

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
Sigena Platform. Galaxy objectives are:

- Make bioinfo Linux tools accessible to biologists.
 - 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

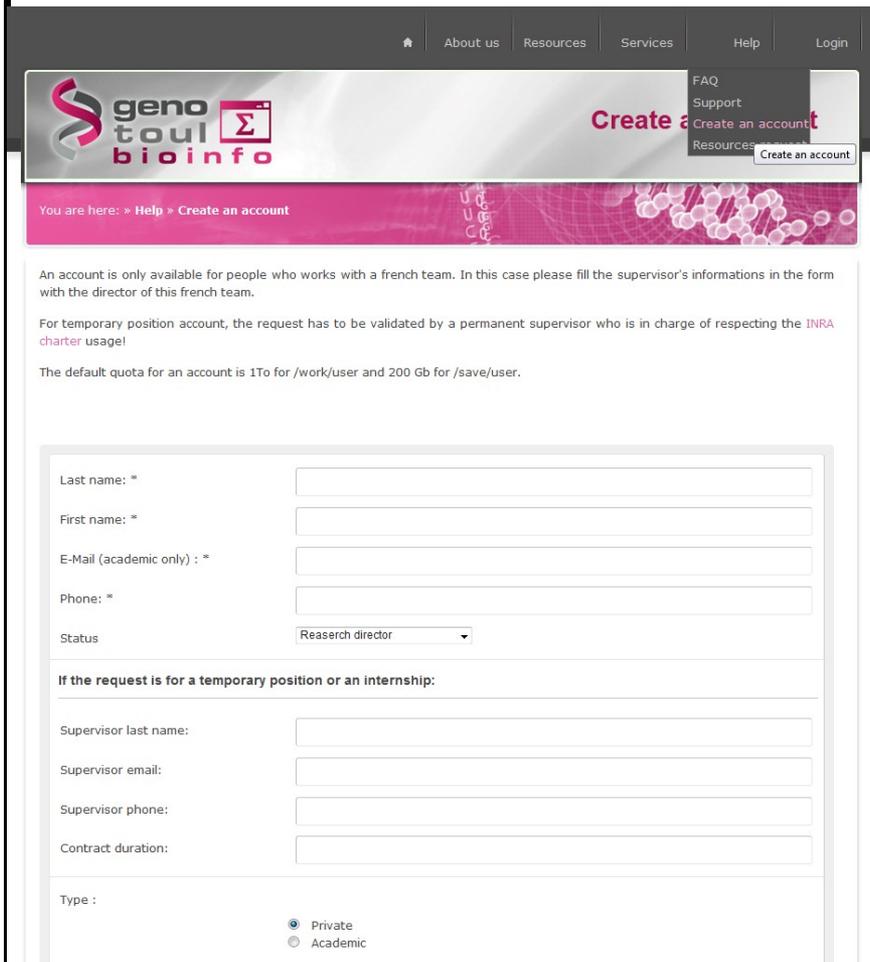


1	2	3	4	5	6
#column	count	min	max	sum	mean
1	99115	2	33	3194703	32.2
2	99115	2	34	3156652	31.8
3	99115	2	34	3145060	31.7
4	99115	2	34	3120431	31.4
5	99115	2	34	3096075	31.2

Etat des lieux Galaxy & Evolutions récentes

Sarah Maman – Ibouniyamine Nabihoudine
24 mars 2014 – GenPhySE

Aperçu général



The screenshot shows the 'Create an account' page on the Genotoul bioinfo website. At the top, there is a navigation bar with links for 'About us', 'Resources', 'Services', 'Help', and 'Login'. Below this is a banner with the Genotoul bioinfo logo and a 'Create an account' button. A breadcrumb trail indicates the user is in 'Help > Create an account'. The main content area contains instructions: '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.' It also mentions that for temporary positions, the request must be validated by a permanent supervisor and that the default quota is 1To for /work/user and 200 Gb for /save/user. Below the text is a form with the following fields: 'Last name: *', 'First name: *', 'E-Mail (academic only) : *', 'Phone: *', 'Status' (with a dropdown menu set to 'Reaserch director'), and a section for temporary positions with fields for 'Supervisor last name:', 'Supervisor email:', 'Supervisor phone:', and 'Contract duration:'. At the bottom, there are radio buttons for 'Type :', with 'Private' selected and 'Academic' unselected.

1 – Ouvrir un compte sur Genotoul :

Formulaire de demande de compte:
<http://bioinfo.genotoul.fr>

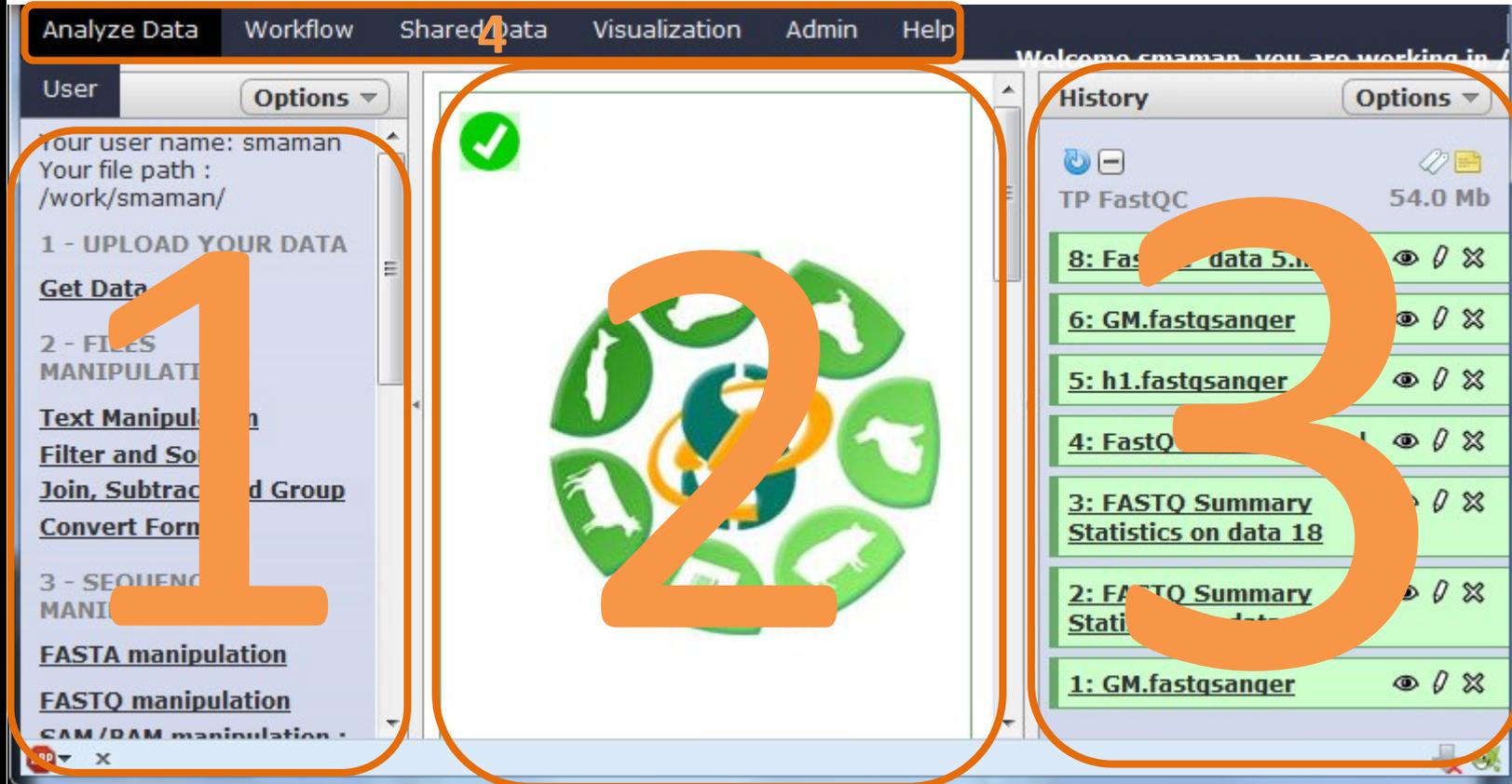


Utiliser un mail académique

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

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

Votre écran est divisé en 4 zones principales :





Analyze Data Workflow Shared Data Visualization Admin Help Using 13%

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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)

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:
phiX174_read

File type:
Fastq ▾

Path to file:
/work/smaman/phiX174_reads.fastqsanger

Execute

History **Options** ▾

Unnamed history 0 bytes

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

Analyze Data Workflow Shared Data Visualization Admin Help Using 13%

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User Options

Your user name: smaman
Your file path: /work/smaman/

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Indel Analysis

RNA-Seq

GATK Tools (beta)

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

File Name:

File type:

Path to file:

History Options

Galaxy sensibilisation - TP 12.1 Mb

2 - BWA and FastQC

14:

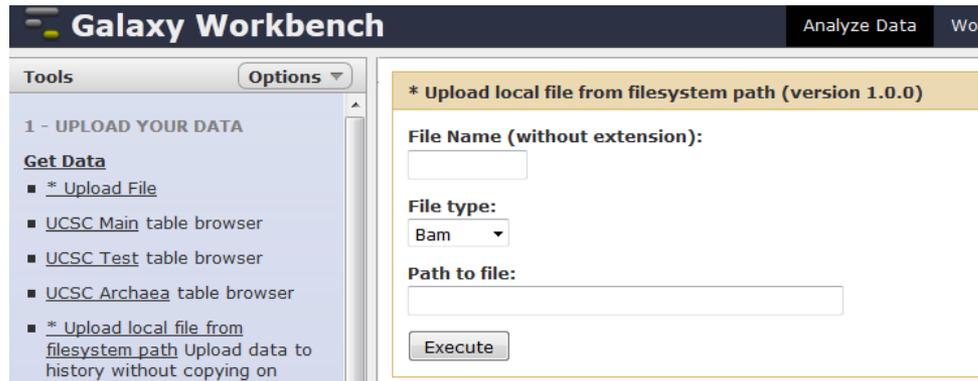
phiX174_reads.fastqsanger

1.0 Mb

format: fastqsanger, database: ?

```
@080917-and-080922:5:1:185:82
GATGTTATTTCTTCATTTGGAGGTAAAACCTCTTAT
+
IIIIIIIIIIIIIIIIIIIIII<III@FI8A/I0II4I
@080917-and-080922:5:1:1366:223
GTTTTCTTCTGCGTCAGTAAGAACGTCAGTGTITCC
```

-Soit fichier par fichier :



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)**

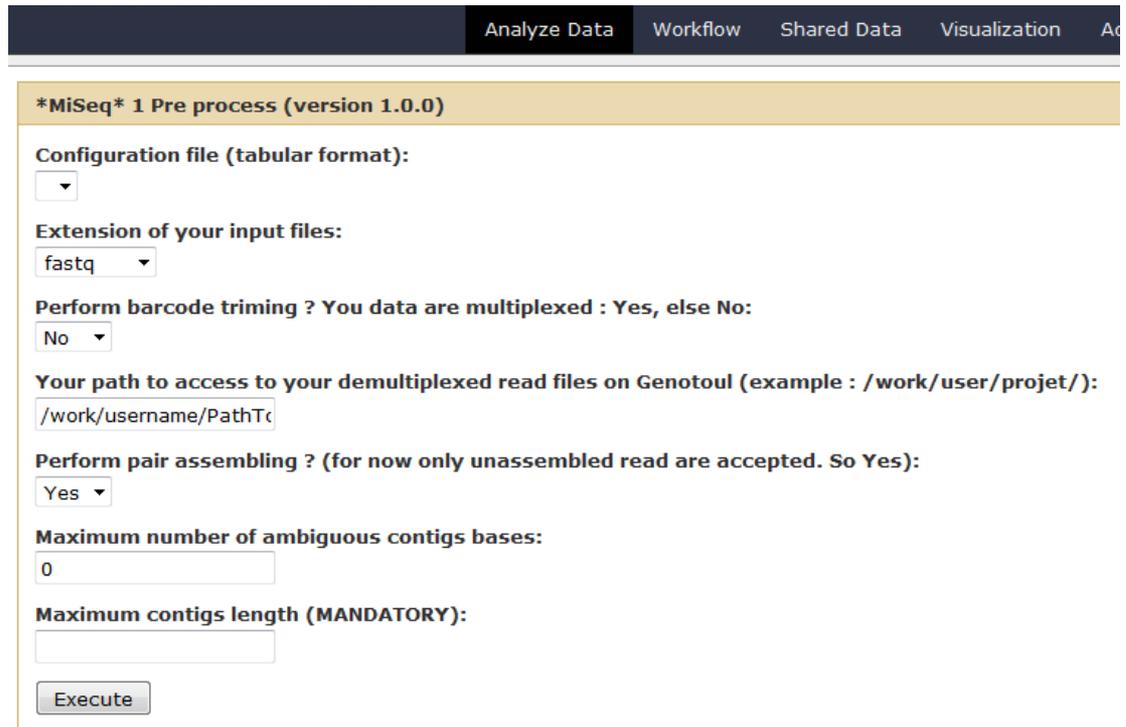
File Name (without extension):

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/):

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

Maximum number of ambiguous contigs bases:

Maximum contigs length (MANDATORY):

Execute

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

Tools Options

1 - UPLOAD YOUR DATA
Get Data

2 - FILES MANIPULATION
Text Manipulation
Filter and Sort
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Convert Formats

3 - SEQUENCES MANIPULATION
FASTA manipulation
FASTQ manipulation
SAM/BAM manipulation : Picard (beta)
SAM/BAM manipulation : SAMtools
Fetch Sequences

Saved Histories

search history names and tags

Advanced Search

Name	Datasets	Tags	Sharing
<input type="checkbox"/> TP Galaxy project	2	1	0 Tags
<input type="checkbox"/> miRNA tests	59	21	0 Tags
<input type="checkbox"/> TP SNPs calling	84	9	0 Tags
<input type="checkbox"/> TP RNAseq	88	1	0 Tags Shared, Accessible
<input type="checkbox"/> test TP miRNA	36	1	0 Tags
<input type="checkbox"/> 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

-Vos jobs :

- Se poursuivent même si vous êtes déconnectés du Galaxy.
- Leurs états sont indiqués par la couleur du dataset.
- Peuvent être lancés en parallèle & sans connaître linux.
- Peuvent être partagés.

-Vos données :

- N'encombrent pas votre disque dur.
- Sont protégées (accès LDAP).

Comment générer une chaîne de traitement ?

-Soit depuis un historique :

Workflow name
 Workflow constructed from history 'IGV bai'

Create Workflow Check all Uncheck all

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

History Options ▼

Using 62%

History Lists

- Saved Histories
- Histories Shared with Me

Current History

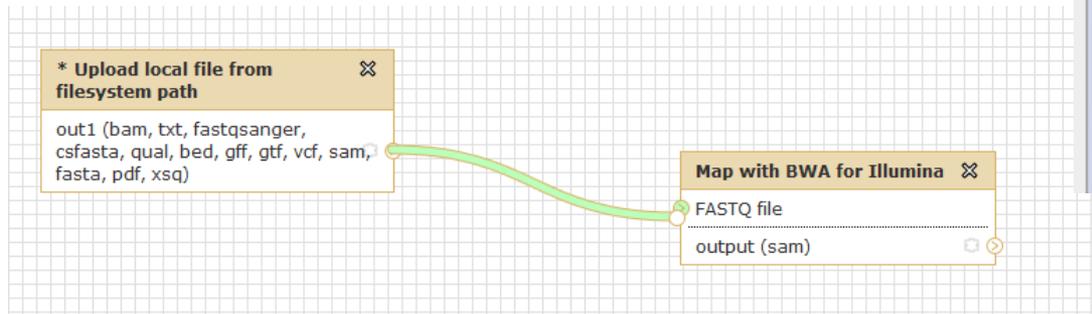
- Create New
- Clone
- Copy Datasets
- Share or Publish
- Extract Workflow**
- Dataset Security
- Show Deleted Datasets
- Show Hidden Datasets
- Purge Deleted Datasets
- Show Structure
- Export to File
- Delete
- Delete Permanently

Other Actions

- Import from File

-Soit depuis une page blanche :

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



Evolution récentes



Des outils plus complets

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

Galaxy Workbench | Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User | Welcome smaman | Using 37%

Tools | Options

- 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
 - RNASEQ RAW EXPRESSION
 - * htseq count
 - * Merge Htseq count output file into a global counting file
 - * Sigcafflinks to obtain raw count of reads
 - * Merge sigcafflinks count file

*** 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.
Execute

(*) Outils Siganae

junctions using RNA-seq data

sRNAseq

7 - CHIP-SEQ

Operate on Genomic Intervals

Nebula

8 - TRAININGS

Galaxy Initiation

Reads alignment and SNP calling

RNA-Seq

sRNAseq

SNP annotation

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

Accès à plus d'options de la ligne de commande

Affichage de la ligne de commande et des étapes de traitement

History | Options

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

85Q VW:1.3 50:coordinate
85Q SN:ENSDART00000112983 LN:2064
85Q SN:ENSDART00000122527 LN:579
85Q SN:ENSDART00000129800 LN:810
85Q SN:ENSDART00000099219 LN:2552
85Q SN:ENSDART00000079354 LN:1245

14:
{{M_Pf_2_ACAGTG_L007_R2.fastqsanger}-BWA.bam
}-bam
97 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 sin /work/galaxy/database/files/011/dataset_11741.d

ENSDART00000112983	2064	0	0
ENSDART00000122527	579	0	0
ENSDART00000129800	810	0	0
ENSDART00000099219	2552	0	0
ENSDART00000079354	1245	0	0
ENSDART0000024841	1605	0	0



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

<input type="checkbox"/>	{PFB-68_8.fastosanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-69_19.fastosanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-69_19.fastosanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-70_20.fastosanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-70_20.fastosanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-71_21.fastosanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-71_21.fastosanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-72_22.fastosanger}-cutadapt.fastq-report.html	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago
<input type="checkbox"/>	{PFB-72_22.fastosanger}-cutadapt.fastq	TESTS ***** Pierre francois mirdeep2	0 Tags	2 days ago

Page: 1 2 3 4 5 6 7 8 9 10 11 ... 17 | Show All

For 0 selected datasets:

3

1: dataset path list

2 lines, 1 comments
format: tabular, database: 2

```
#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

Use file list ?:

Tabular file of datasets to be exported:

Galaxy Workbench
Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User | Welcome smaman

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RNAseq
DEA stats
S-MART
sRNAseq

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Nebula

8 - TRAININGS
Reads alignment and SNP calling
RNA-Seq
sRNAseq
SNP annotation
Metagenomics Mothur 454 and MiSeq



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Connect to our new version of Galaxy

Test it ! [<http://vm-galaxy-dev.toulouse.inra.fr/>]



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/>]



Sigenae e-learning platform

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

Some of the tools have a direct access to the e-learning platform.

Sigenae support : sigenae-support@listes.inra.fr

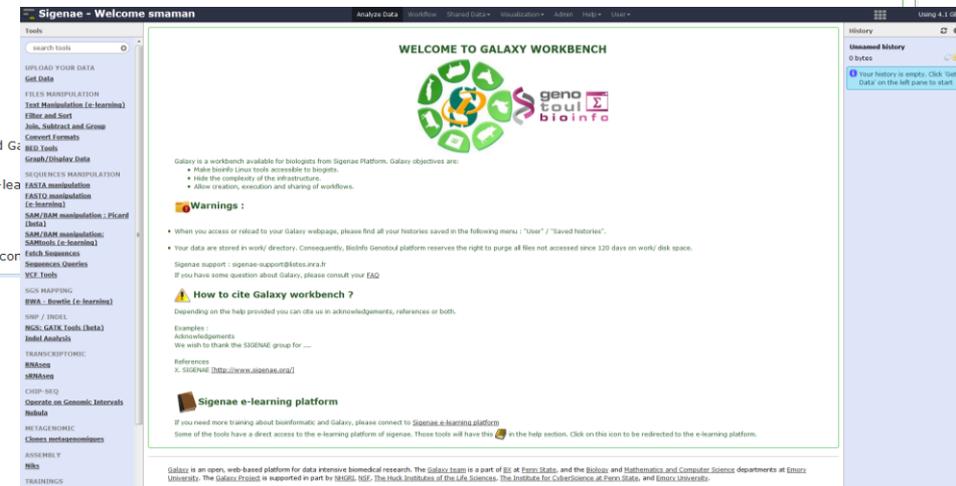
If you have some question about Galaxy, please see our [FAQ](#).

History

Unchanged History

0 bytes

Your history is empty. Click "Get Data" on the left pane to start.



- ~30 nouveaux outils et 5 chaînes de traitements.
- Matériel & méthode : Commandes / versions d'outils Galaxy et bioinfo.
- Machine :
 - ✓ Sur la nouvelle infrastructure (genovcenter)
 - ✓ Plus rapide d'accès sur site distant (multithreading)
 - ✓ Envoi des jobs au nom du user LDAP (workq ou autre q.)
 - ✓ Paramétrage plus fin des jobs en fonction des ressources.

Tool: * NIKS

Name:	* NIKS on data 4, data 6, and others
Created:	Jan 13, 2014
Filesize:	0 bytes
Dbkey:	?
Format:	fasta
Galaxy Tool Version:	1.0.0
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
API ID:	aa03efb04bdce6b0
Full Path:	/work/galaxy-dev/database/files/000/dataset_621.dat
Job Command-Line:	perl /usr/local/bioinfo/src/galaxy-dev/galaxy-dist/tools/sm_niks /sm_niks.pl --pipeline-type KMER --fastqa1 /work/galaxy-dev/database/files/000/dataset_170.dat --fastqa1 /work/galaxy-dev/database/files/000/dataset_168.dat --fastqb1 /work/galaxy-dev/database/files/000/dataset_169.dat --fastqb1 /work/galaxy-dev/database/files/000/dataset_171.dat --insert-size 100 --output-fasta-a /work/galaxy-dev/database/job_working_directory/000/304/galaxy_dataset_620.dat --output-fasta-b /work/galaxy-dev/database/job_working_directory/000/304/galaxy_dataset_621.dat --output-csv /work/galaxy-dev/database/job_working_directory/000/304/galaxy_dataset_622.dat

History

imported: 131220
148.0 GB

30: * NIKS on data 4, data 6, and others

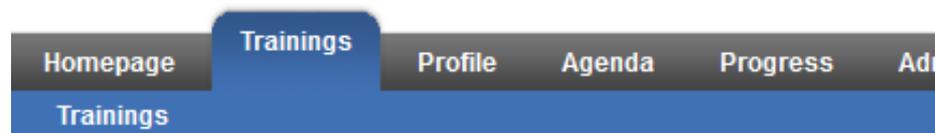
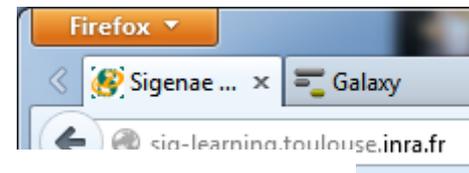
29: * NIKS on data 4, data 6, and others

empty
format: fasta, database: ?
Log: Matched on sed -i -e 's,^FASTQA1=.*,FASTQA1=/work/galaxy-dev/database/files/000/dataset_170.dat /work/galaxy-dev/database/files/000/dataset_168.dat,' /tmp/4211822.1.workq /ZeNIqaDOow/kmerPipeline.sh sed -i -e 's,^FASTQA1=.*,FASTQA1=/work/galaxy-dev/

no peek

Site E-Learning

« sig-learning » : <http://sig-learning.toulouse.inra.fr/>



Enquête 2013 :
Accès ponctuels à sig-learning

- 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
- 4 - Galaxy
GALA01 – SIGENAE Team
- 5 - FastQC : quality control tool & reports interpretation
FASTQC – SIGENAE Team
- 6 - Aligning SGS reads and SNP finding
SGS-SNP – SIGENAE Team
- 7 - NG6
NG6 – SIGENAE Team
- 8 - RNA seq (en construction)
RNASEQ – SIGENAE Team
- Demonstration
DEMO – SIGENAE Team
- Mothur: analyse d'ADN 16S
MOTHUR_16S – bernard maria

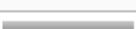
Mise en production

Formations PF BioInfo

Formations PF BioInfo

Formations Roscoff

Formations Roscoff

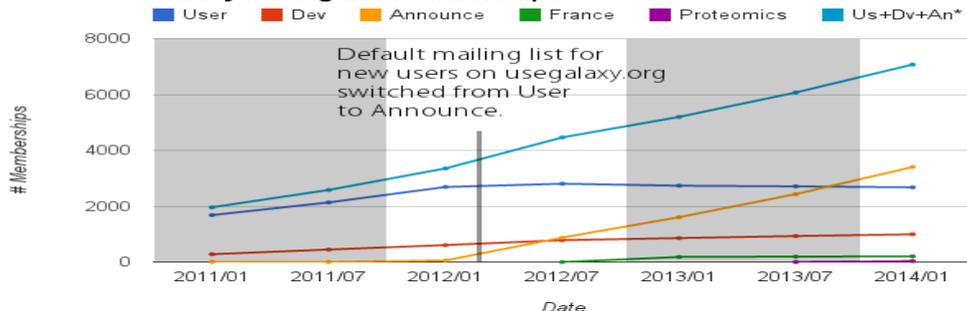
Logins (Month)			
2012 February		103	14,5%
2012 March		34	4,8%
2012 April		33	4,6%
2012 May		92	13,0%
2012 June		103	14,5%
2012 July		15	2,1%
2012 August		13	1,8%
2012 September		14	2,0%
2012 October		42	5,9%
2012 November		11	1,5%
2012 December		12	1,7%
2013 January		29	4,1%
2013 February		19	2,7%
2013 March		6	0,8%
2013 April		4	0,6%
2013 May		11	1,5%
2013 June		6	0,8%
2013 July		18	2,5%
2013 August		6	0,8%
2013 September		22	3,1%
2013 October		5	0,7%
2013 November		13	1,8%
2013 December		71	10,0%
2014 January		21	3,0%
2014 February		7	1,0%
		Total: 710	

Enquête 2013 auprès des ~40 utilisateurs locaux

Statistiques du Galaxy Project

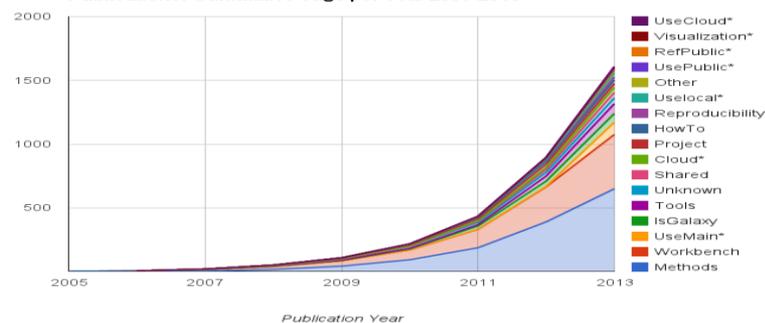
<https://wiki.galaxyproject.org>

Galaxy Mailing List Memberships



Une communauté internationale vivante.
Une communauté française grandissante.

Publications: Cumulative Tags per Year 2005-2013*



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

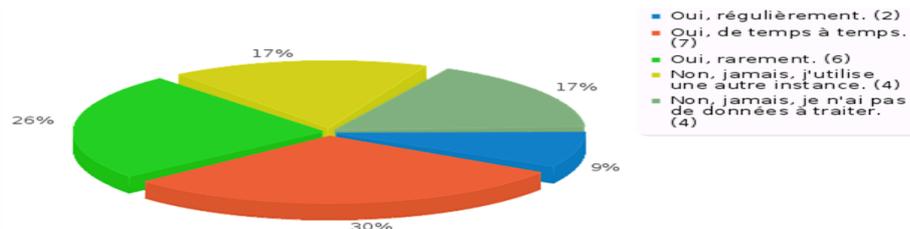


23 réponses sur ~40 utilisateurs

~40 utilisateurs
Les 10 plus gros utilisateurs (hors tests Sigeneae) utilisent Galaxy dans le cadre de leur projet.

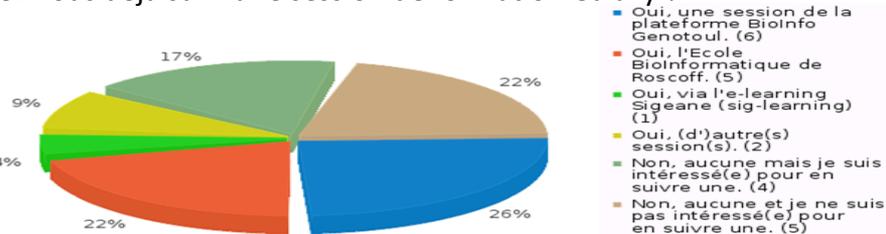
65% des utilisateurs Galaxy ayant répondu à l'enquête utilisent l'instance Sigeneae

Utilisez-vous l'instance Sigeneae de Galaxy ?



Importance de la formation et du e-learning

Avez-vous déjà suivi une session de formation Galaxy ?



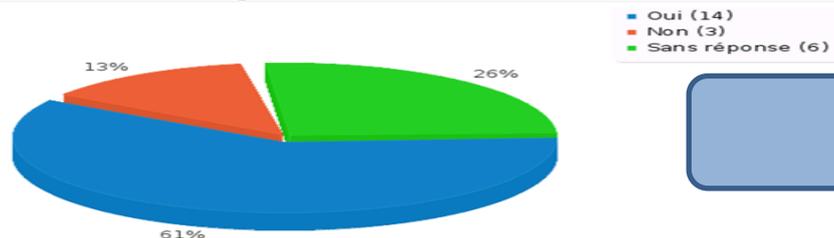
6% des utilisateurs seulement ont déjà suivi une formation en e-learning.

60% des utilisateurs :

- ont déjà suivi une formation Galaxy -> Besoin d'une 'mise en route',
- souhaite plus de support en bioinfo.
- créent et utilisent des workflows.

Les traitements Galaxy sont aussi lancés dans le cadre de projets

Galaxy vous permet-il de traiter vos données bio-informatiques ?



~60% traitent leurs données dans Galaxy.
... Et 60% de ces 60% utilisent ces données dans leur projet.

Principalement des applications de type SNP et RNAseq

Quels sont les principaux outils utilisés ?



Les formations avec Galaxy

- Formations PF BioInfo Genotoul
- UPS Master 2 BioInformatique

Galaxy training :

- Galaxy : First step
- Galaxy : Reads alignment and SNP calling
- Galaxy : RNAseq alignment and transcripts assemblies
- Galaxy : sRNAseq
- Galaxy : metagenomic : sequence analysis of 16S DNA reads

<http://bioinfo.genotoul.fr>

Training calendar :

The table below gives you information on the training subject, session, date, and the number of remaining free places. To register **fill out the registration form** (Unix, Cluster, ...). You will then be in a **waiting list** and you will be informed if you have been selected for the next session or scheduled in an other one.

Title	Date	Organizers	Vacancies	Registration
Metagenomic: 16S DNA reads	05.02.2014	Jerome Mariette, Christophe Klopp, Maria Bernard, Sarah Maman, Laurent Cauquil	fully booked	
Unix / Linux	07.04.2014	Didier Laborie	3 ■	Register now
Cluster	08.04.2014	Didier Laborie, Celine Noirot	5 ■	Register now
Reads alignment and SNP calling	09.04.2014	Jerome Mariette, Philippe Bardou	3 ■	Register now
RNAseq alignment and transcripts assemblies	10.04.2014	Celine Noirot, Delphine Labourdette	7 ■	Register now
Galaxy training days	12.-14.05.2014	Jerome Mariette, Philippe Bardou, Sarah Maman, Celine Noirot, Delphine Labourdette	fully booked ■	Register for the waiting list (0 registrations on the waiting list)



Objectifs
& Missions

Instituts thématiques
multi-organismes

Membres
d'Aviesan

Actions
& Initiatives

Accueil > Toute l'actualité > Ecole de bioinformatique :...

Taille du texte English

Ecole de bioinformatique : Initiation au traitement des données de génomique obtenues par séquençage à haut débit

Ecoutez 14 jan 2013



Du 14 au 18 Janvier 2013 à la Station Biologique de Roscoff

Cette école organisée par l'ITMO Génétique, génomique et bioinformatique avec le support de 9 plateformes de bioinformatique, accueillera 40 participants.

Consulter la plaquette de l'école (397,7 ko)

Contact : ecole-bioinfo@aviesan.fr

[Consulter le programme \(école bioinformatique\)](#)

- Pré-traitement et alignement des données exome-seq (M. Bernard, R. Daveau, S. Gallina, E. Girard, B. Job, Y. Luo, N. Servant)
- Détection et annotation fonctionnelle de variants (M. Bernard, R. Daveau, S. Gallina, E.Girard, B. Job, Y. Luo, S. Marthey, N. Servant)
- Prédiction de miRNA avec MirDeep2 et autres outils. Annotation des reads : miRNA et autres ncRNA (C. Gaspin, S. Maman, O. Rué)
- Analyse des données des participants.

Les liens avec les communautés et groupes de travail



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.



Anton Nekrutenko
Penn State

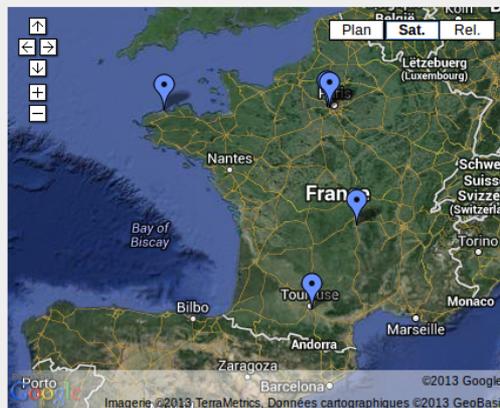


Nate Coraor
Penn State



James Taylor
Emory

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



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

Liste des instances

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

Merci à toutes celles / tous ceux qui travaillent sur Galaxy !

✓ Les wrappers boys & girls

Maria Bernard

Frédéric Escudié

Ibouniyamine Nabihoudine

Olivier Rué

Sabrina Rodriguez

✓ Les admins

Patrice Dehais

Didier Laborie

Marie-Stephane Trotard

✓ Les formateurs

Philippe Bardou

Christophe Klopp

Delphine Labourdette

Jérôme Mariette

Céline Noirot

✓ Les personnes ayant utilisés Galaxy pour leurs projets

Maria Bernard

Sandrine Laguerre

Olivier Monestier

Jérôme Montfort

...

Merci pour votre écoute

sigenae-support@listes.inra.fr