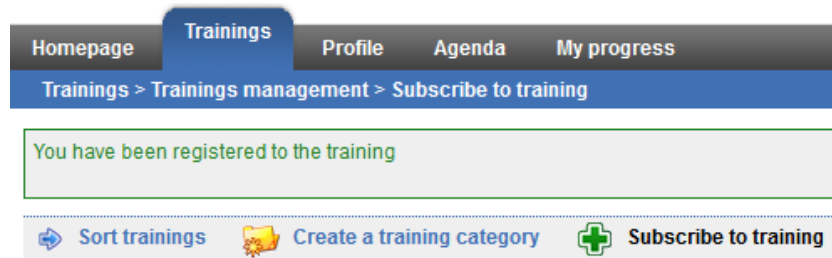


Homepage **Trainings** Profile Agenda Reporting Administration

Trainings

-  **1 - Linux & Unix**  
UNIX1 – SIGENAE Team
-  **2 - Cluster (en construction)**  
CLUSTER – SIGENAE Team
-  **3 - Management of large files on Unix and Galaxy**  
UNIX2 – SIGENAE Team

Il vous est possible de vous inscrire directement en ligne à une formation : « Trainings »  
« Trainings management » puis « Subscribe to training » :



L'inscription s'effectue via une recherche de la formation par mots clés.  
Voici donc la liste des formations :



Training home

Galaxy



57%

Galaxy > Galaxy User Interface

## 1 - Galaxy User Interface

Build Organize Display

- Galaxy menu
  - Galaxy presentation ✓
  - Galaxy connexion ✓
  - Your screen is divided in 3 parts ✓
  - Menu ✓
- Import Dataset
  - How to get data ? ✓
  - Upload without copy on server ✓
  - Upload with copy on server ✓
  - Dataset from NG6 ✓
  - UCSC ✓
  - NCBI ✓
  - BIOMART: Extract tab files ✓
- Datasets, tools and history
  - History creation ✓
  - Manage histories
  - Share histories
  - Datasets and tools are listed in your history
- Edit, run and share a workflow
  - Create a workflow
  - Edit and run a workflow
  - Share workflows
  - Import your workflow
  - Export workflow
  - Main steps

1 – When you open Galaxy, an empty history is automatically created :

2 – Rename this history :

Commentaires Comments

Lorsque vous vous connectez à Galaxy, un historique vide est automatiquement créé de gauche.

Tout d'abord, il est recommandé de renommer votre historique et de télécharger vos jeux de données avec les outils disponibles dans « G »

# Merci pour votre écoute

Questionnaire

<https://enquetes.inra.fr/index.php?sid=84236&lang=en>



# Remerciements



Fonds Européen  
de Développement Régional

