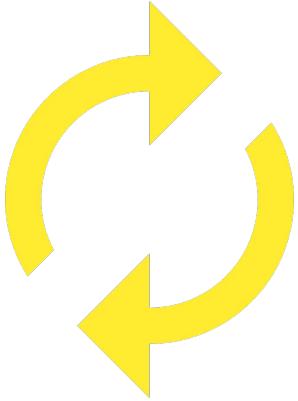




Session de formation 2019





Bioinformatics platform dedicated to the genetics and genomics of tropical and Mediterranean plants and their pathogens

comparative genomics
phylogenetics
GWAS
population genetics
polypliody

genome assembly
transcriptome assembly
metagenomics

SNP detection
structural variation
differential expression



Rice



Banana



Palm



Sorghum



Coffee



Cassava



Magnaporthe

South Green

bioinformatics platform



Charte



Larmande Pierre
Sabot François
Tando Ndomassi
Tranchant-Dubreuil
Christine



Comte Aurore
Dereeper Alexis



Orjuela-Bouniol Julie



Bocs Stephanie
De Lamotte Fredéric
Droc Gaetan
Dufayard Jean-François
Hamelin Chantal
Martin Guillaume
Pitollat Bertrand
Ruiz Manuel
Sarah Gautier
Summo Marilyne



Rouard Mathieu
Guignon Valentin
Catherine Breton



Mahé Frédéric
Ravel Sébastien

Sempere Guilhem





Workflow manager

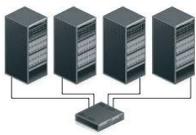
TOGGLE

Toolbox for generic NGS analyses



Galaxy

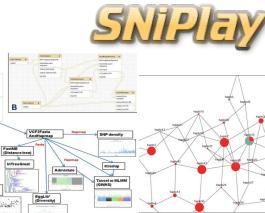
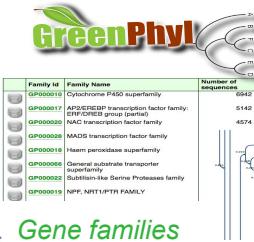
HPC and trainings....



Genome Hubs & Information System



SNPs and Indels





Erwan Corre



Marie Simonin
Sébastien Cunnac



Etienne Loire
Julie Reveillaud



Florentin Constancias



Valentin Klein



Valérie Noël



Emmanuelle Beyne



And more collaborators !

18-19/03	Guide de survie à Linux - IRD
21/03	Initiation à l'utilisation du cluster CIRAD - CIRAD
22/03	Initiation à l'utilisation du cluster itrop - IRD
15-16/04	Initiation au gestionnaires de workflow SG & Gigwa - IRD
18-19/04	Guide du Jedi en Linux & bash - CIRAD
13-16/05	Python - IRD
17/05	Initiation aux analyses de données transcriptomiques - IRD
21/05	Utilisation avancée du cluster IRD - IRD
23-24/05	Initiation aux analyses de données métagénomiques - IRD
6/06	Manipulation de données et figures sous R - CIRAD
26-28/06	Assemblage et annotation de transcriptomes - IRD



Modules de formation 2019

- Toutes nos formations :
<https://southgreenplatform.github.io/trainings/>
- Environnement de travail : **bioinfo-inter.ird.fr:8080**





Workflow Manager

TOEGLe

Galaxy
PROJECT

www.southgreen.fr

<https://southgreenplatform.github.io/trainings>



Objectifs de la formation

objectifs:

Utiliser les gestionnaires de Workflow de South Green afin de construire de manière automatique vos propres pipelines.

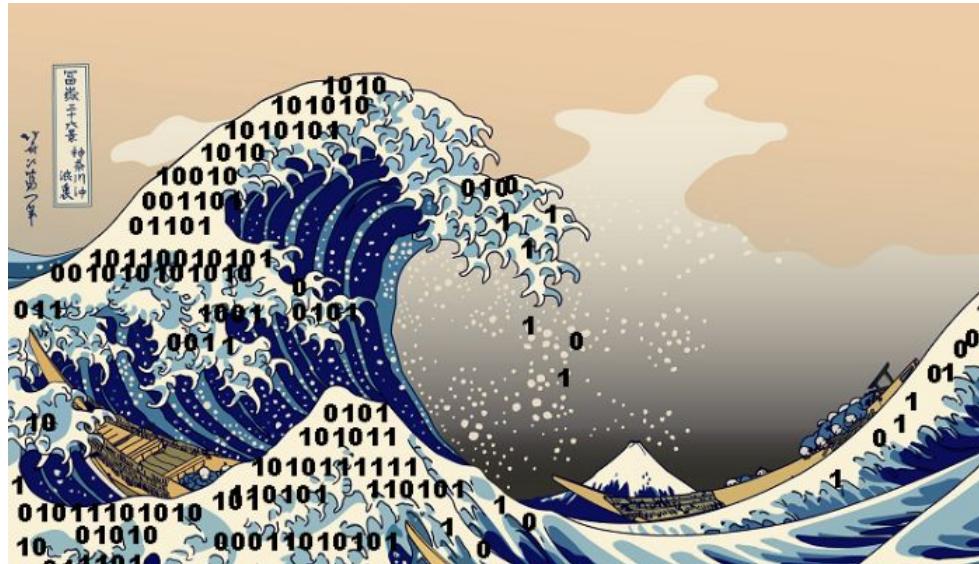


Applications

Tout savoir sur les 2 principaux gestionnaires de workflow

- Utiliser les outils
- Construire son propre workflow
- Pratiquer sur un même cas d'utilisation : Appel de SNPs à partir de reads Illumina de 3 échantillons

Pourquoi utiliser un gestionnaire de workflow?



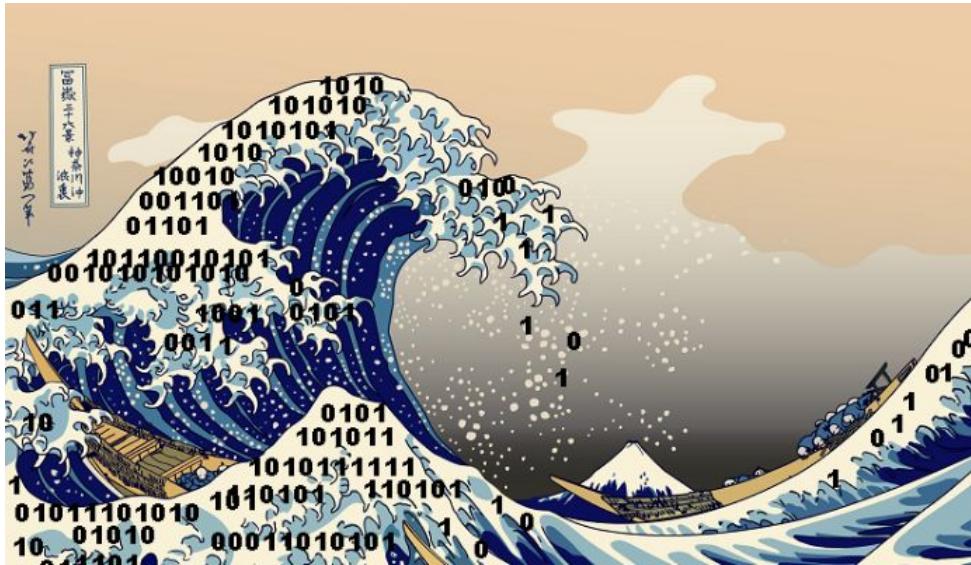
The Great Wave off Kanagawa, Hokusai

@amitechsolutions.com



© D.Fletcher for CloudTweaks.com

Pourquoi utiliser un gestionnaire de workflow?



Créer son propre pipeline via une méthode facile et conviviale

Données brutes



Résultats
Intermédiaires



Résultats
Intermédiaires



Résultat
Final

- 3 solutions proposées par



GUI tools



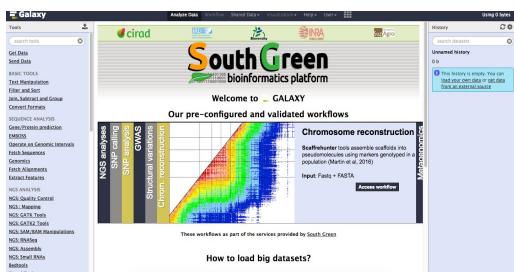
CLI tools



GUI tools



Galaxy



Facilité d'utilisation
Bonne documentation

Pourquoi utiliser un gestionnaire de workflow?

CLI tools



TOGGLE



Snakemake



genome assembly
comparative genomics
GWAS
population genetics
phylogeny
pangenomics
polyploidy
SNP detection
structural variation
transcriptome assembly
differential expression

Facilité de
développement

Contrôle du pipeline
et des données

Apporte un cadre robuste



Vérifie le format des fichiers

Valide l'enchaînement des outils



Automatisation de certaines étapes clefs
(ex : indexation de la référence)

Pourquoi utiliser un gestionnaire de workflow?

Contrôle du pipeline
et des données

Reproductibilité
& traçabilité

**Apporte un cadre
robuste**

Sauvegarde des options, version des logiciels,
partage des analyses

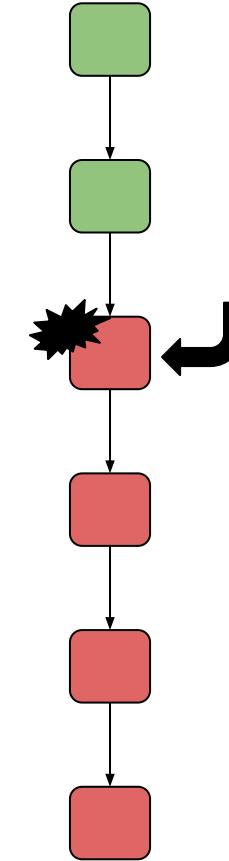
Pourquoi utiliser un gestionnaire de workflow?

Contrôle du pipeline
et des données

Apporte un cadre
robuste

Reproductibilité
& traçabilité

Suivi des erreurs
& reprise en cours



Pourquoi utiliser un gestionnaire de workflow?

Contrôle du pipeline
et des données

Apporte un cadre
robuste

Reproductibilité
& traçabilité

Suivi des erreurs
& reprise en cours



Analyse de gros
jeu de données

Pourquoi utiliser un gestionnaire de workflow?

Contrôle du pipeline
et des données



Connection HPC
Parallélisation

Apporte un cadre
robuste

Reproductibilité
& traçabilité

Suivi des erreurs
& reprise en cours

Analyse de gros
jeu de données



Interface	Command line	GUI (Web interface)
Predefined Pipelines	SNP calling, RNASeq and WGS large scale ...	Metagenomics, RNASeq, SNP calling, post-analyses ...
Number of Samples	+++	++
Quota (related to infra)	Disk space "/data/projects"	IRD 100Go data Cirad 100Go => 300Go
Parallelization (related to infra conf)	IRD 300 cores Cirad 600 cores	IRD 16 cores / one node Cirad 200 cores
Number of tools available	++ (120)	++++ (5500 avail)
Post-analyses Graphical figures	Not yet	Yes

Introduction au gestionnaire de
workflow:



Galaxy : Introduction

- Plateforme de fouille et de gestion de données
- Rendre la bioinformatique accessible sans compétence en programmation informatique



Instance IRD : <http://bioinfo-inter.ird.fr:8080>

Instance SouthGreen : <http://galaxy.southgreen.fr/galaxy/>



Connectez-vous sur la plateforme Galaxy IRD à l'adresse suivante :

<http://bioinfo-inter.ird.fr:8080/>

Utilisez pour aujourd'hui le compte formationN/formationN



The header shows the Galaxy logo, a navigation menu with items like "Analyse de données", "Workflow", "Visualize", "Données partagées", "Aide", and "Authentification", and a file icon.

This Galaxy instance has been configured such that only users who are logged in may use it.

Login

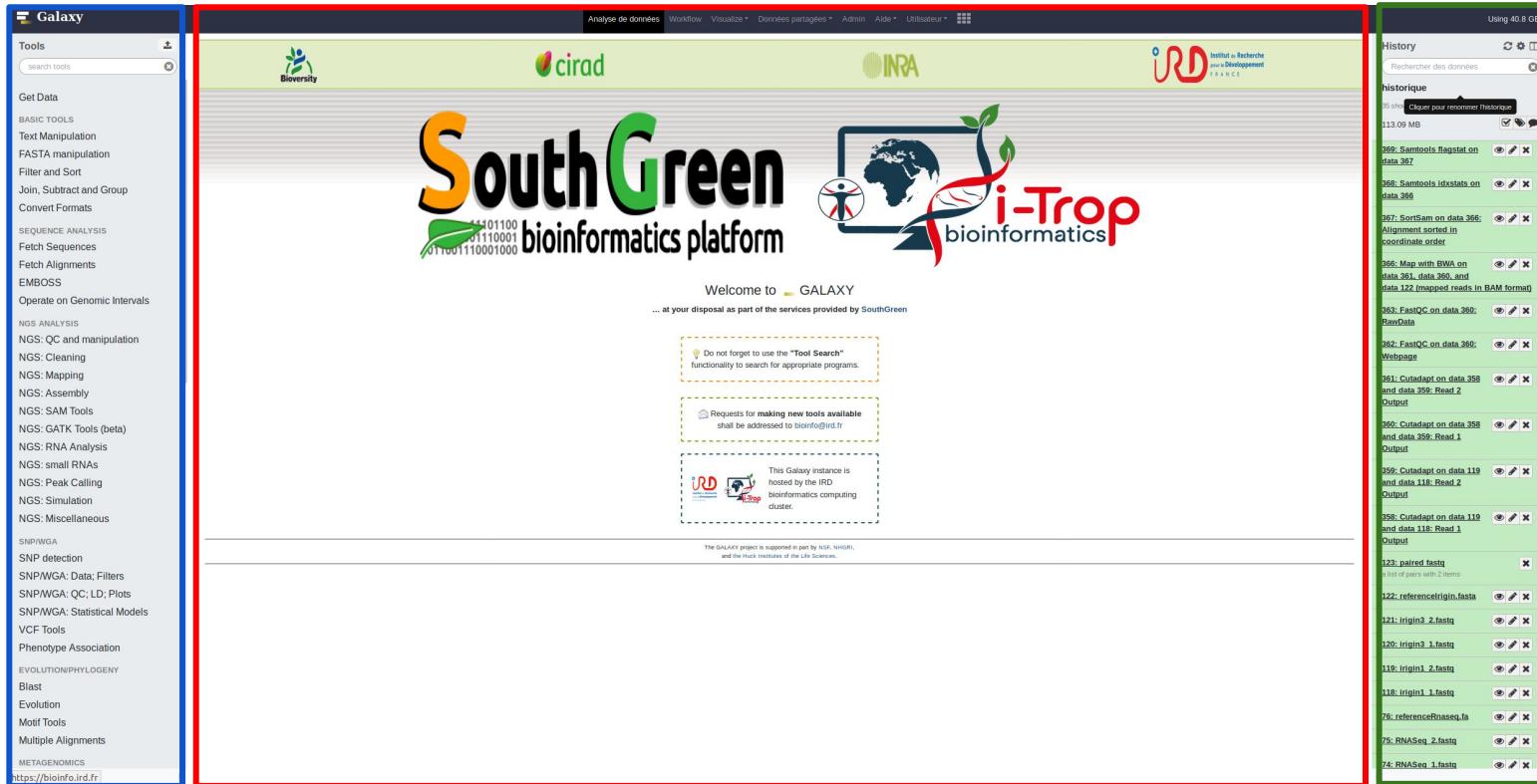
Username / Email Address:

Password:

Forgot password? Reset here

Login

Interface principale



The screenshot displays the main interface of the SouthGreen bioinformatics platform, featuring three main panels:

- outils (Left Panel):** Shows the Galaxy tool panel with various bioinformatics tools categorized under BASIC TOOLS, SEQUENCE ANALYSIS, NGS ANALYSIS, SNP/WGA, and EVOLUTION/PHYLOGENY.
- Panel principal (Center Panel):** Displays the SouthGreen bioinformatics platform logo, the i-Trop bioinformatics logo, and the Galaxy welcome message. It also includes a "Tool Search" tip, a "New tools available" request, and information about the Galaxy instance being hosted by IRD.
- historique (Right Panel):** Shows the history of data analysis, listing 74 items such as "Samtools flagstat on data 367", "SortSam on data 366", "Map with BWA on data 361, data 360, and data 122 (mapped reads in BAM format)", and "FastQC on data 360".

outils

Panel principal

historique

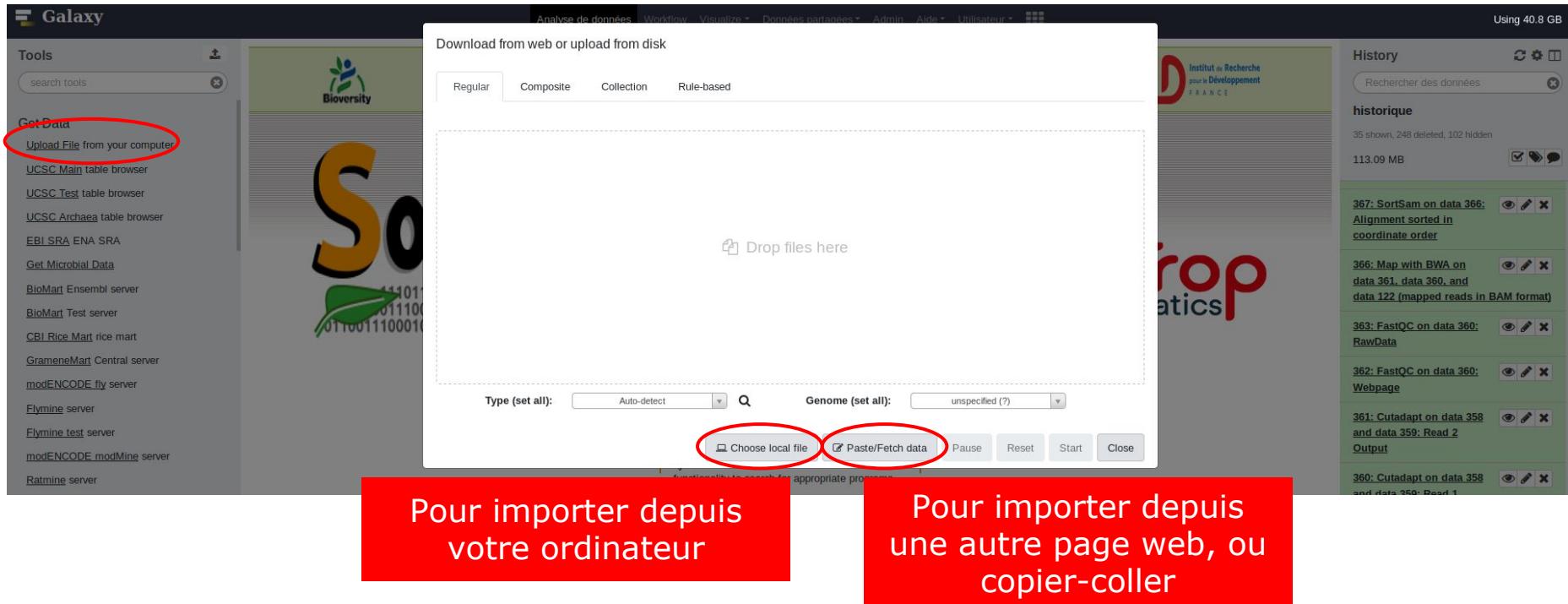
Panel supérieur



Lien	Utilisation
<i>Analyse de données</i>	Retour sur la page principale
<i>Workflow</i>	Accès aux workflows existant ou créé un nouveau workflow
<i>Visualize</i>	Environnement interactif de visualisation de données
<i>Shared data</i>	Accès aux libraries, historiques et workflows publics ou partagés avec vous
<i>Aide</i>	Lien à l'aide de galaxy
<i>Utilisateur</i>	Préférence du compte et accès aux sauvegardes de l'utilisateur

Galaxy : Import de fichiers

→ Import depuis l'ordinateur ou un site externe



The screenshot shows the Galaxy web interface. On the left, the 'Tools' panel is visible with various bioinformatics tools listed. A red circle highlights the 'Get Data' section, which contains a link 'Upload File from your computer'. The main area displays a 'Download from web or upload from disk' dialog. This dialog has tabs for 'Regular', 'Composite', 'Collection', and 'Rule-based'. It features a large central area with a dashed border labeled 'Drop files here' and a 'Type (set all):' dropdown set to 'Auto-detect'. Below this are 'Genome (set all):' dropdowns and two buttons highlighted with red circles: 'Choose local file' and 'Paste/Fetch data'. To the right of the dialog, the Galaxy history panel is shown, listing recent analysis steps like 'SortSam', 'Map with BWA', 'FastQC', 'Cutadapt', and 'Cutadapt' again. Red boxes at the bottom of the image contain text instructions: 'Pour importer depuis votre ordinateur' pointing to the 'Choose local file' button, and 'Pour importer depuis une autre page web, ou copier-coller' pointing to the 'Paste/Fetch data' button.

Galaxy

Analyse de données Workflow Visualize Données partagées Admin Aide Utilisateur Using 40.8 GB

Tools

search tools

Get Data

Upload File from your computer

UCSC Main table browser

UCSC Test table browser

UCSC Archaea table browser

EBI SRA ENA SRA

Get Microbial Data

BioMart Ensembl server

BioMart Test server

CBI Rice Mart rice mart

GrameneMart Central server

modENCODE fly server

Flymine server

Flymine test server

modENCODE modMine server

Ratmine server

Download from web or upload from disk

Regular Composite Collection Rule-based

Drop files here

Type (set all): Auto-detect

Genome (set all): unspecified (?)

Choose local file Paste/Fetch data Pause Reset Start Close

Historique

35 shown, 248 deleted, 102 hidden

113.09 MB

367: SortSam on data 366: Alignment sorted in coordinate order

366: Map with BWA on data 361, data 360, and data 122 (mapped reads in BAM format)

363: FastQC on data 360: RawData

362: FastQC on data 360: Webpage

361: Cutadapt on data 358 and data 359: Read 2 Output

360: Cutadapt on data 358 and data 359: Read 1

Pour importer depuis votre ordinateur

Pour importer depuis une autre page web, ou copier-coller

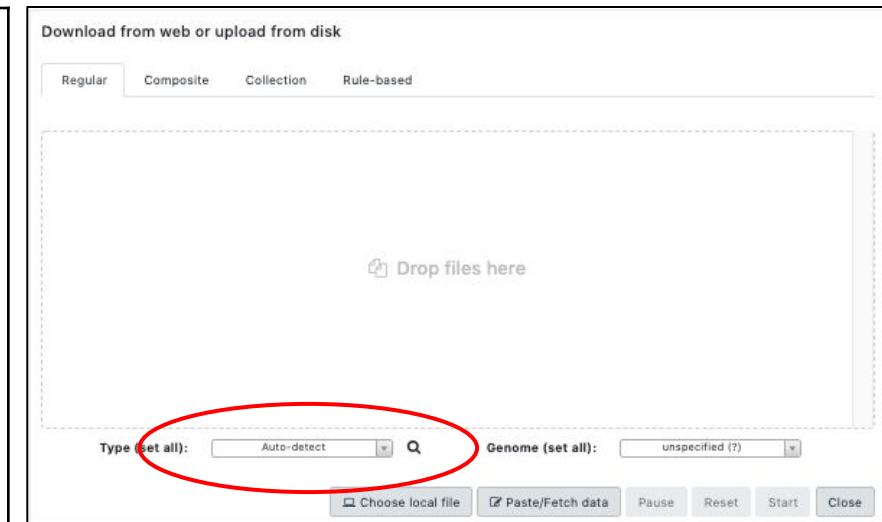
Galaxy : Import de fichiers

→ Import depuis l'ordinateur ou un site externe

- Au chargement d'un fichier :
 - On peut choisir le type de fichier (txt, fasta, ...)
 - Galaxy peut détecter le type automatiquement

Il est possible après chargement de visualiser, supprimer ou éditer les attributs d'un fichier:

- Pour changer le type d'un dataset:
 - *Edit Attributes* → *Datatype*



The History panel displays two datasets:

- Formation_13Nov2014**
87.2 MB
- 37: fastq2.cleaned**
- 35: fastq1.cleaned**

In the second screenshot, a cursor is over the 'Edit attributes' icon for '37: fastq2.cleaned'. In the third screenshot, the 'Edit attributes' dialog is open for '35: fastq1.cleaned'.

Galaxy : Import de fichiers

→ Il y a plusieurs solutions pour importer un fichier :

- Importer un fichier **stocké localement** sur votre ordinateur en cliquant sur «choisissez un fichier »
- Importer un fichier à partir d'une **URL** en copiant l'adresse dans le cadre « URL/Text »
- Copier directement le texte du fichier dans le cadre « URL/Text »
- Importer un **fichier partagé** par une personne / public dans les “données partagées”

→ Pour les gros jeux de données

- Importer un fichier **déposé sur un serveur FTP**
- **Créer un lien symbolique** vers un fichier sur un cluster (voir avec les admins)

→ Depuis la library partagée

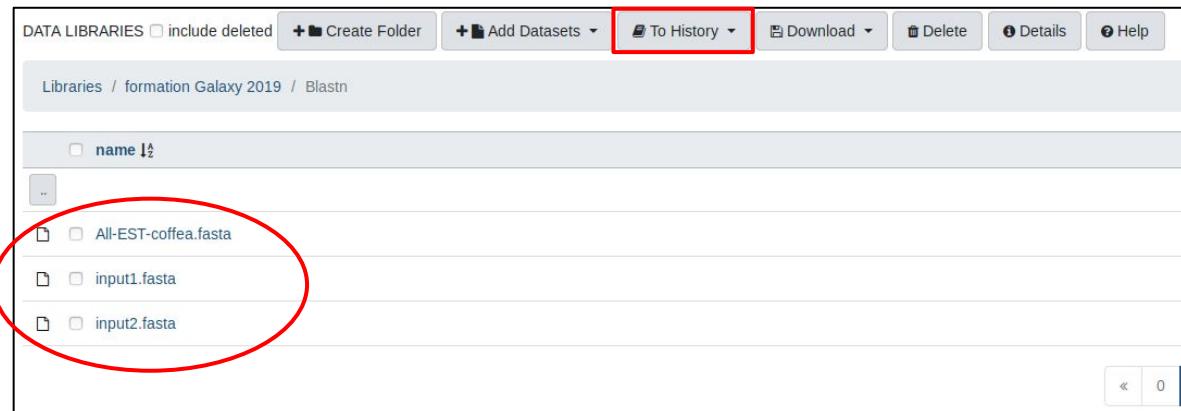
Accédez aux données partagées

(Données partagées → Bibliothèque de données → formation Galaxy 2019 → Blastn)

1) Cliquez sur la library
Formation Galaxy 2019
Blastn

2) Cochez les fichiers:
input1.fasta
input2.fasta
All-EST-coffea.fasta

3) Cliquez sur le bouton “To history” pour importer les données.
→ as Datasets



The screenshot shows the Galaxy web interface with a library list. At the top, there's a toolbar with buttons for 'Create Folder', 'Add Datasets', 'To History' (which is highlighted with a red box), 'Download', 'Delete', 'Details', and 'Help'. Below the toolbar, the library path 'Libraries / formation Galaxy 2019 / Blastn' is shown. The library list contains three items: 'All-EST-coffea.fasta' (highlighted with a red circle), 'input1.fasta', and 'input2.fasta'. At the bottom right of the list, there are navigation arrows and a page number '0'.

Suivi des imports sans l'historique:

Bleu : le job a été soumis

Jaune : le job est en cours de traitement

Vert : le job s'est terminé avec succès

Rouge : le job est en erreur

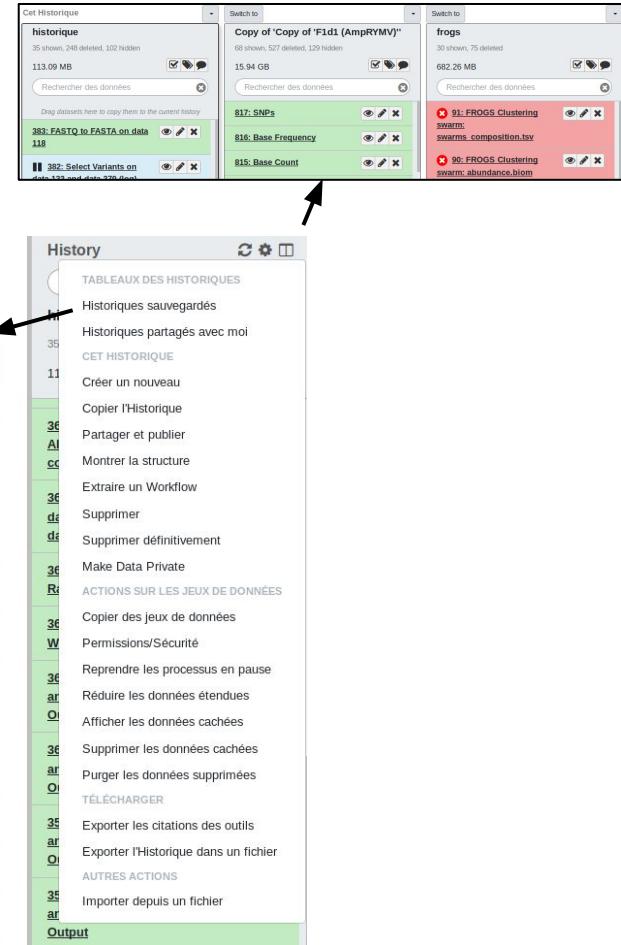
Galaxy : Historique

Vous pouvez avoir autant d'historiques que vous voulez et naviguer entre différents historiques.

- 1 historique = 1 analyse**
- Nommer les historiques de façon reconnaissable

Saved Histories

Name	Items	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated	Status
historique	383	23 2 248 102			113.1 MB	Mar 21, 2019	il y a 1 heure	current history
Copy of 'Copy of F1d1 (AmpRVMV)'	817	68 527 129			15.9 GB	Feb 21, 2019	il y a 2 jours	
frogs	105	21 9 75			682.3 MB	Sep 19, 2018	il y a 6 jours	
Unnamed history	8	2 6			73.2 MB	Mar 20, 2019	Mar 20, 2019	
RNASEQ	105	13 72 32			143.1 MB	Jan 15, 2019	Mar 19, 2019	
traceancestor	60	20 31 9			167.0 MB	Mar 04, 2019	Mar 13, 2019	
vana	849	42 216 138			18.3 GB	Mar 12, 2019	Mar 12, 2019	
KDEClassifier	105	4 82 31			291.6 MB	Mar 04, 2019	Mar 07, 2019	
benchmark calling variant	191	13 2 149 41		Shared, Accessible	14.6 MB	Jan 16, 2019	Feb 20, 2019	
Unnamed history	56	12 4 40			243.5 MB	Dec 13, 2017	Feb 06, 2019	
mapping	7	4 3 1			3.1 MB	Sep 26, 2018	Jan 03, 2019	
frogs 2	21	6 2 13			137.7 MB	Sep 19, 2018	Sep 21, 2018	



The screenshot shows the Galaxy History interface. On the left is a sidebar menu with various options:

- TABLEAUX DES HISTORIQUES
 - Historiques sauvegardés
 - Historiques partagés avec moi
 - CET HISTORIQUE
 - Créer un nouveau
 - Copier l'Historique
 - Partager et publier
 - Montrer la structure
 - Extraire un Workflow
 - Supprimer
 - Supprimer définitivement
 - Make Data Private
- ACTIONS SUR LES JEUX DE DONNÉES
 - Copier des jeux de données
 - Permissions/Sécurité
 - Reprendre les processus en pause
 - Réduire les données étendues
 - Afficher les données cachées
 - Supprimer les données cachées
 - Purger les données supprimées
- TELECHARGER
 - Exporter les citations des outils
 - Exporter l'Historique dans un fichier
- AUTRES ACTIONS
 - Importer depuis un fichier
- Output

The main area is divided into two panes:

- Cet Historique** (Current History):
 - historique (35 shown, 248 deleted, 102 hidden)
 - 113.09 MB
 - Rechercher des données
 - Drag datasets here to copy them to the current history
 - 383: FASTQ to FASTA on data 118
 - 382: Select Variants on data 123 and data 329 (done)
- Switch to** (Switched to 'frogs'):
 - Copy of 'Copy of F1d1 (AmpRVMV)' (68 shown, 527 deleted, 129 hidden)
 - 15.94 GB
 - Rechercher des données
 - 917: SNPs
 - 816: Base Frequency
 - 815: Base Count

Pour trouver facilement un outil vous pouvez taper son nom dans la case de recherche « search tools ».

Cherchez
BLASTN



Tools

blastn

NGS: Mapping

Megablast compare short reads against htgs, nt, and wgs databases

Blast

NCBI BLAST+ makeprofiledb Make profile database

NCBI BLAST+ blastn Search translated nucleotide database with protein query sequence(s)

NCBI BLAST+ psiblast Search protein domain database (PSSMs) with translated nucleotide query sequence(s)

NCBI BLAST+ blastn Search nucleotide database with nucleotide query sequence(s)

Metagenomic analyses

MetaPhiAn metagenomic profiler

MetaPhiAn Metagenomic Phylogenetic Analysis

FROGS

OTUS RECONSTRUCTION

FROGS_Affiliation_OTU Step 4 in metagenomics analysis : Taxonomic affiliation of each OTU's seed by RDTools and BLAST

Vizualisation

JBrowse genome browser

NCBI BLAST+ blastn Search nucleotide database with nucleotide query sequence(s) (Galaxy Version 0.3.1)

Nucleotide query sequence(s)
1: input1.fasta
(-query)

Subject database/sequences
FASTA file from your history (see warning note below)

Nucleotide FASTA subject file to use instead of a database
3: All-EST-coffea.fasta
(-subject)

Type of BLAST

megablast - Traditional megablast used to find very similar (e.g., intraspecies or closely related species) sequences

blastn - Traditional BLASTN requiring an exact match of 11, for somewhat similar sequences

blastn-short - BLASTN program optimized for sequences shorter than 50 bases

Ddc-megablast - Discontiguous megablast used to find more distant (e.g., interspecies) sequences

(-task)

Set expectation value cutoff
0.001
(-eval)

Output format
Tabular (standard 12 columns)
(-outfmt)

Advanced Options

Hide Advanced Options

Execute

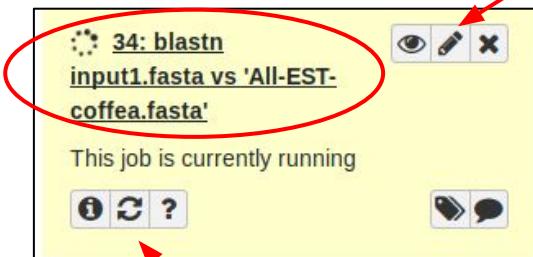
1) Lancez BLASTN avec les paramètres suivants :

- Query = input1.fasta
- Banque Fasta de l'historique = all-EST-coffea.fasta
- Output = fichier tabulé de 12 colonnes

Blast (*Basic local alignment Search tool*) = permet de trouver des régions similaires entre 2 séquences de nucléotides (*blastn*) ou d'acides aminés



Nom automatique



34: blastn
input1.fasta vs 'All-EST-coffea.fasta'
This job is currently running

Modifier nom / extension

Relancer blastn avec les mêmes paramètres

Télécharger

Voir les données

Supprimer

aperçu

The screenshot shows a Galaxy tool interface for a running job. The job ID is 34, the tool is blastn, and the parameters are input1.fasta vs 'All-EST-coffea.fasta'. A red circle highlights the job title and parameters. Below the job status, there are several small icons. To the right, a red box labeled 'Modifier nom / extension' has an arrow pointing to the 'input1.fasta' part of the parameters. Another red box labeled 'Relancer blastn avec les mêmes paramètres' has an arrow pointing to the 'Télécharger' button. A third red box labeled 'Télécharger' has an arrow pointing to the download icon. Red arrows also point from the 'Voir les données' and 'Supprimer' buttons to their respective counterparts in the detailed view window.

Modifier nom / extension

Télécharger

Voir les données

Supprimer



34: blastn input1.fasta vs 'All-EST-coffea.fasta'
2,897 lines
format: tabular, database: ?

gi 33391745 gb AY273814.1	gi 31580930
gi 33391745 gb AY273814.1	gi 82472623
gi 33391745 gb AY273814.1	gi 31585146
gi 33391745 gb AY273814.1	gi 31575874
gi 33391745 gb AY273814.1	gi 31118113

aperçu

The screenshot shows the results of the blastn job. It displays the command used (blastn input1.fasta vs 'All-EST-coffea.fasta'), the number of lines (2,897), and the format (tabular). Below this, a preview window shows the first few lines of the output, which consists of two columns of identifiers. A red box labeled 'aperçu' has an arrow pointing to the preview window.

Galaxy : Util



34: blastn
input1.fasta vs 'All-EST-coffea.fasta'
This job is currently running





34: blastn input1.fasta vs 'All-EST-coffea.fasta'
2,897 lines
format: tabular, database: ?



1	2
gi 33391745 gb AY273814.1	gi 31580930
gi 33391745 gb AY273814.1	gi 82472623
gi 33391745 gb AY273814.1	gi 31585146
gi 33391745 gb AY273814.1	gi 31575874
gi 33391745 gb AY273814.1	gi 31118113

- Output tabular format (6 or 7):
 1. query id
 2. subject id
 3. percent identity
 4. alignment length
 5. number of mismatches
 6. number of gap openings
 7. query start
 8. query end
 9. subject start
 10. subject end
 11. expect value
 12. bit score

gi 33391745 gb AY273814.1	gi 315809301 gb GW481759.1 GW481759	94.922	709	14	2	188	896	1	687	0.0	1128
---------------------------	-------------------------------------	--------	-----	----	---	-----	-----	---	-----	-----	------



- 1) Lancez BLASTN pour obtenir un fichier tabulé
- 2) Lancez FILTER et ne gardez que les lignes où le pourcentage d'identité est de plus de 98
- 3) Lancez CUT et ne gardez que les “subject ID” sur le fichier précédent

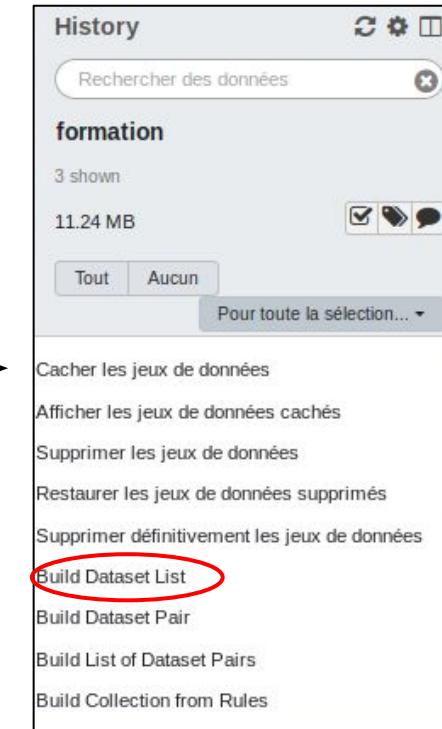
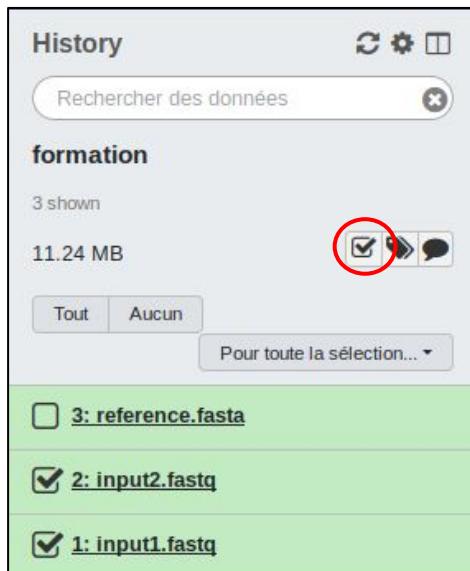
- Output tabular format (6 or 7):
 1. query id
 2. subject id
 3. percent identity
 4. alignment length
 5. number of mismatches
 6. number of gap openings
 7. query start
 8. query end
 9. subject start
 10. subject end
 11. expect value
 12. bit score

Galaxy : Collections



Collection = Permet d'effectuer une même analyse sur plusieurs échantillons

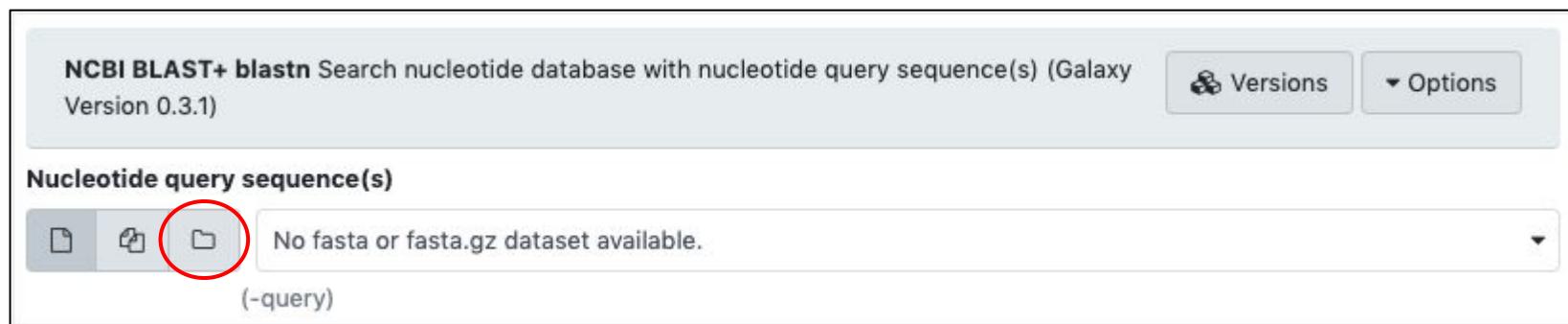
1) Créez une collection avec les deux sets de reads input1.fastq et input2.fastq



The image shows two screenshots of the Galaxy interface. On the left, the 'History' panel displays three datasets: '3: reference.fasta', '2: input2.fastq', and '1: input1.fastq'. The dataset '2: input2.fastq' has its checkbox icon circled in red. An arrow points from this panel to the right. On the right, a context menu is open over the same dataset, listing options like 'Cacher les jeux de données', 'Afficher les jeux de données cachés', 'Supprimer les jeux de données', etc. The 'Build Dataset List' option is also circled in red.

Collection = Permet d'effectuer une même analyse sur plusieurs échantillons

- 1) Créez une collection avec les deux sets de reads
- 2) Lancez blastn sur la collection et observez le résultat



NCBI BLAST+ blastn Search nucleotide database with nucleotide query sequence(s) (Galaxy Version 0.3.1)

Nucleotide query sequence(s)

No fasta or fasta.gz dataset available.

(-query)

A screenshot of a Galaxy web interface for the NCBI BLAST+ blastn tool. The title bar says "NCBI BLAST+ blastn Search nucleotide database with nucleotide query sequence(s) (Galaxy Version 0.3.1)". Below the title, there's a "Versions" button and an "Options" dropdown. The main area is titled "Nucleotide query sequence(s)". It shows three icons: a file icon, a refresh icon, and a folder icon. The folder icon is circled in red. To its right is a text input field containing the message "No fasta or fasta.gz dataset available." and a dropdown arrow. Below the input field is the text "(-query)".

Galaxy : Workflows

Créer un nouveau Workflow

Analyse de données Workflow Visualize ▾ Données partagées ▾ Admin Aide ▾ Utilisateur ▾

Your workflows

search for workflow...

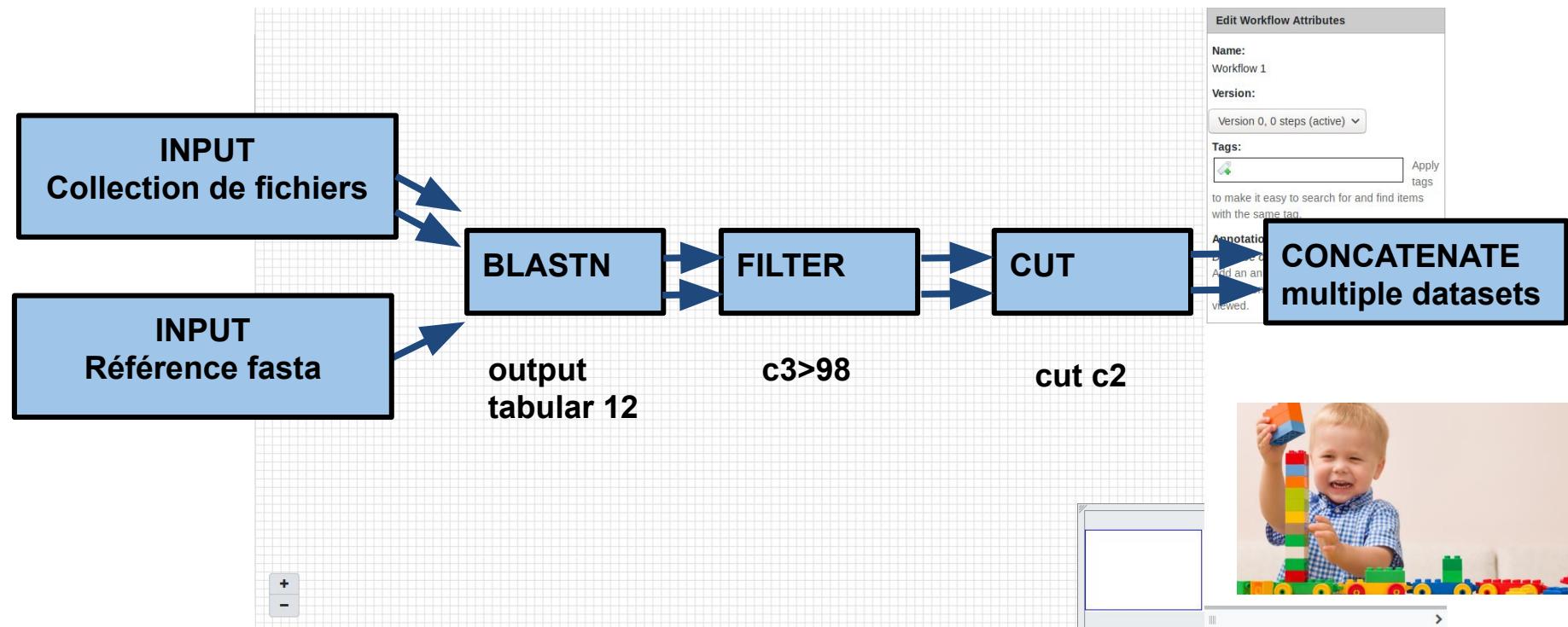


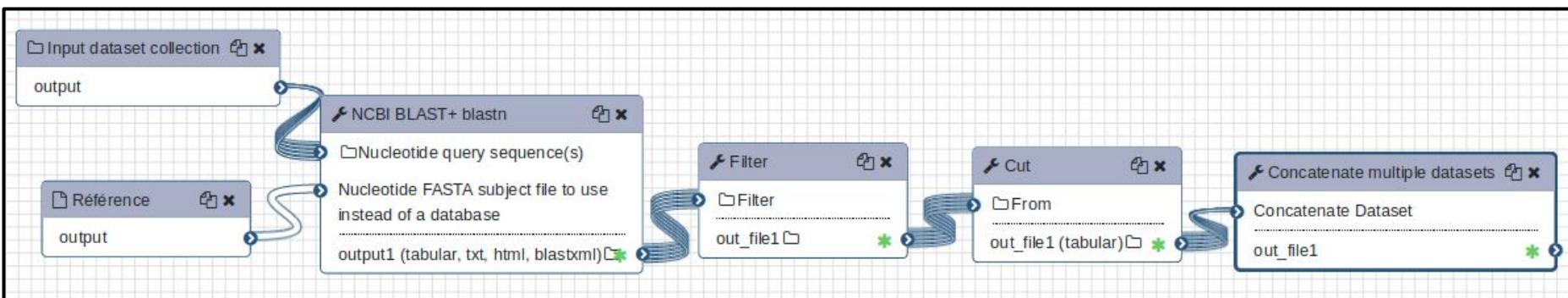
Name	Tags	Owner	# of Steps	Published	Show in tools panel
BlastN et tri	 You	6	Yes	<input type="checkbox"/>	
SNP Calling - multi	 You	8	Yes	<input type="checkbox"/>	
SNPCalling - mapping - multi	 You	9	Yes	<input type="checkbox"/>	
SNP Calling	 You	8	No	<input type="checkbox"/>	
kallistoEdgeR	 You	7	Yes	<input type="checkbox"/>	
imported: Virus_haplotype_network	 You	4	No	<input type="checkbox"/>	

Liste de mes workflows



Créez votre premier Workflow : BLASTN, paramétrez le et lancez le !





TIPS:

Cochez l'astérisque verte pour afficher votre résultat intermédiaire ou décochez la pour le cacher !

Il est possible d'effectuer une copie d'un workflow

- par exemple pour rajouter une brique ou modifier les paramètres
- type de données en entrée (collection, paires, simple fichier)

Your workflows

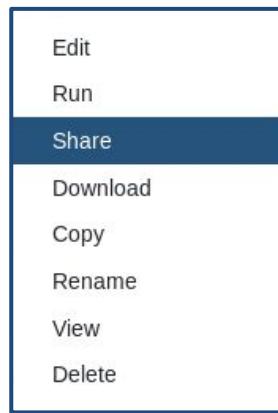
search for workflow... + +

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Workflow 1		You	5	No	<input type="checkbox"/>
SNPCalling - mapping - multi		You	9	No	<input type="checkbox"/>
SNP Calling - multi		You	8	No	<input type="checkbox"/>
SNPCalling - mapping		You	10	Yes	<input type="checkbox"/>
SNP Calling		You	8	Yes	<input type="checkbox"/>
kallistoEdgeR		You	7	Yes	<input type="checkbox"/>
imported: Virus_haplotype_net		You	4	No	<input type="checkbox"/>

A context menu is open over the second workflow row, listing options: Edit, Run, Share, Download, Copy (which is highlighted in blue), Rename, View, and Delete.

Galaxy : Workflows

Partager un workflow (ou un historique)



Share

This workflow is currently restricted so that only you and the users listed below can access it.

[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.

You have not shared this workflow with any users yet

[Share with a user](#)

Export

[Download](#) workflow as a file so that it can be saved or imported into another Galaxy server.

This workflow must be accessible. Please use the option above to "Make Workflow Accessible and Publish" before receiving a URL for importing to another Galaxy.

[Create image](#) of workflow in SVG format

Export to the www.myexperiment.org site.

myExperiment username:

myExperiment password:

[Export to myExperiment](#)

A une ou plusieurs personnes en particulier

Public à tous les utilisateurs

Télécharger et exporter vers un site externe

SNP-Calling avec:

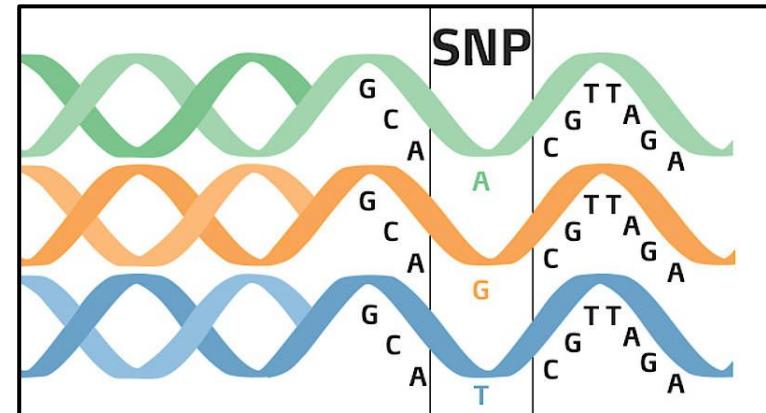


Objectifs :

Avec le séquençage NGS on obtient de nombreux reads présentant des différences / mutations au niveau de certains nucléotides. Ce sont des SNP. Comment les détecter?

Pré-requis:

- Une séquence de référence (Fasta)
- Des reads (FastQ)



SNP-CALLING : introduction

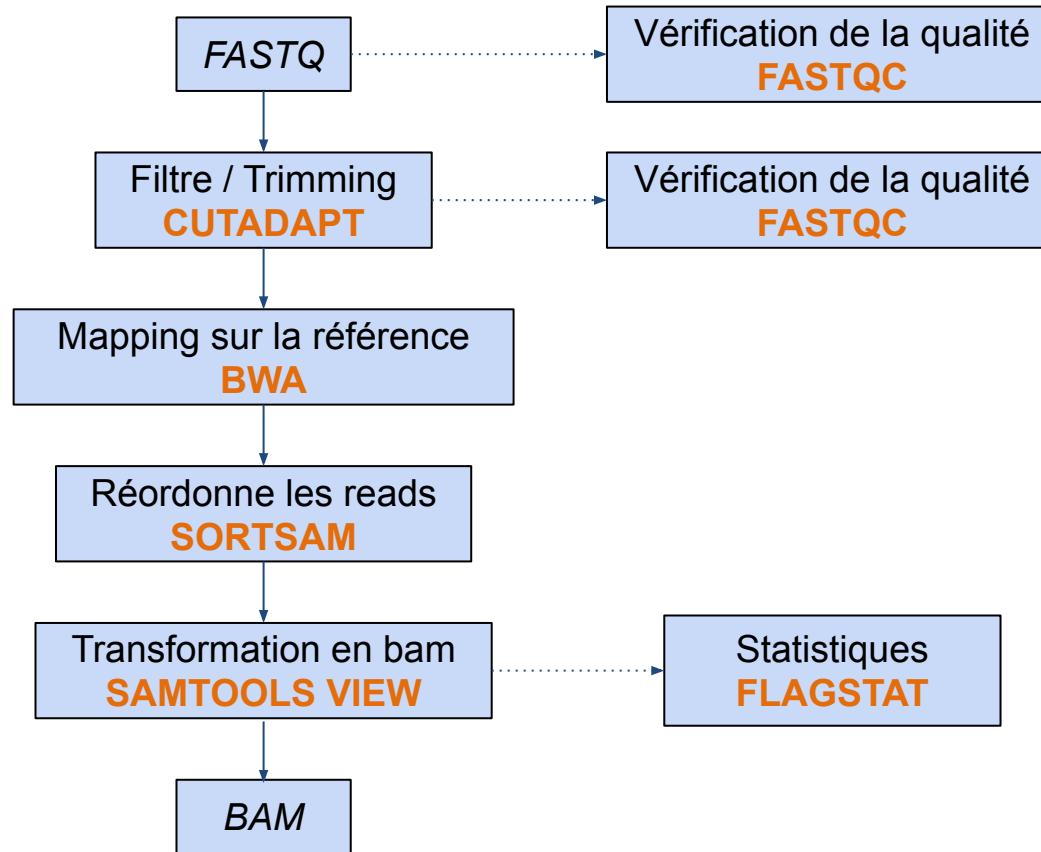
Le format FastQ

Format concis et compact qui stocke à la fois séquence et qualité de séquençage.

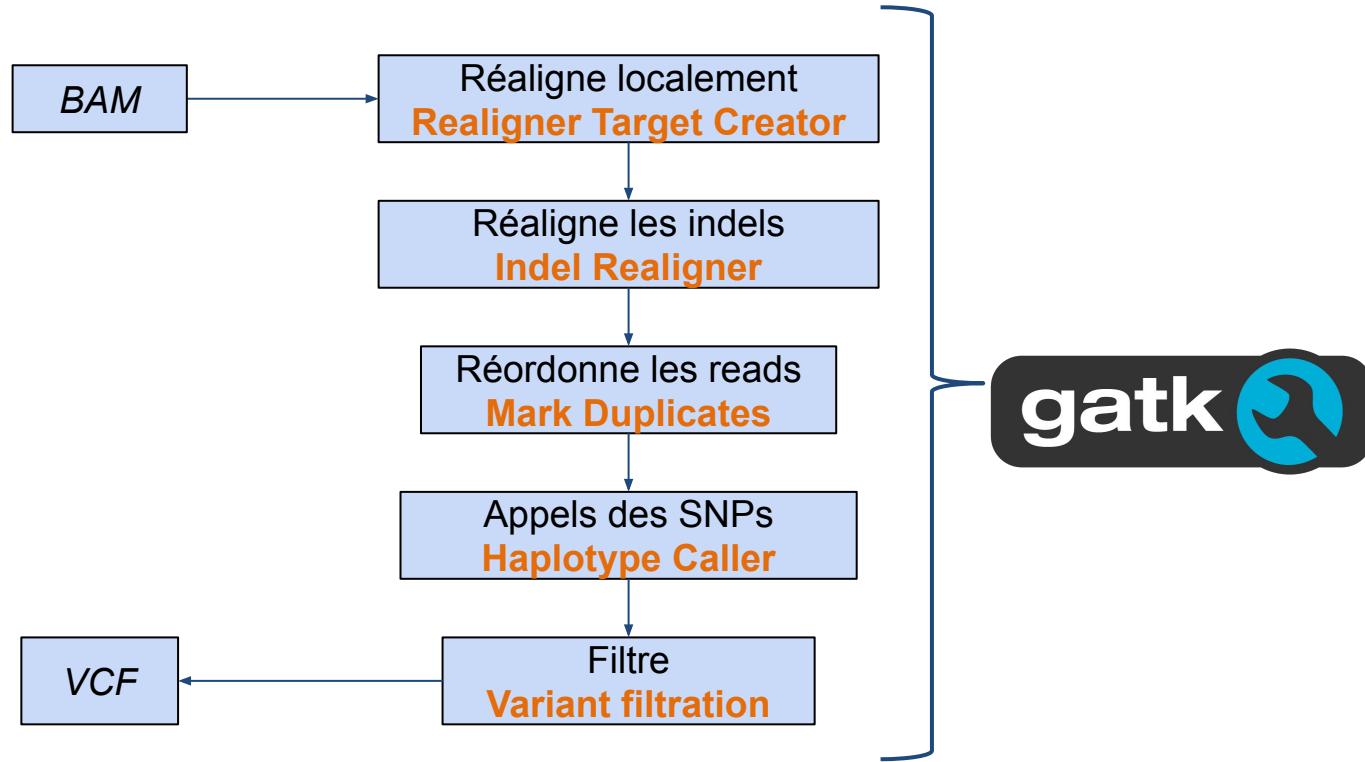
Identifier	• @SRR566546.970 HWUSI-EAS1673_11067_FC7070M:4:1:2299:1109 length=50
Sequence	• TTGCCTGCCTATCATTAGTGCCTGTGAGGTGGAGATGTGAGGATCAGT
'+' sign	• +
Quality scores	• hhhhhhhhhhhghhhhhhhfhhhhfffffe'ee[‘X]b[d[ed‘[Y[^Y
Identifier	• @SRR566546.971 HWUSI-EAS1673_11067_FC7070M:4:1:2374:1108 length=50
Sequence	• GATTGTATGAAAGTATAACAACTAAAACTGCAGGTGGATCAGAGTAAGTC
'+' sign	• +
Quality scores	• hhggfhhcgghggfcffdhfehhhhcehdchhdhahehffffde‘bVd

SNP-CALLING : introduction

1) Mapping



2) SNP calling



SNP-CALLING : introduction

VCF : Description des variants par position + assignation génotypique

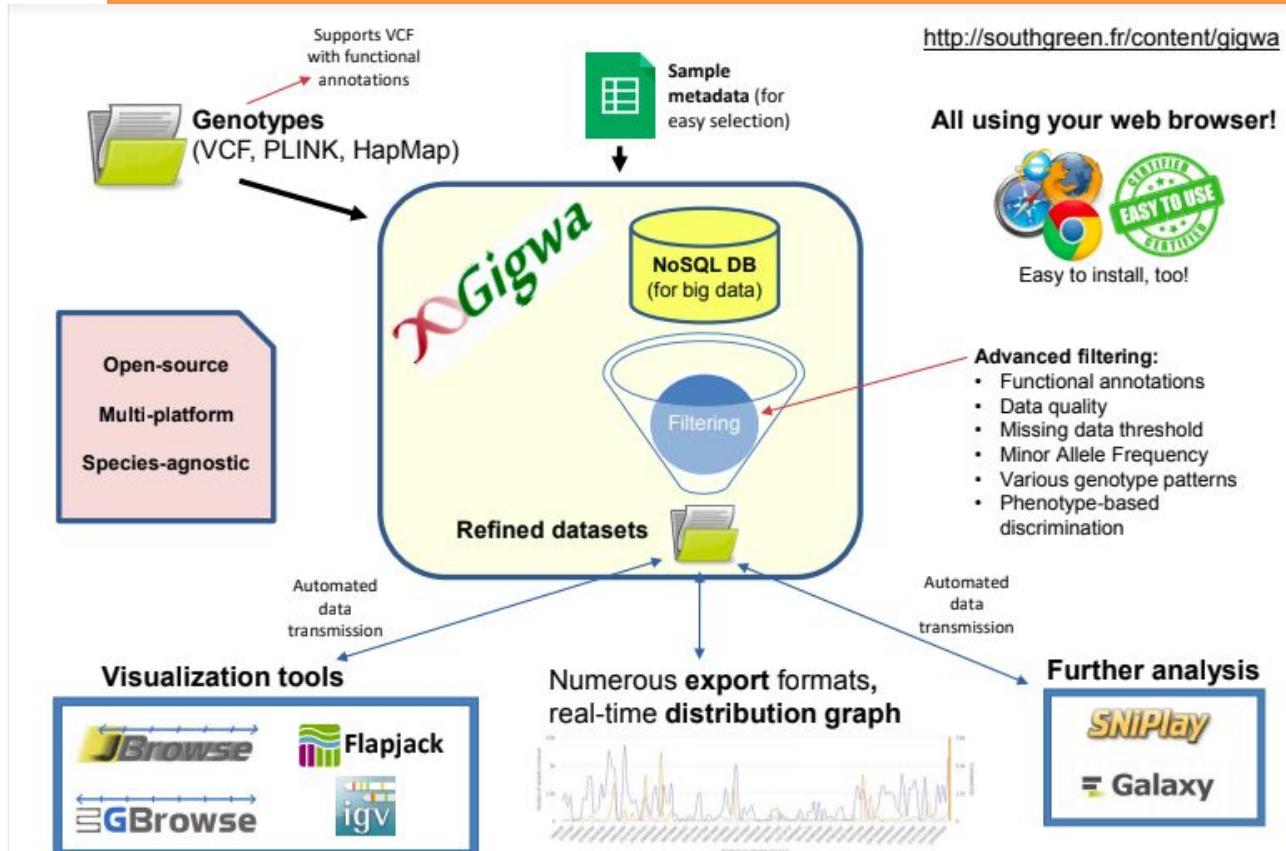
#fileformat=VCFv4.0											
##fileDate=20110705											
##reference=1000GenomesPilot-NCBI37											
##phasing=partial											
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">											
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">											
##INFO=<ID=AF,Number=.,Type=Float,Description="Allele Frequency">											
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">											
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">											
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">											
##FILTER=<ID=q10,Description="Quality below 10">											
##FILTER=<ID=s50,Description="Less than 50% of samples have data">											
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">											
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">											
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">											
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">											
CHROM	POS	ID	REF	ALT	QUAL	FILTER INFO	FORMAT	Sample1	Sample2	Sample3	
2	4370	rs6057	G	A	29	.	NS=2;DP=13;AF=0.5;DB;H2	GT:GQ:DP:HQ	0 0:48:1:52,51	1 0:48:8:51,51	1/1:43:5:..,
2	7330	.	T	A	3	q10	NS=5;DP=12;AF=0.017	GT:GQ:DP:HQ	0 0:46:3:58,50	0 1:3:5:65,3	0/0:41:3
2	110696	rs6055	A	G,T	67	PASS	NS=2;DP=10;AF=0.333,0.667;AA=T;DB	GT:GQ:DP:HQ	1 2:21:6:23,27	2 1:2:0:18,2	2/2:35:4
2	130237	.	T	.	47	.	NS=2;DP=16;AA=T	GT:GQ:DP:HQ	0 0:54:7:56,60	0 0:48:4:56,51	0/0:61:2
2	134567	microsat1	GTCT	G,GTACT	50	PASS	NS=2;DP=9;AA=G	GT:GQ:DP	0/1:35:4	0/2:17:2	1/1:40:3

VCF : Description des variants par position + assignation génotypique

The figure displays a genomic sequence alignment between two samples, Sample1 and Sample2, across chromosome chr1. The sequence is represented by a grid of letters, where each row corresponds to a nucleotide position and each column corresponds to a base pair. The sequence starts with A, C, C, T, followed by a long stretch of T's. A vertical bracket on the right indicates that the sequence continues beyond the visible portion. The alignment shows that Sample1 has a G at position 1, while Sample2 has an A. Both samples have a C at position 2. At positions 3 through 10, both samples show a T. Sample1 has an A at position 11, while Sample2 has a T. Both samples have a C at position 12. At positions 13 through 18, both samples show a G. Sample1 has a C at position 19, while Sample2 has a T. Both samples have an A at position 20. A vertical bracket on the right indicates that the sequence continues beyond the visible portion.

#CHR	POS	ID	REF	ALT	QUAL	FILTER	[INFO\$]	FORMAT	Sample1	Sample2
chr1	7	.	C	T	247.82	.	[INFO]	GT/AD/DP/GQ/PL	0/1:2,3:5:9.2:20,0,15	./.
chr1	19	.	G	A	124.34	.	[INFO]	GT/AD/DP/GQ/PL	0/0:5,0:5:20.2:0,42,94	./.

Gigwa : Genotype investigator for genome wide analyses



Galaxy : Import de fichiers



→ Depuis la library partagée

Accédez aux données partagées

(Données partagées → Bibliothèque de données → formation Galaxy 2019 → SNPCalling)

1) Cliquez sur la library

Formation Galaxy 2019
SNPCalling

2) Cochez les fichiers:

RCX_raw_RX.fastq
Reference.fasta

3) Cliquez sur le bouton “To history”
pour importer les données.

DATA LIBRARIES include deleted + Create Folder + Add Datasets To History Download Delete Details Help

Libraries / formation Galaxy 2019 / SNPCalling

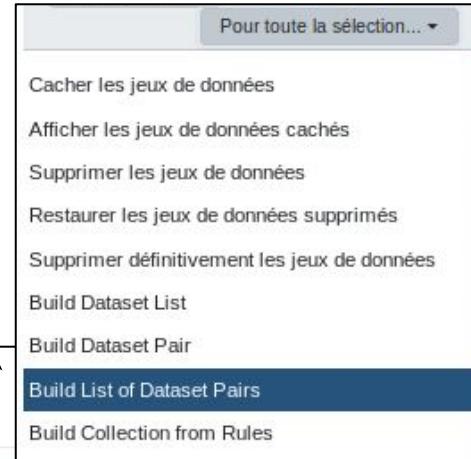
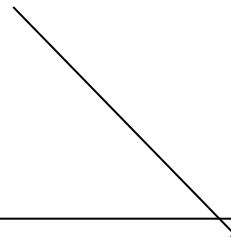
<input type="checkbox"/> name	description	data type	size	time updated (UTC)	state		
<input type="checkbox"/> RC1_raw_R1.fastq		fastqsanger	1.6 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> RC1_raw_R2.fastq		fastqsanger	1.6 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> RC2_raw_R1.fastq		fastqsanger	1.5 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> RC2_raw_R2.fastq		fastqsanger	1.5 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> RC3_raw_R1.fastq		fastqsanger	1.6 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> RC3_raw_R2.fastq		fastqsanger	1.6 MB	2019-04-11 08:06 AM			
<input type="checkbox"/> Reference.fasta		fasta	6.5 KB	2019-04-11 08:06 AM			

SNP-CALLING : Workflows



1) Créer une collection pour des données pairées

Create a collection of paired datasets



Could not automatically create any pairs from the given dataset names. You may want to choose or enter different filters and try auto-pairing again. Close this message using the X on the right to view more help.

3 unpaired forward - (3 filtered out)

R1

RC1_raw_R1.fastq

RC2_raw_R1.fastq

RC3_raw_R1.fastq

Choose filters Clear filters

Auto-pair

3 unpaired reverse - (3 filtered out)

R2

RC1_raw_R2.fastq

RC2_raw_R2.fastq

RC3_raw_R2.fastq

Pair these datasets

Pair these datasets

Pair these datasets

SNP-CALLING : Workflows



1) FastQC : Read Quality reports

FastQC Read Quality reports (Galaxy Version 0.72)

Short read data from your current history

6: input
 This is a batch mode input field. Separate jobs will be triggered for each dataset selection.

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

Adapter list

Nothing selected

list of adapters adapter sequences which will be explicitly searched against the library. tab delimited file with 2 columns: name and sequence. (--adapters)

Submodule and Limit specifying file

Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for each submodules warning parameter

Disable grouping of bases for reads >50bp

Yes No

Using this option will cause fastqc to crash and burn if you use it on really long reads, and your plots may end up a ridiculous size. You have been warned! (--nogroup)

Lower limit on the length of the sequence to be shown in the report

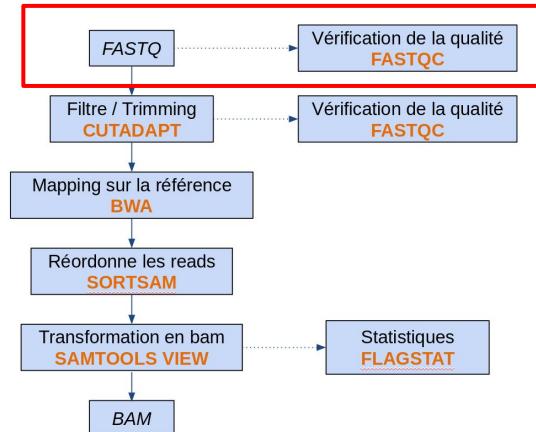
As long as you set this to a value greater or equal to your longest read length then this will be the sequence length used to create your read groups. This can be useful for making directly comparable statistics from datasets with somewhat variable read lengths. (--min_length)

length of Kmer to look for

7

note: the Kmer test is disabled and needs to be enabled using a custom Submodule and limits file (--kmers)

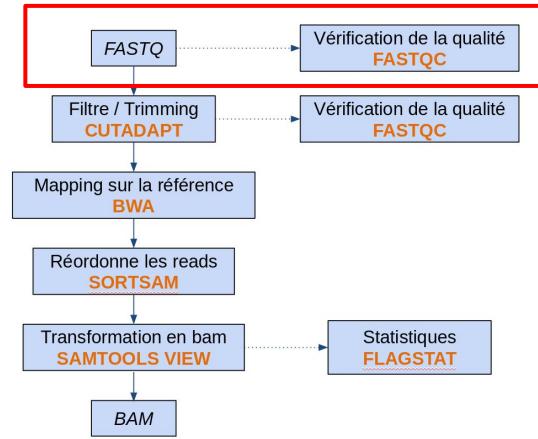
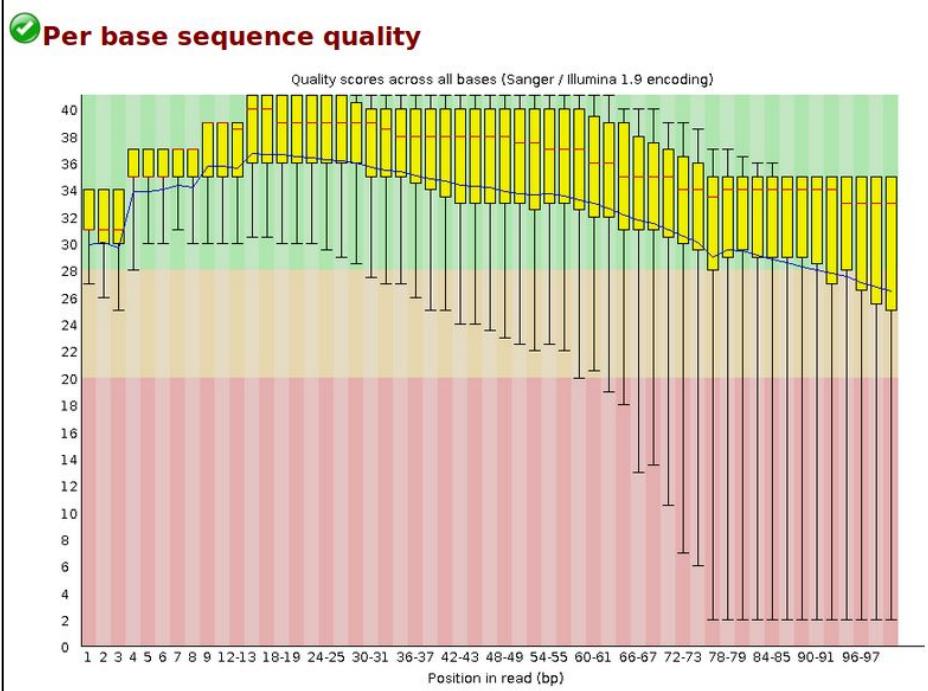
Execute





1) FastQC : Read Quality reports

Produit 2 datasets en sortie : Rawdata & webpage



Explication détaillées de toutes les sorties:
https://dnacore.missouri.edu/PDF/FastQC_Manual.pdf



2) Cutadapt : Remove adapter sequences from Fastq/Fasta

Paramètres :

Adapter Option:

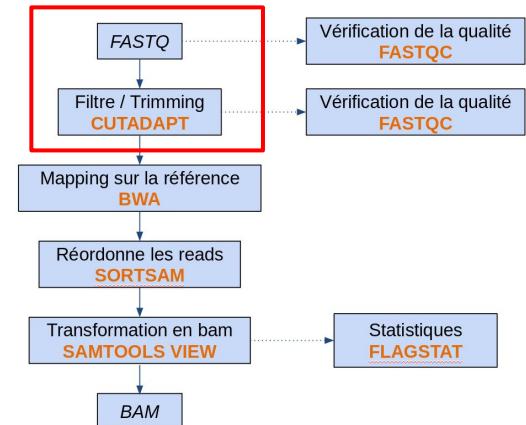
Minimum overlap length = 7

Filter Option:

minimum-length=35

Read Modification Options:

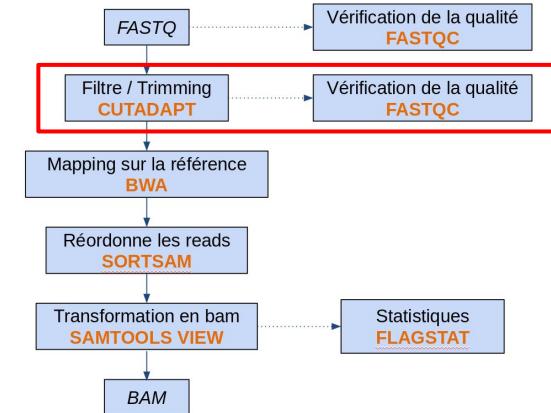
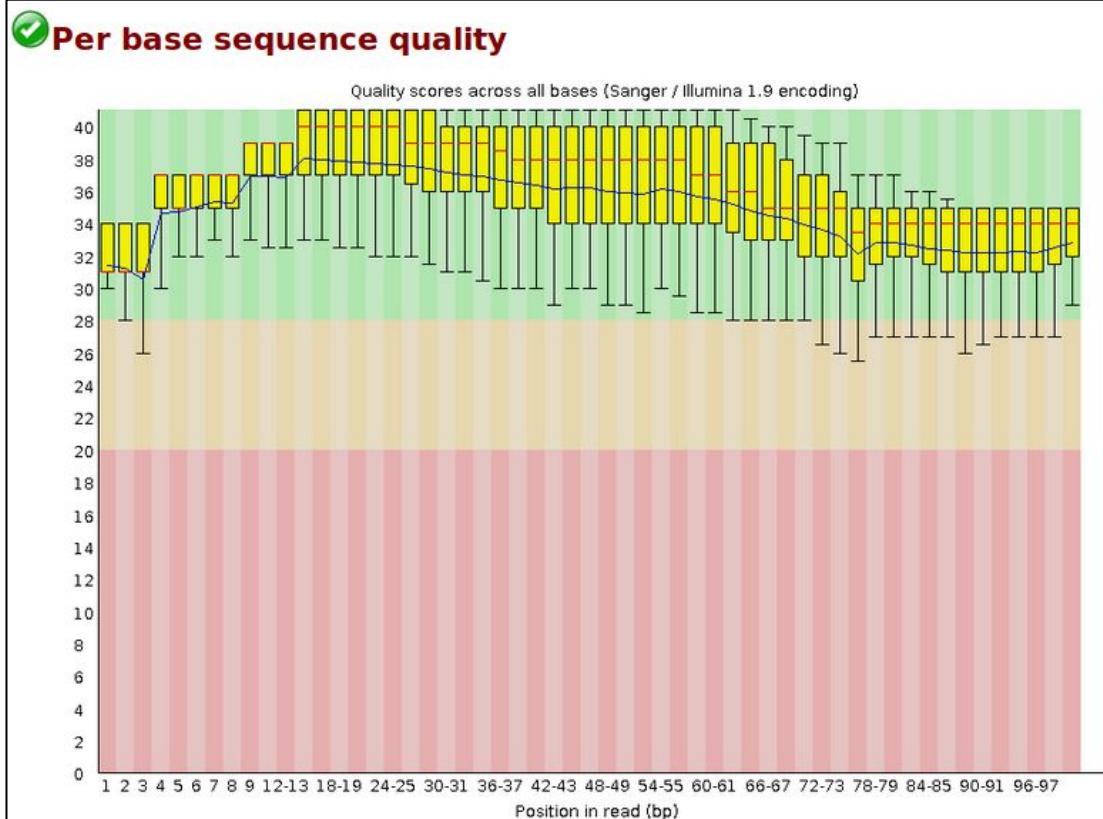
Quality cutoff=20,20



→ reads fastq filtrés en fonction de la qualité



3) FastQC : Read Quality reports





4) BWA map short reads against reference genome

Will you select a reference genome from your history or use a built-in index?

Use a genome from history and build index

Built-ins were indexed using default options. See 'Indexes' section of help below

Use the following dataset as the reference sequence

7: Reference.fasta

You can upload a FASTA sequence to the history and use it as reference

Select input type

Paired fastq

Select between fastq and bam datasets and between paired and single end data

Select first set of reads

23: Cutadapt on collection 8: Read 1 Output

This is a batch mode input field. Separate jobs will be triggered for each dataset selection.

Specify dataset with forward reads

Select second set of reads

24: Cutadapt on collection 8: Read 2 Output

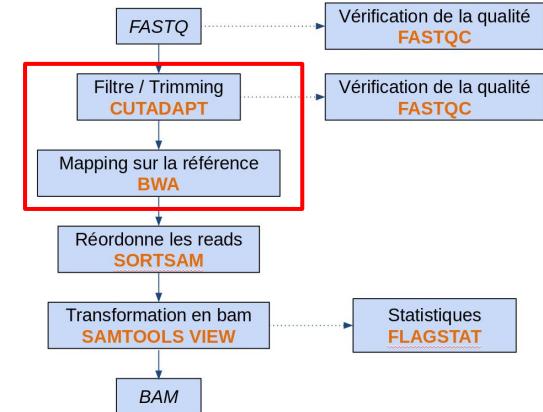
This is a batch mode input field. Separate jobs will be triggered for each dataset selection.

Specify dataset with reverse reads

Set advanced paired end options?

Do not set

Provides additional controls



→ Collection de 3 bam

SNP-CALLING : Workflows



Map with BWA on collection 23 and collection 24 (mapped reads in BAM format)

a list with 3 items

Add tags



RC1 raw

929.9 KB

format: **bam**, génome de référence: ?

Reference genome size is 6632 bytes,
generating BWA index with is algorithm
[bwa_index] Pack FASTA... 0.00 sec
[bwa_index] Construct RWT for the packed

```
sequence...
[bwa_index] 0.00 seconds elapse.
[bwa_index] Update BWT. 0.00 sec
[bwa_index] Pack forward.
```



display with IGV local

display in IGB View

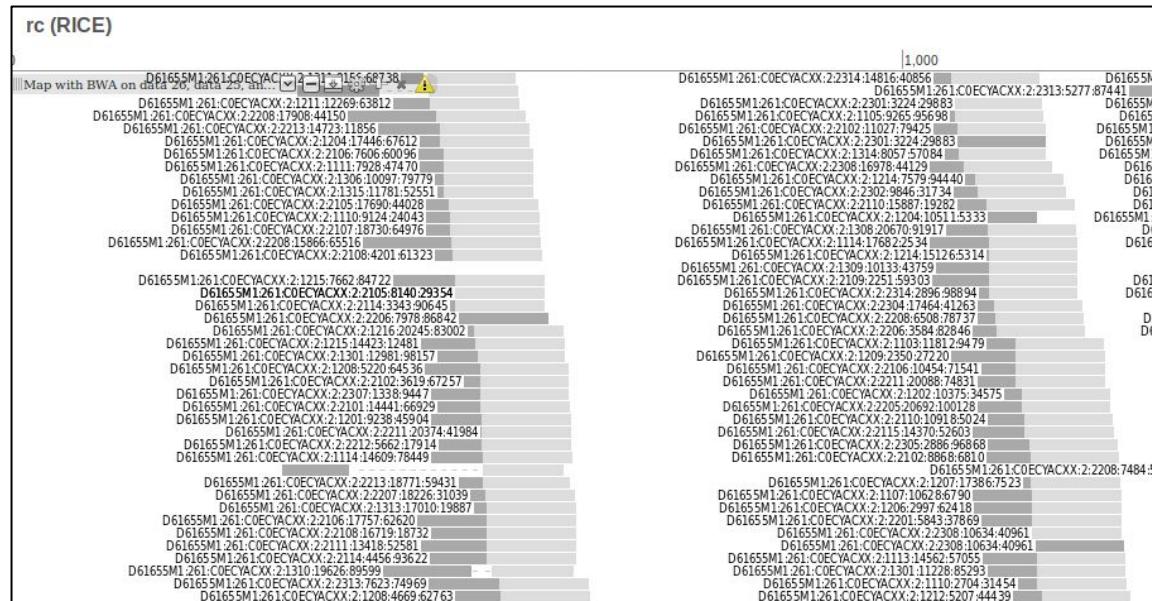
display at bam.io/bio bam.io/bio.io

Binary bam alignments file



RC2 raw

Visualisation du mapping dans Trackster



SNP-CALLING : Workflows



Map with BWA on collection 23 and collection 24 (mapped reads in BAM format)

a list with 3 items

Add tags

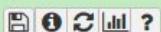


RC1 raw

929.9 KB

format: **bam**, génome de référence: ?

Reference genome size is 6632 bytes, generating BWA index with is algorithm [bwa_index] Pack FASTA... 0.00 sec [bwa_index] Construct BWT for the packed sequence... [bwa_index] 0.00 seconds elapse. [bwa_index] Update BWT... 0.00 sec [bwa_index] Pack forwa



display with IGV local

display in IGB View

display at bam.iobio bam.iobio.io

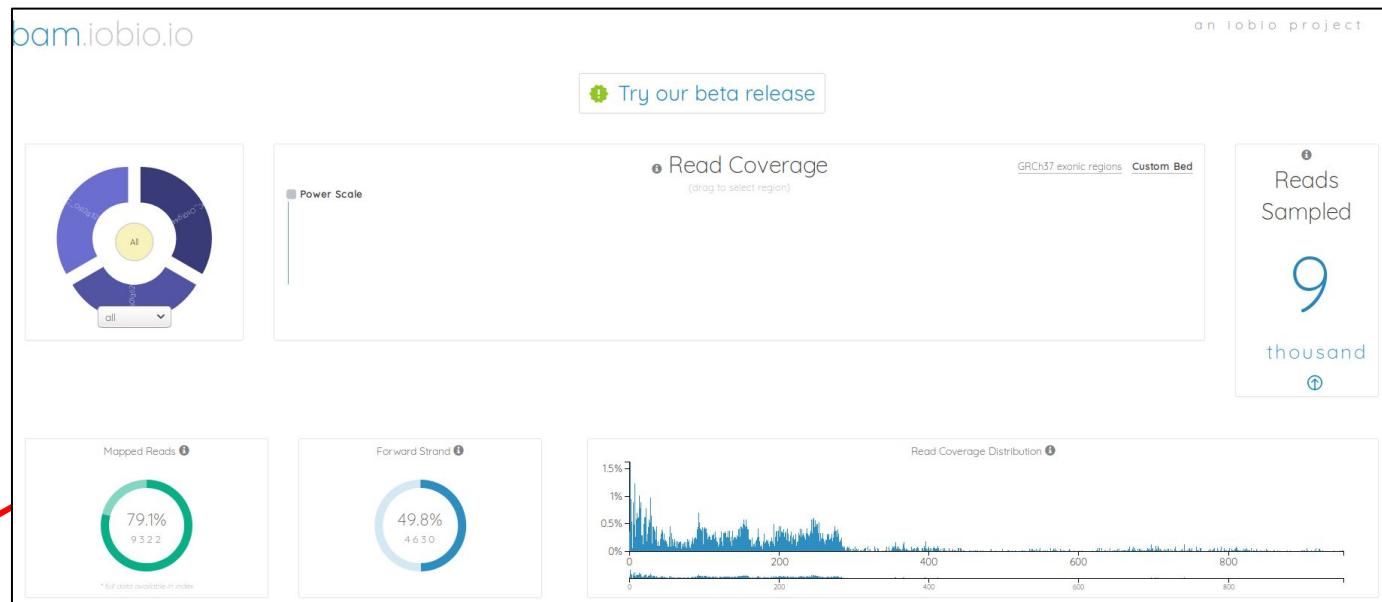
Binary bam alignments file

RC3 raw

RC2 raw



Données statistiques du mapping dans bam.iobio.io





5) SortSAM : sort SAM/BAM dataset

Paramètres :

Sort order = coordinate

Select validation Stringency = Silent

SortSam sort SAM/BAM dataset (Galaxy Version 2.18.2.0)

Select SAM/BAM dataset or dataset collection

47: Map with BWA on collection 23 and collection 24 (mapped reads in BAM format)

This is a batch mode input field. Separate jobs will be triggered for each dataset selection.

If empty, upload or import a SAM/BAM dataset

Sort order

Coordinate
 Queryname

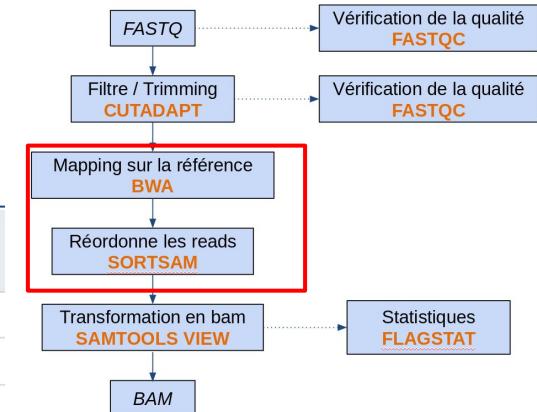
SORT_ORDER; default=coordinate. Selecting Queryname will output SAM file, as Galaxy does not support BAM files that are not coordinate sorted.

Select validation stringency

Silent

Setting stringency to SILENT can improve performance when processing a BAM file in which variable-length data (read, qualities, tags) do not otherwise need to be decoded.

Execute



→ Collection de 3 bam ordonnés

SNP-CALLING : Workflows



6) Samtools view : reformat, filter, or subsample

SAM/BAM/CRAM data set

52: (hidden) SortSam on data 48: Alignment sorted in coordinate order

Output type

BAM (-b)

Select output type. In case of counts only the total number of alignments is returned. All filters are taken into account (-b/-C/-c)

Filter alignment

Yes

Filter by regions

No

Filter by readgroup

No

Filter by quality

Skip alignments with MAPQ smaller than INT. (-q)

Filter by library

Only output alignments in library STR (-l)

Filter by number of CIGAR bases consuming query sequence

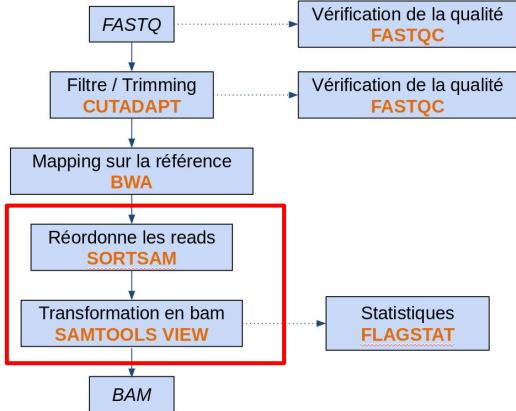
Only output alignments with number of CIGAR bases consuming query sequence greater than or equal INT. (-m)

Require that these flags are set

Select/Unselect all

read is mapped in a proper pair

(-f)



Paramètres :
Output Type = BAM
Require that these flags are set =
read is mapped in a proper pair

→ Collection de 3 bam finaux

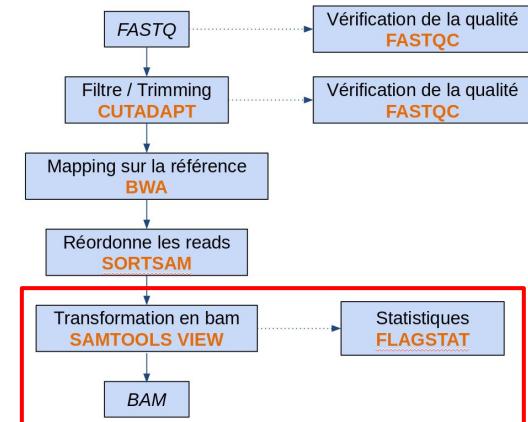
7) Samtools Flagstat : tabulate descriptive stats for BAM dataset

BAM File to report statistics of

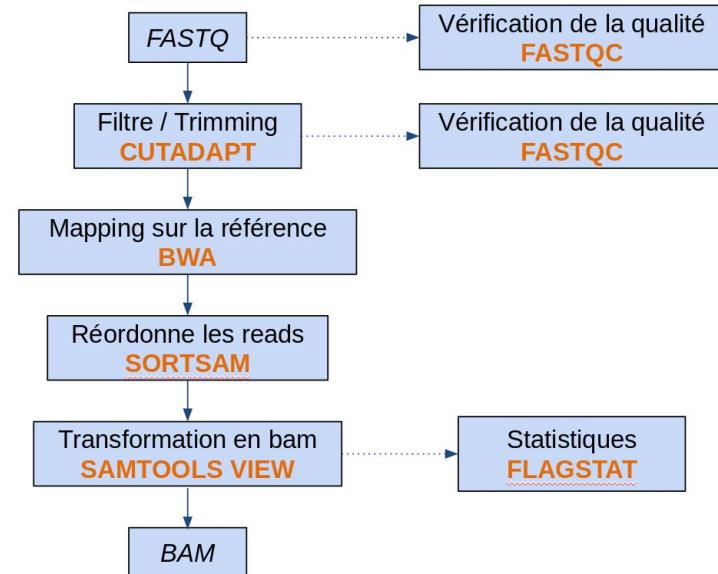
52: (hidden) SortSam on data 48: Alignment sorted in coordinate order

Execute

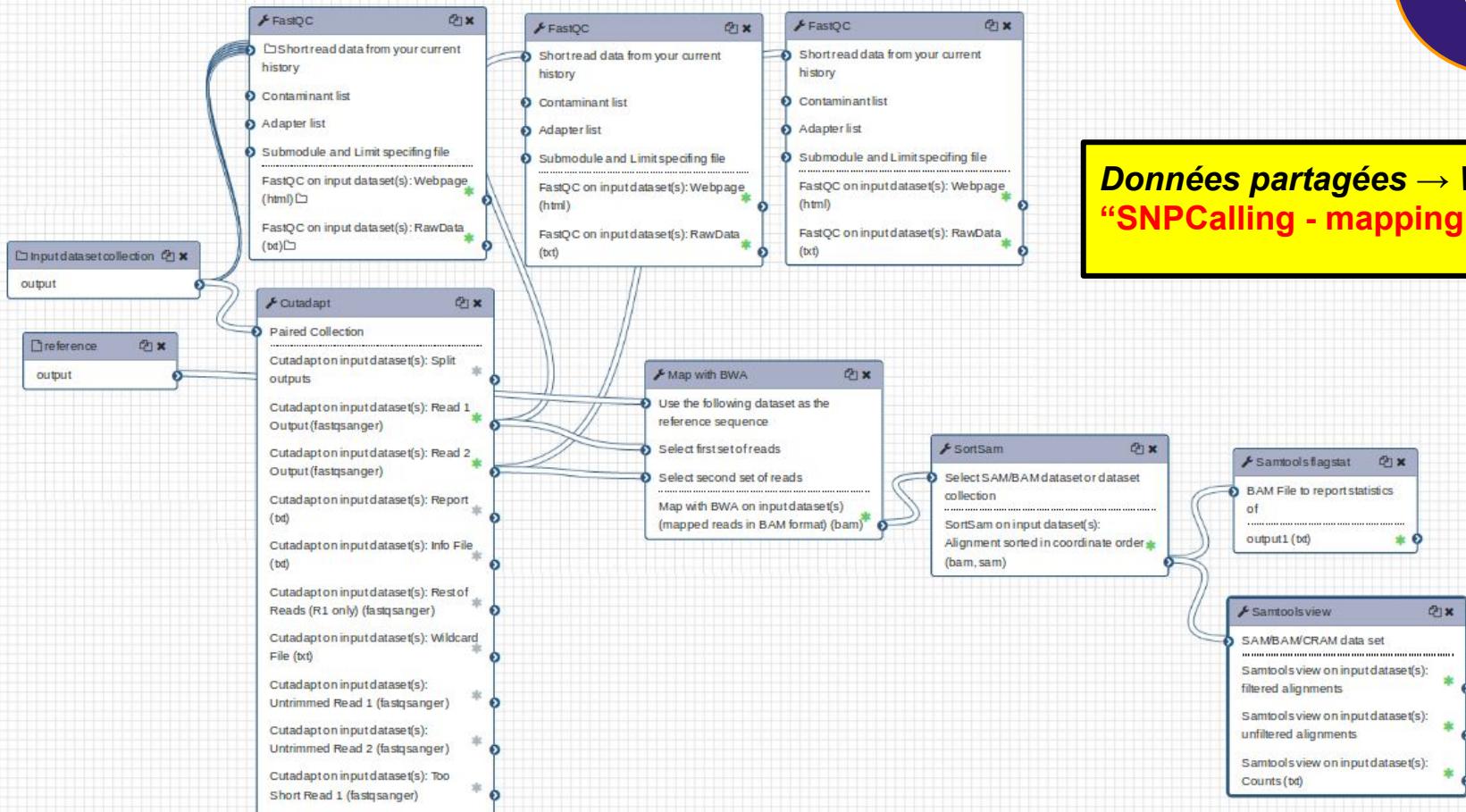
```
11812 + 0 in total (QC-passed reads + QC-failed reads)
0 + 0 secondary
0 + 0 supplementary
0 + 0 duplicates
9322 + 0 mapped (78.92% : N/A)
11812 + 0 paired in sequencing
5906 + 0 read1
5906 + 0 read2
9078 + 0 properly paired (76.85% : N/A)
9292 + 0 with itself and mate mapped
30 + 0 singletons (0.25% : N/A)
0 + 0 with mate mapped to a different chr
0 + 0 with mate mapped to a different chr (mapQ<=5)
```



1) CONSTRUISEZ LE WORKFLOW MAPPING



SNP-CALLING : Workflows

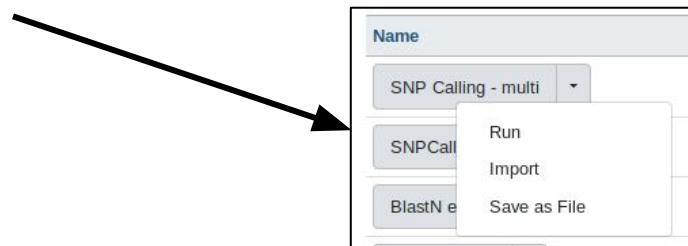
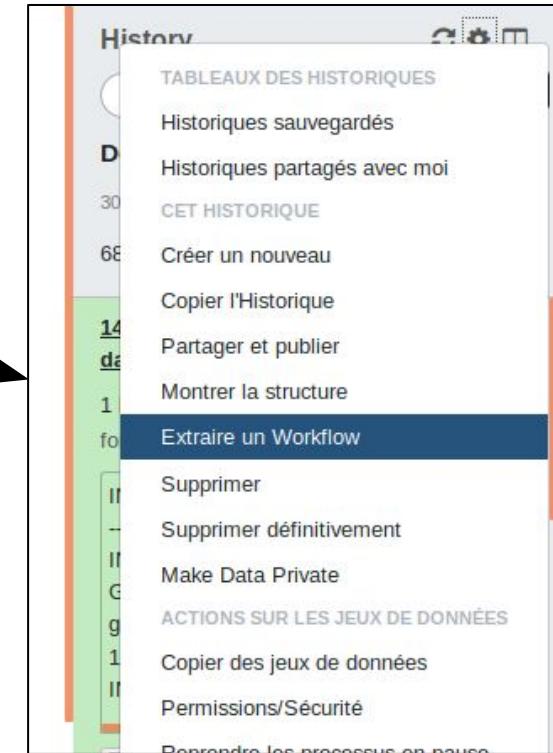


**Données partagées → WF
“SNPCalling - mapping - multi”**

Galaxy : Workflows

Pour lancer un **WORKFLOW** on peut :

- L'extraire de l'**historique** après avoir lancé tous les outils
- Le construire manuellement avec le canva
- L'importer depuis les données partagées



Dans vos Workflows personnels !

SNP-CALLING : Workflows



- 1) Télécharger le workflow “SNPCalling - multi” depuis les données partagées
- 2) Le lancer sur le BAM obtenu précédemment

Tools

search tools

Get Data

BASIC TOOLS

- Text Manipulation
- FASTA manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats

SEQUENCE ANALYSIS

- Fetch Sequences
- Fetch Alignments
- EMBOSS
- Operate on Genomic Intervals

NGS ANALYSIS

- NGS: QC and manipulation
- NGS: Cleaning
- NGS: Mapping
- NGS: Assembly
- NGS: SAM Tools
- NGS: GATK Tools (beta)
- NGS: RNA Analysis
- NGS: small RNAs
- NGS: Peak Calling
- NGS: Simulation

Workflow: SNP Calling - multi

History Options

Send results to a new history

Yes No

1: Input dataset collection

227: MarkDuplicates on collection 194: MarkDuplicates BAM output

2: reference

161: reference.fasta

3: Realigner Target Creator (Galaxy Version 2.8.1)

4: Indel Realigner (Galaxy Version 2.8.1)

5: MarkDuplicates (Galaxy Version 2.18.2.0)

6: Haplotype Caller (Galaxy Version 2.8.2)

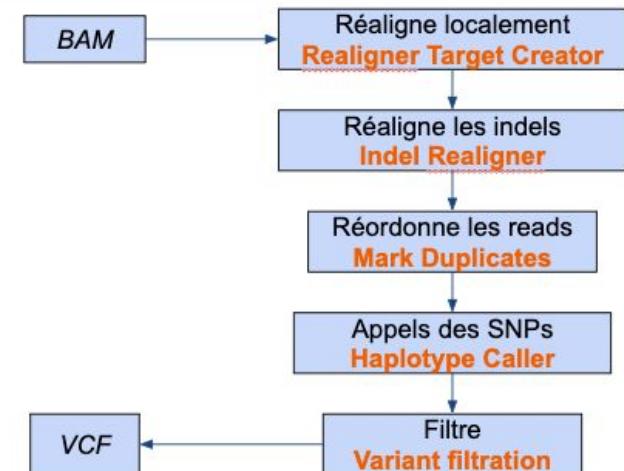
Covariates table recalibration file

No gatk_report dataset available.

The input covariates table file which enables on-the-fly base quality score recalibration. Enables on-the-fly recalibrate of base qualities. The covariates tables are produced by the BaseQualityScoreRecalibrator tool. Please be aware that one should only run recalibration with the covariates file created on the same input bam(s) (-BQSR,--BQSR <recal_file>).

Choose the source for the reference list

Run workflow



SNP-CALLING : Workflows



```

##INFO=<ID=InbreedingCoeff,Number=1>Type=Float,Description="Inbreeding coefficient as estimated from the genotype likelihoods per-sample when compared a
##INFO=<ID=MLEAC,Number=A>Type=Integer,Description="Maximum likelihood expectation (MLE) for the allele counts (not necessarily the same as the AC), for e
##INFO=<ID=MLEAF,Number=A>Type=Float,Description="Maximum likelihood expectation (MLE) for the allele frequency (not necessarily the same as the AF), for e
##INFO=<ID=MQ,Number=1>Type=Float,Description="RMS Mapping Quality"
##INFO=<ID=MQRankSum,Number=1>Type=Float,Description="Z-score From Wilcoxon rank sum test of Alt vs. Ref read mapping qualities"
##INFO=<ID=QD,Number=1>Type=Float,Description="Variant Confidence/Quality by Depth"
##INFO=<ID=ReadPosRankSum,Number=1>Type=Float,Description="Z-score from Wilcoxon rank sum test of Alt vs. Ref read position bias"
##INFO=<ID=SOR,Number=1>Type=Float,Description="Symmetric Odds Ratio of 2x2 contingency table to detect strand bias"
##contig=<ID=LOC_Os01g44110.1,length=2608>
##contig=<ID=LOC_Os01g62920.1,length=2879>
##contig=<ID=LOC_Os12g32240.1,length=1088>
##reference=file:///scratch2/galaxy/galaxy-19.01/galaxy/database/tmp/tmp-gatk-kyTSPp/gatk_input.fasta
#CHROM
LOC_Os01g44110.1
LOC_Os01g62920.1
LOC_Os12g32240.1
LOC_Os12g32240.1
LOC_Os12g32240.1
LOC_Os12g32240.1
LOC_Os12g32240.1

```

History

Rechercher des données

Donnees alexis

30 shown, 61 deleted, 90 hidden
68.87 MB

144: Variant Filtration on data 7 and data 141 (log)

143: Variant Filtration on data 7 and data 141 (Variant File)

142: Haplotype Caller on data 7, data 140, and others (log)

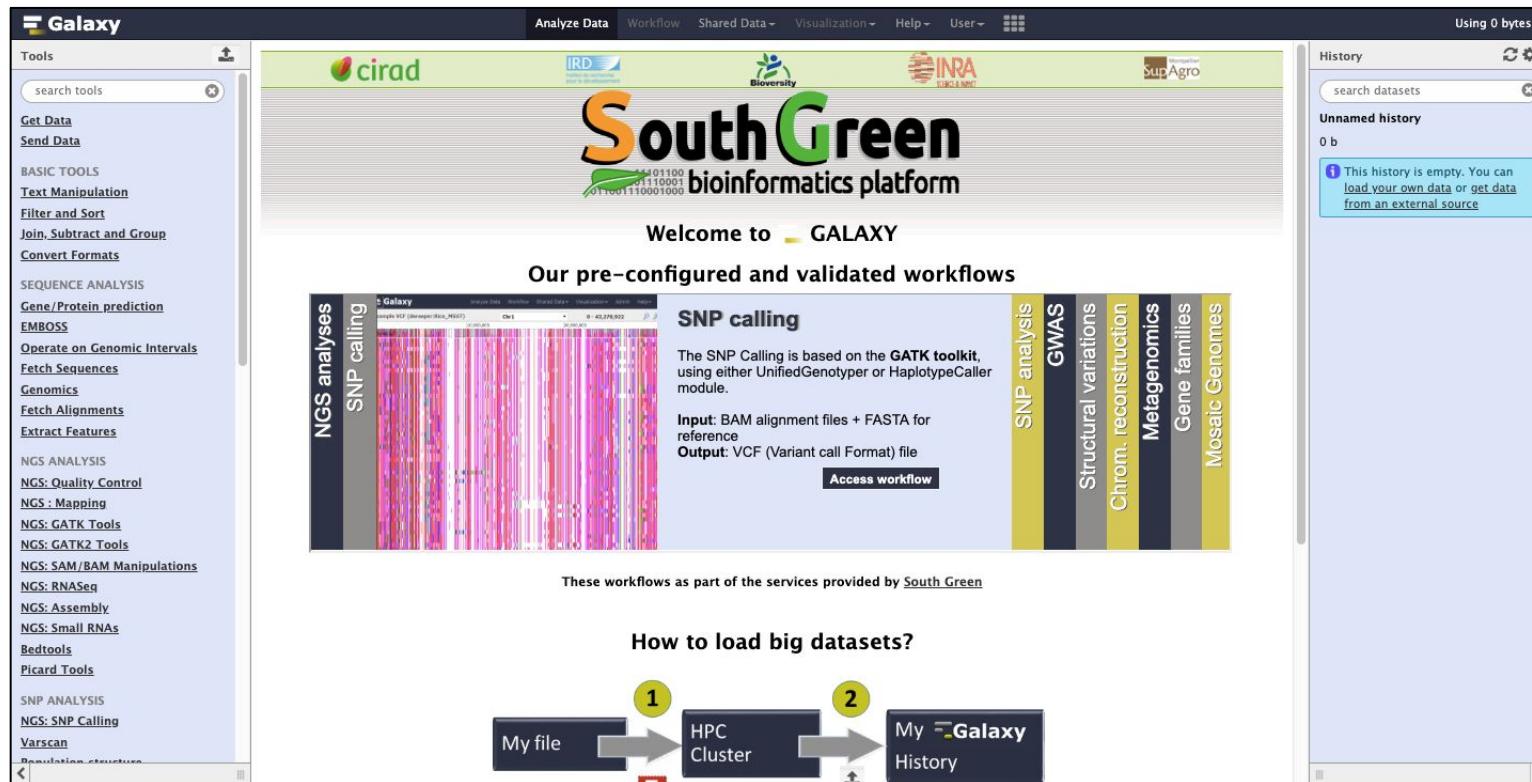
141: Haplotype Caller on data 7, data 140, and others (VCF)

134: MarkDuplicates on collection 125: MarkDuplicates BAM output
a list with 3 items

133: MarkDuplicates on collection 125: MarkDuplicate metrics
a list with 3 items

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme



The screenshot shows the Galaxy web interface with the SouthGreen bioinformatics platform integrated. The top navigation bar includes links for Analyze Data, Workflow, Shared Data, Visualization, Help, User, and a search bar. The main header features logos for cirad, IRD, Biodiversity, INRA, and AgroParisTech, followed by the SouthGreen logo and the text "Welcome to GALAXY". Below this, a banner reads "Our pre-configured and validated workflows". A sidebar on the left lists various tool categories such as BASIC TOOLS, SEQUENCE ANALYSIS, and NGS ANALYSIS. The central area displays a workflow titled "SNP calling" which uses the GATK toolkit. It shows a visualization of a BAM file and provides input and output specifications. To the right, other validated workflows are listed: SNP analysis, GWAS, Structural variations, Chrom. reconstruction, Metagenomics, Gene families, and Mosaic Genomes. At the bottom, a section titled "How to load big datasets?" illustrates a two-step process: "My file" leads to "HPC Cluster", which then leads to "My Galaxy History".

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme

NGS analyses



NGS analyses

We propose several workflows for NGS analyses in different scenarii (transcriptome vs transcriptome, transcriptome vs genome...) It includes cleaning and mapping steps using commonly used softwares.

Input: Fastq files + FASTA for reference
Output: BAM alignment files

[Access workflow](#)



G. Sarah



F. Homa



SNP calling

SNP calling

The SNP Calling is based on the **GATK toolkit**, using either UnifiedGenotyper or HaplotypeCaller module.

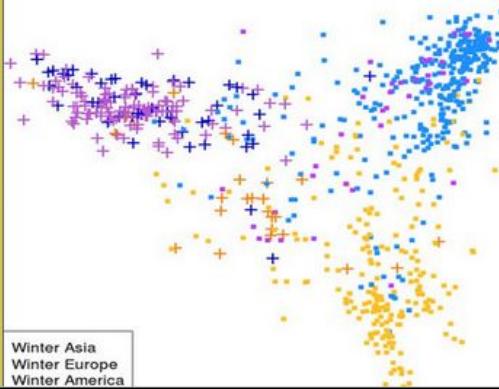
Input: BAM alignment files + FASTA for reference
Output: VCF (Variant call Format) file

[Access workflow](#)

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme

SNP analysis



Winter Asia
Winter Europe
Winter America

SNP analysis

SNiPlay3 complete workflow: a package for exploration and large scale analyses of SNP polymorphisms (filtering, SNP density, diversity, linkagedisequilibrium) (Dereeper et al, 2015)

Input: VCF

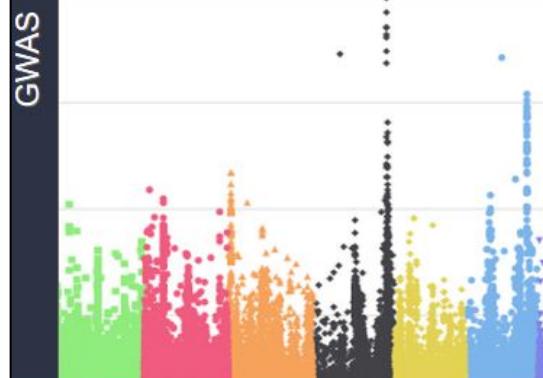
[Access workflow](#)



A. Dereeper



G. Andres



GWAS

SNiPlay3 GWAS workflow: Tassel-based GWAS workflow (GLM model) including population structure and correction for structure (Dereeper et al, 2015)

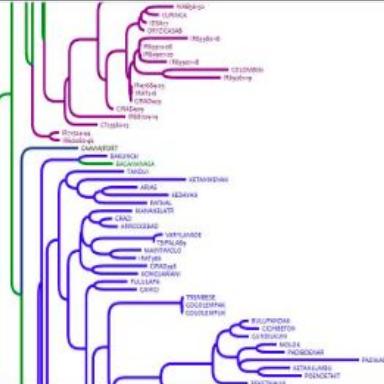
Input: VCF + Phenotypic tabulated file

[Access workflow](#)

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme

Gene families



Gene families

GreenphyL / GenFam : comparative and functional genomics in plants (Rouard et al, 2011).

Input: FASTA file, Species tree file

[Access workflow](#)



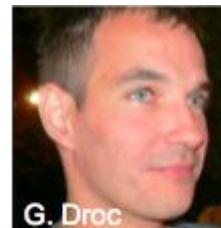
J.F. Dufayard



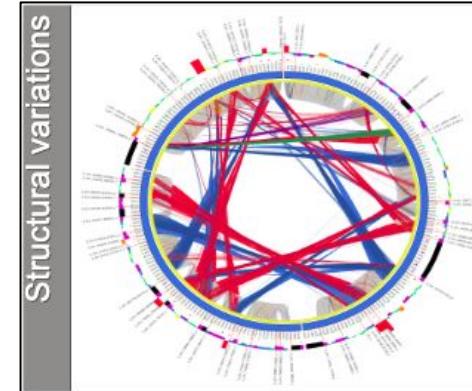
M. Rouard



G. Martin



G. Droc



Structural variations

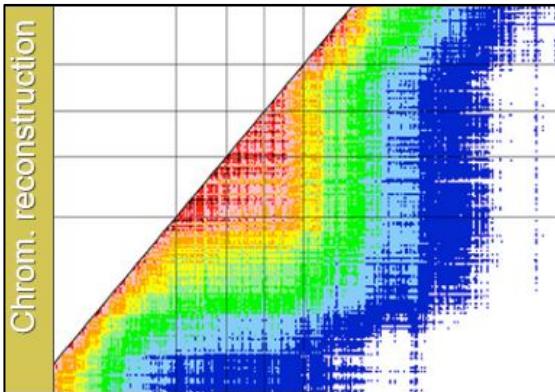
Scaffremodeler can be used to detect large structural variations between a reference sequence and a resequenced genome (Martin et al, 2016)

Input: Fastq + FASTA

[Access workflow](#)

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme



Chromosome reconstruction

Scaffehunter tools assemble scaffolds into pseudomolecules using markers genotyped in a population (Martin et al, 2016)

Input: Fastq + FASTA

[Access workflow](#)

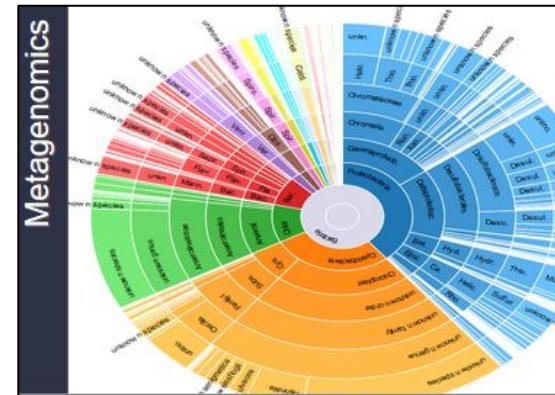


G. Martin



G. Droc

GenPhySE
Génétique Physiologie et Systèmes d'Elevage



Metagenomics

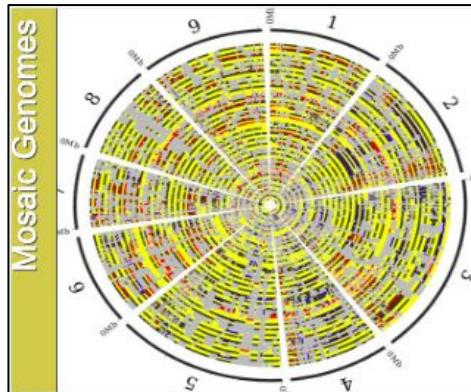
FROGS: Find Rapidly OTU with Galaxy Solution (Pascal et al, 2015)

Input: Fastq files

[Access workflow](#)

Aperçu des Workflows de SouthGreen

> 9 workflows préconfigurés et validés par la plateforme



Mosaic Genomes

Mosaic genome reconstruction

TraceAncestor / KDE_Classifier : Two approaches to analyze the mosaic structure of plant genomes

Input: VCF file + structure file

[Access workflow](#)



F. Curk



A. Comte



J. Santos

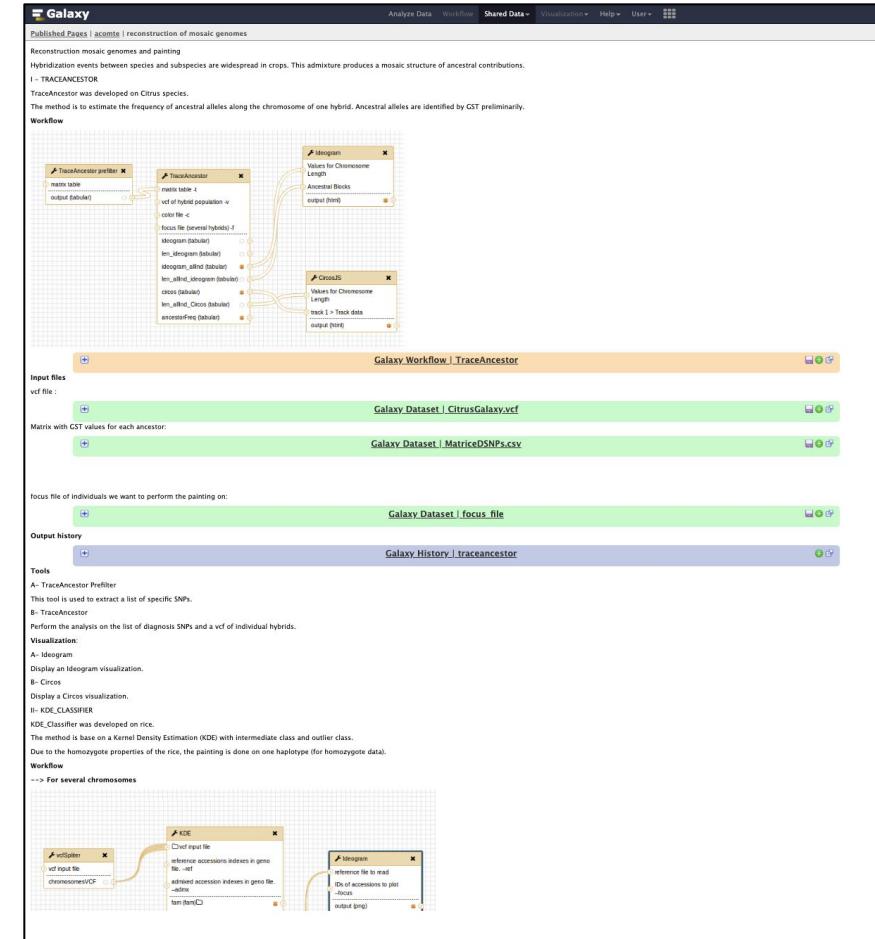


P. Ollitrault

Aperçu des Workflows de SouthGreen

Une documentation est disponible dans les Galaxy pages

> Workflow / Jeux de données / Historique d'analyses



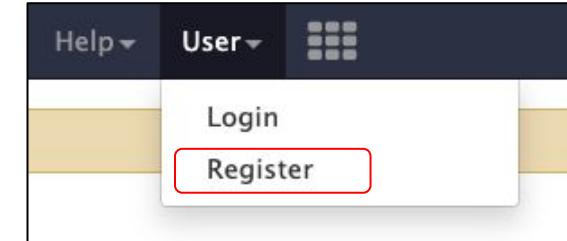
Galaxy : Bonnes pratiques

Galaxy CIRAD : <http://galaxy.southgreen.fr/galaxy/>

Comment créer un compte:

Directement sur Galaxy : <http://galaxy.southgreen.fr/galaxy/user/create>

Contactez : admin.bioinfo@cirad.fr pour augmenter l'espace alloué.



Pour tout problème ou demande (briques...): Contactez : admin.bioinfo@cirad.fr

Galaxy IRD : <http://bioinfo-inter.ird.fr:8080/>

Comment créer un compte:

Formulaire disponible sur le site web du plateau: <https://bioinfo.ird.fr/index.php/platform/galaxy-account>.

- La durée d'un compte est de 3 ans renouvelable sur demande au plateau bioinformatique.
- Quota utilisateur à fixer lors de la création du compte

Pour tout problème ou demande (briques...): contactez : bioinfo@ird.fr

Bonnes pratiques:

- Pensez à supprimer vos données / historique après analyse
→ galaxy n'est pas une plateforme de stockage
- Connaissez bien vos données et vos objectifs
→ configurations / paramètres

Galaxy : Bonnes pratiques

Comment citer Galaxy?

"The authors acknowledge the South Green Platform (<http://www.southgreen.fr>) for providing the galaxy instance (<http://bioinfo-inter.ird.fr:8080/> or <http://galaxy.southgreen.fr/galaxy/>) that have contributed to the research results reported within this paper."

→ N'oubliez pas de citer aussi les outils utilisés !

Comment citer les clusters?

"The authors acknowledge the IRD i-Trop HPC at IRD Montpellier for providing HPC resources that have contributed to the research results reported within this paper. URL: <http://bioinfo.ird.fr/> "

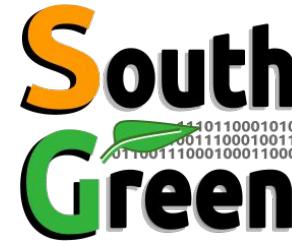
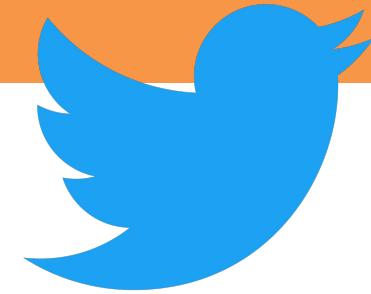
"The authors acknowledge the CIRAD UMR-AGAP HPC (South Green Platform) at CIRAD montpellier for providing HPC resources that have contributed to the research results reported within this paper. URL: <http://www.southgreen.fr>"

Formateurs

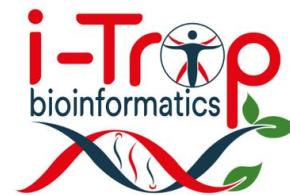
- Christine Tranchant-Dubreuil
- **Sebastien Ravel**
- Alexis Dereeper
- **Jean-François Dufayard**
- Ndomassi Tando
- Bertrand Pitollat
- **François Sabot**
- **Julie Orjuela-Bougnol**
- Gautier Sarah
- **Aurore Comte**
- **Marilyne Summo**
- **Guilhem Sempere**
- **Emmanuelle Beyne**



SUIVEZ NOUS SUR TWITTER !



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i-Trop : [@ItropBioinfo](https://twitter.com/ItropBioinfo)



Galaxy Project : [@galaxyproject](https://twitter.com/galaxyproject)

Merci pour votre attention !



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