

Galaxy

Galaxy is an open source, web-based platform for data intensive biomedical research. A universal **GUI** and **workflow manager** for lots of tools.

Official website: <https://galaxyproject.org/main/>

There are approximately **120 public servers**, **dozens** of private **academic servers** and even several **commercial servers**. Lots of which are highly specialised or modified as Galaxy project is completely **open access**.

Anyone can use one of public servers, with or without an account, but **Galaxy user accounts** are simple to create (email, password and go!). Advantages are: **increased data quotas**, **more resources** available, **parallel jobs** and **extended functionality** across sessions (i.e., **Histories**), such as **naming**, **saving**, **sharing**, and **publishing**.

Usegalaxy.org

The main Galaxy server at <http://usegalaxy.org>

- combines many **common tools** with **data sources**;
- is available since 2007 for **anyone** to analyze their data **free of charge**;
- provides **substantial CPU and disk space**, making it possible to analyze large datasets;
- supports **thousands of users** and **hundreds of thousands of jobs** per month (see [Statistics](#));
- sustained by [TACC](#) hardware using allocation generously provided by the [CyVerse](#) project.

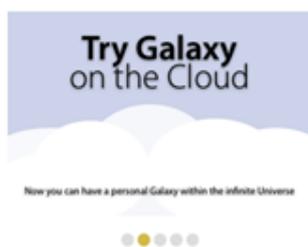
Notation: **History, Dataset, Tool panel, Job, Workflow, Visualization, Library**

Tools

search tools

- Get Data
- Send Data
- Lift-Over
- Collection Operations
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- NGS: QC and manipulation
- NGS: DeepTools
- NGS: Mapping
- NGS: RNA Analysis
- NGS: SAMtools
- NGS: BamTools
- NGS: Picard
- NGS: VCF Manipulation
- NGS: Peak Calling
- NGS: Variant Analysis
- NGS: RNA Structure
- NGS: Du, Novo
- NGS: Geminl
- NGS: Assembly
- NGS: Chromosome Conformation
- NGS: Mothur
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- BEDTools
- Genome Diversity
- EMBOSS
- Regional Variation
- FASTA manipulation
- Multiple Alignments
- Metagenomic Analysis
- Multiple regression
- Multivariate Analysis
- Motif Tools
- STR-FM: Microsatellite Analysis
- NCBI SRA Tools

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy [start here](#) or consult our [help resources](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).



The Galaxy Team is a part of the [Center for Comparative Genomics and Bioinformatics](#) at Penn State, the [Department of Biology](#) and at [Johns Hopkins University](#) and the [Computational Biology Program](#) at [Oregon Health & Science University](#).

This instance of Galaxy is utilizing infrastructure generously provided by the [CyVerse](#) at the [Texas Advanced Computing Center](#), with support from the [National Science Foundation](#).

The Galaxy Project is supported in part by [HSE](#), [NIHGR1](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

This is a free, public, internet accessible resource. Data transfer and data storage are not encrypted. If there are restrictions on the way your research data can be stored and used, please consult your local institutional review board or the project PI before uploading it to any public site, including this Galaxy server. If you have protected data, large data storage requirements, or short deadlines you are encouraged to setup your own [local Galaxy instance](#) or run [Galaxy on the cloud](#).

Galaxy version 17.09.rc1, commit [266c48c386f41c856ae3ba997197929605abdc](#)

Tweets by @galaxyproject

Galaxy Project @galaxyproject
#usegalaxy openings at 5 organizations in US and France (including @galaxyproject) [galaxyproject.org/galaxy-updates...](#)

Who's Hiring

The Galaxy is expanding! Please help it grow.

- The Warburg Lab in the Genomic Medicine Institute at the Cleveland Clinic Lerner Research Institute is hiring positions.
- Galaxy Project is hiring software engineers and positions at Johns Hopkins, Baltimore, Maryland, United States
- Implémentation d'outils d'analyse et de visualisation de variations structurales et génomes mitochondriaux, IRD (Institut de Recherche pour le Développement), Montpellier, France.

Embed

View on Twitter

History

search datasets

Unnamed history

21 shown, 28 deleted, 1 hidden

31.99 GB

48: Wla/BedGraph-to-bigWig on data 47

47: Genome Coverage on data 46 and data 29

46: Cut on data 45

45: IdxStats on data 29

36: RNA STAR on data 12 and data 11: mapped.bam

35: RNA STAR on data 12 and data 11: splice Junctions.bed

34: RNA STAR on data 12 and data 11: J 99

32: bamCoverage on data 29

30: featureCounts on data 22 and data 2 9

29: RNA STAR on data 20 and data 19: mapped.bam

28: RNA STAR on data 20 and data 19: splice Junctions.bed

27: RNA STAR on data 20 and data 19: J 99

26: FastQC on data 12: RawData

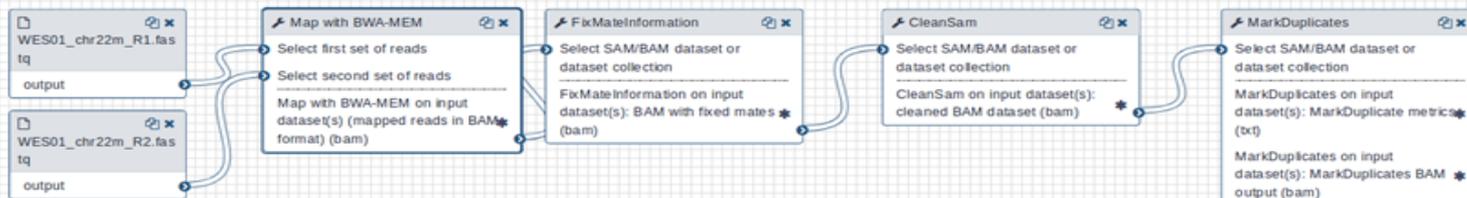
25: FastQC on data 12: Webpage

24: FastQC on data 19: RawData

imported: 01-ngs-bwa-mem-markdupe-filter



Details



Map with BWA-MEM



Map with BWA-MEM - map medium and long reads (> 100 bp) against reference genome (Galaxy Version 0.7.12.1)

Label

Add a step label.

Annotation

Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

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

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

 Using reference genome

Select genome from the list

Single or Paired-end reads

Select between paired and single end data

 Select first set of reads

Data input 'fastq_input1' (fastqsanger)

Specify dataset with forward reads

 Select second set of reads

Data input 'fastq_input2' (fastqsanger)

Specify dataset with reverse reads

90%



CEITEC Galaxy server

Public Galaxy is quite **versatile** and **flexible** (but not that much).

You can always install your **own Galaxy instance**. Advantages:

- (simple) installation of **additional tools, visualizations**, etc.
- own computational **resources** and **personalised quotas** in data storages
- easy to **share datasets, workflows**, etc.
- adjustable **access security level** (from no authentication to fully restricted access)

Our Galaxy server can be found here:

<https://galaxy.ceitec.muni.cz/>

To login please use your **university UCO** and **secondary password**

CEITEC Galaxy server

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 82.7 GB

CEITEC

Welcome to the CEITEC MU private Galaxy server

It is maintained by [Bioinformatics Core Facility](#). In the case of a problem or with any question about Galaxy do not hesitate to contact our administrator, Martin Demko, at 325073@mail.muni.cz.

If you used the services of this Galaxy server for your published research, we expect you to acknowledge these contributions: [Core Facility Bioinformatics of CEITEC Masaryk University](#) is gratefully acknowledged for the obtaining of the scientific data presented in this paper. and [MetaCentrum Computational resources](#) were provided by the [CESNET LM2015042](#) and the [CERIT Scientific Cloud LM2015085](#), provided under the programme "Projects of Large Research, Development, and Innovations Infrastructures".

Please, do not forget to cite the [Galaxy project itself](#) [Enis Afgan](#), [Dannon Baker](#), [Marius van den Beek](#), [Daniel Blankenberg](#), [Dave Bouvier](#), [Martin Čech](#), [John Chilton](#), [Dave Clements](#), [Nate Coraor](#), [Carl Eberhard](#), [Björn Grüning](#), [Aysam Guerler](#), [Jennifer Hillman-Jackson](#), [Greg Von Kuster](#), [Eric Rasche](#), [Nicola Soranzo](#), [Nitesh Turaga](#), [James Taylor](#), [Anton Nekrutenko](#), and [Jeremy Goecks](#). *The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update*. *Nucleic Acids Research* (2016) doi: [10.1093/nar/gkw343](https://doi.org/10.1093/nar/gkw343)

as well as the individual tools you used in your analysis. For more information about how to cite Galaxy please follow [this link](#).

Galaxy is an open platform for supporting data intensive research. It is developed by [The Galaxy Team](#) with the support of [many contributors](#). The [Galaxy Project](#) is supported in part by [NH&GRI](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

Tools

search tools

- General
- Phylogeny
- RNA-seq
- smallRNA-seq
- DNA variants
- Repeats
- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- BEDTools suite
- Cufflinks suite
- Picard Tools
- Primary
- Seqtk Toolkit
- RSeQC
- Genome assembly
- Samtools
- FASTX-Toolkit
- DeepTools
- BLAST+ tools
- Transcriptome assembly
- VSearch
- QIIME
- QIIME2
- Workflows
- All workflows

History

search datasets

imported: qiime test
11 shown, 19 deleted
1.15 GB

- 46: Pick representatively a set of sequences on data 2 and data 1: Log
- 46: Pick representatively a set of sequences on data 2 and data 1: Representative sequences
- 47: Pick representatively a set of sequences on data 6 and data 2: Log
- 45: pick_otus_on_data 6 and data 2: failures.txt
- 18: pick_otus_through_otu_table on data 2: log

error

An error occurred with this dataset:

```
Error running /bin/sh: 1: pick_otus_through_otu_table.p
```

WARNING:galaxy.model.Datatype class n
WARNING:galaxy.model.Datatype class n

- 6: 97_otus_16S.fasta
- 5: taxonomy_all_levels.txt
- 4: param_file.txt
- 3: gold.fa
- 2: input_galaxy.fa
- 1: mapa.txt

Upload data

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 82.7 GB

Tools

- General
- Phylogeny
- RNA-seq
- smallRNA-seq
- DNA variants
- Repeats
- Get Data
 - Upload File** from your computer
 - UCSC Main table browser
 - UCSC Archaea table browser
 - EBI SRA ENA SRA
 - modENCODE fly server
 - InterMine server
 - Flymine server
 - modENCODE modMine server
 - MouseMine server
 - Ratmine server
 - YeastMine server
 - modENCODE worm server
 - WormBase server
 - ZebrafishMine server
 - EuPathDB server
 - HbVar Human Hemoglobin Variants and Thalassemias
 - GenomeSpace Importer - receive data from GenomeSpace
- Send Data
- Collection Operations
- Lift-Over

CEITEC

Welcome to the CEITEC MU private Galaxy server

It is maintained by [Bioinformatics Core Facility](#). In the case of a problem or with any question about Galaxy do not hesitate to contact our administrator, Martin Demko, at 325073@mail.muni.cz.

If you used the services of this Galaxy server for your published research, we expect you to acknowledge these contributions: *Core Facility Bioinformatics of CEITEC Masaryk University is gratefully acknowledged for the obtaining of the scientific data presented in this paper. and MetaCentrum Computational resources were provided by the CESNET LM2015042 and the CERIT Scientific Cloud LM2015085, provided under the programme "Projects of Large Research, Development, and Innovations Infrastructures".*

Please, do not forget to cite the Galaxy project itself *Enis Afgan, Dannon Baker, Marius van den Beek, Daniel Blankenberg, Dave Bouvier, Martin Čech, John Chilton, Dave Clements, Nate Coraor, Carl Eberhard, Björn Grüning, Aysam Guerler, Jennifer Hillman-Jackson, Greg Von Kuster, Eric Rasche, Nicola Soranzo, Nitesh Turaga, James Taylor, Anton Nekrutenko, and Jeremy Goecks. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research (2016) doi: 10.1093/nar/gkw343 as well as the individual tools you used in your analysis. For more information about how to cite Galaxy please follow [this link](#).*

[Galaxy](#) is an open platform for supporting data intensive research. It is developed by [The Galaxy Team](#) with the support of [many contributors](#). The [Galaxy Project](#) is supported in part by [NHGRI](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

History Unnamed History (empty)

Upload data - sources

Galaxy

Analyze Data Workflow Visualize Shared Data Admin Help User

Using 82.7 GB

Tools

search tools

General
Phylogeny
RNA-seq
smallRNA-seq
DNA variants
Repeats
Get Data
Send Data
Collection Operations
Lift-Over
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
Operate on Genomic Intervals
Statistics
Graph/Display Data
Phenotype Association
BEDTools suite
Cufflinks suite
Picard Tools

Download from web or upload from disk

Regular Composite Collection Rule-based

Drop files here

Type (set all): Auto-detect Q Genome (s) Additional Species Are B...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

History

search datasets

Unnamed history (empty)

This history is empty. You can load your own data or get data from an external source

Upload data into History

Download from web or upload from disk

Regular Composite Collection Rule-based

You added 3 file(s) to the queue. Add more files or click "Start" to proceed.

Name	Size	Type	Genome	Settings	Status
<input type="text" value="chrom_sizes_test.fa"/>	31 b	Auto-detect	----- Additional Speci...		
<input checked="" type="checkbox"/> <input type="text" value="New File"/>	11 b	Auto-detect	----- Additional Speci...		
You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.					
<input type="text" value="ACGTGCGAAAA"/>					
<input checked="" type="checkbox"/> <input type="text" value="New File"/>	131 b	Auto-detect	----- Additional Speci...		
You can tell Galaxy to download data from web by entering URL in this box (one per line). You can also directly paste the contents of a file.					
<input type="text" value="ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz"/>					

Type (set all): Genome (set all):

History (empty)

This history is empty. You can [load your own data](#) or [get data from an external source](#).

Upload data into History



Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 82.7 GB

Tools

- General
- Phylogeny
- RNA-seq
- smallRNA-seq
- DNA variants
- Repeats
- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- BEDTools suite
- Cufflinks suite
- Picard Tools
- Primary
- Seqtk Toolkit
- RSeQC
- Genome assembly

 **CEITEC**

Welcome to the CEITEC MU private Galaxy server

It is maintained by [Bioinformatics Core Facility](#). In the case of a problem or with any question about Galaxy do not hesitate to contact our administrator, Martin Demko, at 325073@mail.muni.cz.

If you used the services of this Galaxy server for your published research, we expect you to acknowledge these contributions: *Core Facility Bioinformatics of CEITEC Masaryk University is gratefully acknowledged for the obtaining of the scientific data presented in this paper. and MetaCentrum Computational resources were provided by the CESNET LM2015042 and the CERIT Scientific Cloud LM2015085, provided under the programme "Projects of Large Research, Development, and Innovations Infrastructures".*

Please, do not forget to cite the Galaxy project itself *Eris Afgan, Dannon Baker, Marius van den Beek, Daniel Blankenberg, Dave Bouvier, Martin Čech, John Chilton, Dave Clements, Nate Coraor, Carl Eberhard, Björn Grüning, Aysam Guerler, Jennifer Hillman-Jackson, Greg Von Kuster, Eric Rasche, Nicola Soranzo, Nitesh Turaga, James Taylor, Anton Nekrutenko, and Jeremy Goecks. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research (2016) doi: 10.1093/nar/gkw343 as well as the individual tools you used in your analysis. For more information about how to cite Galaxy please follow [this link](#).*

[Galaxy](#) is an open platform for supporting data intensive research. It is developed by [The Galaxy Team](#) with the support of [many contributors](#). The [Galaxy Project](#) is supported in part by [NHGRI](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

History

Unnamed history
3 shown
(empty)

- [3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/86/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz](ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/86/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz)
- 2: Pasted Entry**
- 1: chrom_sizes_test.fa**

History

Using 83.2 GB

History

search datasets

Unnamed history
3 shown
441.74 MB

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/nomic.gff.gz

2: Pasted Entry

1: chrom sizes test.fa

Size of History

axy server

y do not hesitate to contact our

se these contributions: Core Facility data presented in this paper. Scientific Cloud LM2015085, provided

niel Blankenberg, Dave Bouvier, Jennifer Hillman-Jackson, Greg Von Kuster. The Galaxy platform for genomics. doi: 10.1093/nar/gkw343 Please follow [this link](#).

Contributors. The Galaxy Project is hosted at Johns Hopkins University.

Total usage across the Histories

Reload, Advanced options, Multy-history panel

Search field (looks in names, tags, comments, metadata)

History name (adjustable anytime, recommended to use)

Multi-dataset operations, History tags, History annotation

Dataset with ID and name

History - advanced options

Lot of useful features:

- **Copy** whole History
- **Share** or **Publish** History
- **Extract Workflow**
- **Permanent delete** of History or Datasets
- **Export citations** from used Tools

The screenshot shows a 'History' menu with the following sections and items:

- HISTORY LISTS**
 - Saved Histories
 - Histories Shared with Me
- CURRENT HISTORY**
 - Create New
 - Copy History
 - Share or Publish
 - Show Structure
 - Extract Workflow
 - Delete
 - Delete Permanently
- DATASET ACTIONS**
 - Copy Datasets
 - Dataset Security
 - Resume Paused Jobs
 - Collapse Expanded Datasets
 - Unhide Hidden Datasets
 - Delete Hidden Datasets
 - Purge Deleted Datasets
- DOWNLOADS**
 - Export Tool Citations
 - Export History to File
- OTHER ACTIONS**
 - Import from File

Dataset

HID - History ID of Dataset (*increasing*)
Name of Dataset (usually name of uploaded file or description of job result, *strongly recommended to change*)

Information about **length, format** and associated **genome database**

Download Dataset
Show **Details** of Dataset or Job
Show **available Visualizations**
Show **Help** page

Peek into Dataset (first several lines)

441.74 MB

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/nomic.gff.gz

~1,800,000 lines
format: **gff3**, database: ?

uploaded gff3 file

1. Seqid
##gff-version 3
#!gff-spec-version 1.21
#!processor NCBI annotwriter
#!genome-build Bra_napus_v2.0
#!genome-build-accession NCBI_Assembly

2: Pasted Entry

1: chrom sizes test.fa

View content of Dataset
Edit attributes (name, datatype, access)
Delete Dataset (*not permanently*)

Adjustable **Info** panel

Edit tags of Dataset (*very usefull*)
Edit attributes (name, datatype, access)
Delete Dataset (*not permanently*)

Dataset content

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User 83.2 GB

Tools search tools

General
Phylogeny
RNA-seq
smallRNA-seq
DNA variants
Repeats
Get Data
Send Data
Collection Operations
Lift-Over
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
Operate on Genomic Intervals
Statistics
Graph/Display Data
Phenotype Association
BEDTools suite
Cufflinks suite
Picard Tools
Primary
Seqtk Toolkit
RSeQC

Seqid	Source	Type	Start	End	Score	Strand	Phase	Attributes
##gff-version 3								
##gff-spec-version 1.21								
#processor NCBI annotwriter								
#genome-build Bra_napus_v2.0								
#genome-build-accession NCBI_Assembly:GCF_000686985.2								
#annotation-source NCBI Brassica napus Annotation Release 101								
##sequence-region NC_027757.2 1 35822559								
##species https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=3708								
NC_027757.2	RefSeq	region	1	35822559	.	+	.	ID=id0,Dbxref=taxon:3708,Name=A1,chromosome=A1,cultivar=ZS11.gbkey=Src:genome=chromosome7
NC_027757.2	Gnomon	gene	6637	9236	.	-	.	ID=gene0,Dbxref=GeneID:106345161,Name=LOC106345161.gbkey=Gene:gene=LOC106345161.g
NC_027757.2	Gnomon	mRNA	6637	9236	.	-	.	ID=ma0,Parent=gene0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2,Name=XM_013814943.2
NC_027757.2	Gnomon	exon	9092	9236	.	-	.	ID=id1,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	8813	8994	.	-	.	ID=id2,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	8688	8744	.	-	.	ID=id3,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	8298	8594	.	-	.	ID=id4,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	8126	8214	.	-	.	ID=id5,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	7727	7988	.	-	.	ID=id6,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	7407	7658	.	-	.	ID=id7,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	exon	6637	7209	.	-	.	ID=id8,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XM_013814943.2.gbkey=mRNA:gene=LOC106345161.g
NC_027757.2	Gnomon	CDS	8813	8950	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	8688	8744	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	8298	8594	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	8126	8214	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	7727	7988	.	-	1	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	7407	7658	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	CDS	6808	7209	.	-	0	ID=cds0,Parent=ma0,Dbxref=GeneID:106345161,Genbank:XP_013670397.1,Name=XP_013670397.1.g
NC_027757.2	Gnomon	gene	15630	16233	.	-	.	ID=gene1,Dbxref=GeneID:106353279,Name=LOC106353279.gbkey=Gene:gene=LOC106353279.g
NC_027757.2	Gnomon	mRNA	15630	16233	.	-	.	ID=ma1,Parent=gene1,Dbxref=GeneID:106353279,Genbank:XM_022689881.1,Name=XM_022689881.1

History search datasets

Unnamed history
3 shown
441.74 MB

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000686985/GCF_000686985.2_Bra_napus_v2.0/genomic.gff.gz
~1,800,000 lines
format: gff3, database: 2
uploaded gff3 file

1: Seqid
##gff-version 3
##gff-spec-version 1.21
#processor NCBI annotwriter
#genome-build Bra_napus_v2.0
#genome-build-accession NCBI_Assembl

2: Pasted Entry

1: chrom_sizes_test.fa

Dataset attributes

Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

Edit dataset attributes

Attributes Convert Datatypes Permissions

Edit attributes

Auto-detect Save

Name

ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz

Info

Genomic reference of Brassica Napus

Annotation

Genomic reference of Brassica Napus
version 2.0
NCBI database
GCF: 000696985

Add an annotation or notes to a dataset; annotations are available when a history is viewed.

Database/Build

----- Additional Species Are Below -----

Number of comment lines

History

search datasets

Unnamed history
3 shown
441.74 MB

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz
~1,800,000 lines
format: gff3, database: 2
Genomic reference of Brassica Napus

```
1. Seqid
##gff-version 3
#igff-spec-version 1.21
#iprocessor NCBI annotwriter
#lgenome-build Bra_napus_v2.0
#lgenome-build-accession NCBI_Assembl
```

2: Pasted Entry

1: chrom_sizes_test.fa

Dataset details



Each **Dataset** is a result of a **Job** using some **Tool** from **Tool panel** (here are useful information about performed Job)

Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

Upload File

Dataset Information

Number: 3
Name: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz
Created: Thu Oct 17 09:53:12 2019 (UTC)
Filesize: 441.7 MB
Dbkey: ?
Format: gff3

Job Information

Galaxy Tool ID:	upload1
Galaxy Tool Version:	1.1.6
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
History Content API ID:	aaabea39ae366df0 (55661)
Job API ID:	a189130306db606c (18693)
History API ID:	fb584e5eeac65a1 (913)
UUID:	f22452aa-3352-4b01-948a-10edf3447c55
Full Path:	/home/galaxy_new/data/datasets/043/dataset_43874.dat

Tool Parameters

Input Parameter	Value	Note for rerun
File Format	auto	
file_count	1	
Specify Files for Dataset (auto)	1 uploaded datasets	
Genome	unspecified (?) ----- Additional Species Are Below -----	
File Format	auto	

Inheritance Chain

ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz

History

search datasets

Unnamed history

3 shown

441.74 MB

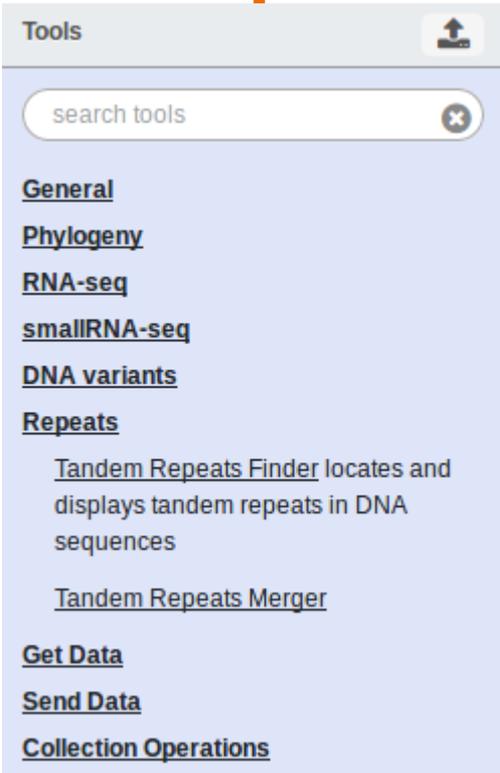
3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz
-1,800,000 lines
format gff3, database: ?
Genomic reference of Brassica Napus

1: Seqid
#gff-version 3
#igff-spec-version 1.21
#processor NCBI annotwriter
#genome-build Bra_napus_v2.0
#genome-build-accession NCBI_Assembl

2: Pasted Entry

1: chrom_sizes_test.fa

Tool panel



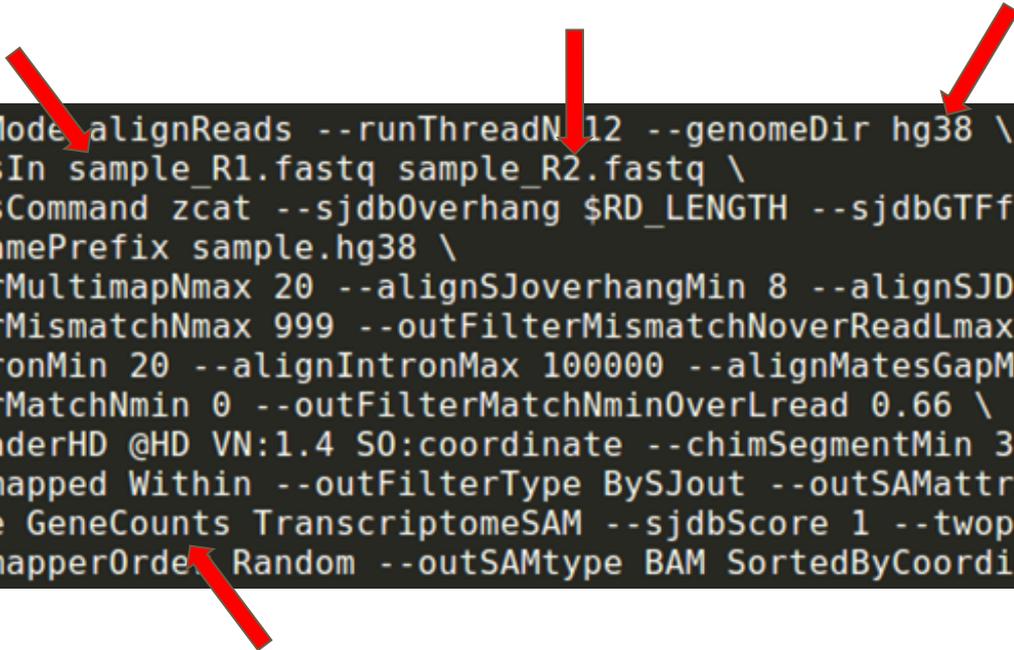
← **Search field** of Tool panel (looks into **names, descriptions, metadata**)

← **Tool panel** with many (named) **groups of tools**.

← Each group can be **unrolled** into a **list of tools**

Command-line Tool

```
STAR --runMode alignReads --runThreadN 12 --genomeDir hg38 \  
--readFilesIn sample_R1.fastq sample_R2.fastq \  
--readFilesCommand zcat --sjdbOverhang $RD_LENGTH --sjdbGTFfile hg38.gtf \  
--outFileNamePrefix sample.hg38 \  
--outFilterMultimapNmax 20 --alignSJoverhangMin 8 --alignSJDBoverhangMin 1 \  
--outFilterMismatchNmax 999 --outFilterMismatchNoverReadLmax 0.04 \  
--alignIntronMin 20 --alignIntronMax 100000 --alignMatesGapMax 1000000 \  
--outFilterMatchNmin 0 --outFilterMatchNminOverLread 0.66 \  
--outSAMheaderHD @HD VN:1.4 S0:coordinate --chimSegmentMin 30 --chimOutType SeparateSAMold \  
--outSAMunmapped Within --outFilterType BySJout --outSAMattributes All \  
--quantMode GeneCounts TranscriptomeSAM --sjdbScore 1 --twopassMode Basic \  
--outMultimapperOrder Random --outSAMtype BAM SortedByCoordinate
```



- Tools
- star
- Text Manipulation**
- Text reformatting with awk
- Convert Formats**
- MAF to BED Converts a MAF formatted file to the BED format
 - MAF to FASTA Converts a MAF formatted file to FASTA format
- NGS: RNA Analysis**
- RNA STAR** Gapped-read mapper for RNA-seq data new
- NGS: SAMtools**
- Convert SAM to interval
- NGS: Picard**
- ValidateSamFile assess validity of SAM/BAM dataset
- NGS: Peak Calling**
- CWPair2 find matched pairs and unmatched orphans
- NGS: Variant Analysis**
- Naive Variant Caller - tabulate variable sites from BAM datasets
- NGS: RNA Structure**
- Get RT Stop Counts derives the reverse transcriptase (RT) stop count on each nucleotide from a mapped file provided by the Iterative Mapping module
 - Reactivity Calculation calculates structural reactivity on each nucleotide based on RT stop counts from the Get RT Stop Counts module
- Operate on Genomic Intervals**
- Intersect the intervals of two datasets
 - Base Coverage of all intervals
 - Get flanks returns flanking region/s for every gene
- BEDTools**

RNA STAR Gapped-read mapper for RNA-seq data (Galaxy Version 2.5.2b-0) Options

Single-end or paired-end reads

Paired-end (as individual datasets)

RNA-Seq FASTQ/FASTA file, forward reads

19: ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR127302/ERR127302_1.fastq

RNA-Seq FASTQ/FASTA file, reverse reads

20: ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR127/ERR127302/ERR127302_2.fastq

Custom or built-in reference genome

Use a built-in index

Built-ins were indexed using default options

Reference genome with or without an annotation

use genome reference without builtin gene-model

Must the index have been created WITH a GTF file (if not you can specify one afterward).

Select reference genome

Human (Homo sapiens) (b38): hg38

If your genome of interest is not listed, contact the Galaxy team (--genomeDir)

Gene model (gff3,gtf) file for splice junctions

Nothing selected

Exon junction information for mapping splices (--sjdbGTFfile)

Length of the genomic sequence around annotated junctions

100

Used in constructing the splice junctions database. Ideal value is ReadLength-1 (--sjdbOverhang)

Count number of reads per gene

Yes No

column 1: gene ID, column 2: counts for unstranded RNA-seq, column 3: counts for the 1st read strand aligned with RNA , column 4: counts for the 2nd read strand aligned with RNA. This requires either (A) an index that was built with an annotation (GTF or GFF3 file) or (B) having specified an annotation (GTF or GFF3 file above). (--quantMode)

Would you like to set output parameters (formatting and filtering)?

No

Other parameters (seed, alignment, and chimeric alignment)

Use Defaults

Job Resource Parameters

Use default job resource parameters

Galaxy Tool

What it does

STAR is an ultrafast universal RNA-seq aligner.

Extra SAM attributes

The standard option includes the following four attributes

Command-line vs Galaxy

Galaxy

- is build **on top of the bioinformatic** (and not only) **tools** providing non-bioinformaticians an access to the tools
- puts a **graphic interface** on the top of the command-line making it much more user-friendly
- allows **sharing** of the data, **workflows, results, visualizations**, etc.
- allows to **repeat** and **edit Job settings** easily
- Is great for **small-scale analyses**
- does **not** support all types of tools (e.g., **online tools**)

Command-line is more **flexible**

For **large amount of data** or **unsupported tools** it is still better to use **command-line**

Job - setup

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

Tools

fasta

extract sequences from a FASTA file

Picard Tools

NormalizeFasta normalize fasta datasets

Primary

Cutadapt Remove adapter sequences from Fastq/Fasta

Seqtk Tools

seqtk_sample sample from subsample of fasta or fastq sequences

seqtk_dropseq drop unpaired from interleaved Paired End FASTA/Q

seqtk_comp get the nucleotide composition of FASTA/Q

seqtk_mutfa point mutate FASTA at specified positions

seqtk_subseq extract subsequences from FASTA/Q files

seqtk_mergefa merge two FASTA/Q files

seqtk_seq common transformation of FASTA/Q

QIIME

Filter fasta to remove sequences based on input criteria (filter_fasta)

Count the sequences in a fasta file (count_seqs)

Pick representative set of sequences (pick_rep_set)

Cutadapt Remove adapter sequences from Fastq/Fasta (Galaxy Version 1.16.1) Options

Single-end or Paired-end reads?
Single-end

FASTQ/A file
1: chrom_sizes_test.fa
Should be of datatype "fastq.gz" or "fasta"

Read 1 Options

3' (End) Adapters
+ Insert 3' (End) Adapters
Sequence of an adapter ligated to the 3' end (paired data: of the first read). The adapter and subsequent bases are trimmed. If a '\$' character is appended ('anchoring'), the adapter is only found if it is a suffix of the read. To search for a linked adapter, separate the 2 sequences with 3 dots (ADAPTER1...ADAPTER2), see Help below.

5' (Front) Adapters
+ Insert 5' (Front) Adapters
Sequence of an adapter ligated to the 5' end (paired data: of the first read). The adapter and any preceding bases are trimmed. Partial matches at the 5' end are allowed. If a '^' character is prepended ('anchoring'), the adapter is only found if it is a prefix of the read. To search for a linked adapter, separate the 2 sequences with 3 dots (ADAPTER1...ADAPTER2), see Help below.

5' or 3' (Anywhere) Adapters
+ Insert 5' or 3' (Anywhere) Adapters
Sequence of an adapter that may be ligated to the 5' or 3' end (paired data: of the first read). Both types of matches as described under 3' and 5' Adapters are allowed. If the first base of the read is part of the match, the behavior is as with 5' Adapters, otherwise as with 3' Adapters. This option is mostly for rescuing failed library preparations - do not use if you know which end your adapter was ligated to!

Cut bases from reads before adapter trimming
0
Remove bases from each read (first read only if paired). If positive, remove bases from the beginning. If negative, remove bases from the end. This is applied "before" adapter trimming. (-u)

Adapter Options

Filter Options

Read Modification Options

Output Options

Execute

History

search datasets

Unnamed history
3 shown, 1 deleted
441.74 MB

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/085/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz
-1,800,000 lines
format: gff3, database: 2
Genomic reference of Brassica Napus

1: seqid
##gff-version 3
##gff-spec-version 1.21
##processor NCBI annotwriter
##genome-build Bra_napus_v2.0
##genome-build-accession NCBI_Assembly

2: Pasted Entry

1: chrom_sizes_test.fa

Job - execution

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

Tools

fasta

extract sequences from a FASTA file

Picard Tools

NormalizeFasta normalize fasta datasets

Primary

Cutadapt Remove adapter sequences from Fastq/Fasta

Seqtk Toolkit

seqtk_sample random subsample of fasta or fastq sequences

seqtk_dropse drop unpaired from interleaved Paired End FASTA/Q

seqtk_comp get the nucleotide composition of FASTA/Q

seqtk_muta point mutate FASTA at specified positions

seqtk_subseq extract subsequences from FASTA/Q files

seqtk_mergefa merge two FASTA/Q files

seqtk_seq common transformation of FASTA/Q

QIIME

Executed Cutadapt and successfully added 1 job to the queue.

The tool uses this input:

1: chrom_sizes_test.fa

It produces this output:

7: Cutadapt on data 1: Read 1 Output

You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

search datasets

Unnamed history

4 shown, 3 deleted

441.74 MB

7: Cutadapt on data 1: Read 1 Output

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/9/95/GCF_000686985.2_Bra_napus_v2.0/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz

~1,800,000 lines

format: gff3, database: 2

Genomic reference of Brassica Napus

```
1. Seqid
##gff-version 3
##gff-spec-version 1.21
#iprocessor NCBI annotwriter
#genome-build Bra_napus_v2.0
#genome-build-accession NCBI_Assembly
```

2: Pasted Entry

1: chrom_sizes_test.fa

Job - error

Indicator of **failed Job**



49: Pick representative set of sequences on data 2 and data 1: Log



Piece of **Error message**



error

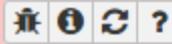
An error occurred with this dataset:

Fatal error: Exit code 1 ()

Traceback (most recent call last):

```
File "/home/galaxy_new/dependencies/_conda/er
__import__('pkg_resources').run_script('qiime==
File
```

Report failed Job (please, do!)



Rerun job (not only failed one)



Report Job error

Dataset Error

An error occurred while running the tool `toolshed.g2.bx.psu.edu/repos/iuc/qiime_pick_rep_set/qiime_pick_rep_set/1.9.1.0`.

Tool execution generated the following messages:

```
Fatal error: Exit code 1 ()
Traceback (most recent call last):
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/bin/pick_rep_set.py", line 4, in <module>
    __import__('pkg_resources').run_script('qiime=1.9.1', 'pick_rep_set.py')
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/lib/python2.7/site-packages/pkg_resources/__init__.py", line 666, in run_script
    self.require(requires)[0].run_script(script_name, ns)
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/lib/python2.7/site-packages/pkg_resources/__init__.py", line 1462, in run_script
    exec(code, namespace, namespace)
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/lib/python2.7/site-packages/qiime-1.9.1-py2.7.egg-info/scripts/pick_rep_set.py", line 125, in <module>
    main()
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/lib/python2.7/site-packages/qiime-1.9.1-py2.7.egg-info/scripts/pick_rep_set.py", line 121, in main
    sort_by=opts.sort_by)
  File "/home/galaxy_new/dependencies/_conda/envs/__qiime@1.9.1/lib/python2.7/site-packages/qiime/pick_rep_set.py", line 190, in __call__
    of.write(">%s %s\n%s\n" % (cluster_id_, seqs[id_]))
KeyError: 'BarcodeSequence'
```

Troubleshoot This Error

There are a number of help resources to self diagnose and correct problems. Start here: [My job ended with an error. What can I do?](#)

Report This Error

Usually the local Galaxy administrators regularly review errors that occur on the server. However, if you would like to provide additional information (such as what you were trying to do when the error occurred) and a contact e-mail address, we will be better able to investigate your problem and get back to you.

Error Report

Your email

Your email address

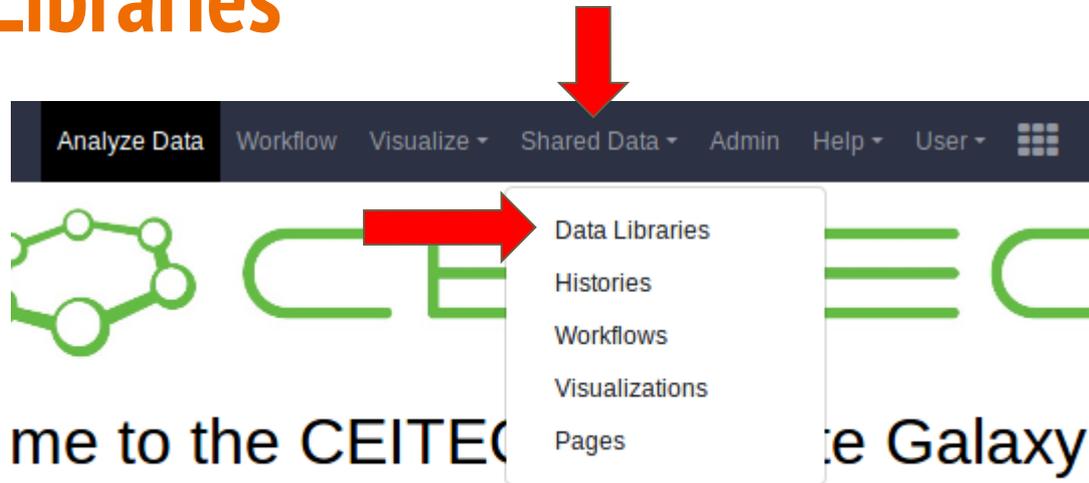
Message

Any additional comments you can provide regarding what you were doing at the time of the bug.

Report



Data Libraries



[atics Core Facility](#). In the case of a problem or with any question about Galaxy do not
at 225072@mail.muni.cz

Data Libraries

Galaxy Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

DATA LIBRARIES < 0 1 2 > 8 libraries shown (change) 8 total include deleted exclude restricted + New Library Help

name↑	description	synopsis	
admin_test	for testing		Edit Manage
BI5444 	Analysis of sequencing data		Edit Manage
Bioda_group	for Bioda users to share data		Edit Manage
CEITEC_Workshop			Edit Manage
galaxy_test			Edit Manage
Honza_lib	personal library of Honza		Edit Manage
Lysak_group_workshop			Edit Manage
Mraz_lab_workshop			Edit Manage

Data Libraries

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

Libraries / B15444

as Datasets
as a Collection

name 11

description

data type

size

time updated (UTC)

state

--

CLIP-Seq

folder

2019-09-19 03:42 PM

Edit

Manage

RNA-Seq

folder

2019-09-16 03:30 PM

Edit

Manage

< 0 1 2 > 2 items shown (change) 2 total

1.

Import into History

Select history:

or create new:

Import

Close

Workflow

Workflow or **pipeline** is an **automatisation** of multi-step **analysis**

Set (or tree) of **tools** taking the **input** from the **output** of another tool (except the very first)

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Admin', 'Help', and 'User'. The 'Workflow' tab is highlighted with a red arrow. The main content area is titled 'Your workflows' and contains a table with the following data:

Name	Tags	Owner	# of Steps	Published	Show in tools panel
Imported: microRNA - Classic		You	14	No	<input type="checkbox"/>
Imported: Ks analysis		You	14	No	<input type="checkbox"/>
Imported: Analysis - RNA-Seq - Counts to Expression		You	9	No	<input type="checkbox"/>
Unnamed workflow		You	0	No	<input type="checkbox"/>

The left sidebar contains a search bar and a list of tool categories. The 'Workflows' category is expanded, and 'All workflows' is highlighted with a red arrow.

Workflow

Your workflows

search for workflow...  

Name	Tags	Owner	# of Steps	Published	Show in tools panel
imported: microRNA - Classic		You	14	No	<input type="checkbox"/>
imported: Ks analysis		You	14	No	<input type="checkbox"/>
imported: Analysis - RNA-Seq -		You	9	No	<input type="checkbox"/>
Unnamed workflow		You	0	No	<input type="checkbox"/>

- Edit
- Run
- Share
- Download
- Copy
- Rename
- View
- Delete

Galaxy

Analyze Data Workflow Visualize Shared Data Admin Help User Using 83.2 GB

Workflow Canvas | Imported: microRNA - Classic

FastQC

- Short read data from your current history
- Contaminant list
- Submodule and Limit specifying file
- html_file (html)
- text_file (txt)

MultiQC

- Results 1 > FastQC output 1 > FastQC output
- Results 2 > Output of Cutadapt
- stats
- html_report (html)
- log (txt)

Filter by quality

- Library to filter
- output

Adapters detection

- Input file in Fastq format
- out (txt)

Cutadapt

- FASTQ/A file
- out1 (fasta)
- out2 (fastqsanger)
- report (txt)
- info_file (txt)
- rest_output (fastqsanger)
- wild_output (txt)
- untrimmed_output (fastqsanger)
- untrimmed_paired_output (fastqsanger)
- too_short_output (fastqsanger)
- too_short_paired_output (fastqsanger)
- too_long_output (fastqsanger)
- too_long_paired_output (fastqsanger)

Filter fastq by size

- Input file(s) in FastQ format
- out (fastqsanger.gz)

fastq_screen

- RNA-Seq FASTQ file
- out_text (tabular)
- out_html (html)
- out_png (png)
- out_html_2 (html)
- out_png_2 (png)

Collapse

- Library to collapse
- output (fasta)

Cutadapt

- FASTQ/A file
- out1 (fasta)
- out2 (fastqsanger)
- report (txt)
- info_file (txt)
- rest_output (fastqsanger)
- wild_output (txt)
- untrimmed_output (fastqsanger)
- untrimmed_paired_output (fastqsanger)
- too_short_output (fastqsanger)
- too_short_paired_output (fastqsanger)
- too_long_output (fastqsanger)
- too_long_paired_output (fastqsanger)

Input reads (FASTQ format)

- output

FastQC Read Quality reports (Galaxy Version 0.72)

Label

Add a step label.

Annotation

Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

Short read data from your current history

Data input 'input_file' (fastq, fastq.gz, fastq.bz2, bam or sam)

Contaminant list

Data input 'contaminants' (tabular)

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

Submodule and Limit specifying file

Data input 'limits' (txt)

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

Email notification

Yes No

An email notification will be sent when the job has completed.

Output cleanup

Yes No

Upon completion of this step, delete non-starred outputs from completed workflow steps if they are no longer required as inputs.

Configure Output: 'html_file'

Configure Output: 'text_file'

Purpose

FastQC aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines. It provides a modular set of analyses which you can use to give a quick impression of whether your data has any problems of which you should be aware before doing any further analysis.

The main functions of FastQC are:

- Import of data from BAM, SAM or FastQ/FastQ.gz files (any variant).
- Providing a quick overview to tell you in which areas there may be problems
- Summary graphs and tables to quickly assess your data

Workflow - build

Tools can be drag&dropped from Tool panel and connected together only if **output** and **input** Dataset format matches

Parameters, Annotation, etc.

Workflow - execution

History Options

Send results to a new history

Yes No

1: Input raw counts 1 (featureCounts)



6: HUGO Gene information

2: Input raw counts 2 (featureCounts)



6: HUGO Gene information

3: Input raw counts 3 (featureCounts)



6: HUGO Gene information

4: Entrez to HUGO (tsv)



6: HUGO Gene information

5: edgeR (Galaxy Version 3.20.7.2)

6: DESeq2 (Galaxy Version 2.11.40.2)

7: Join two Datasets (Galaxy Version 2.1.1)

8: Join two Datasets (Galaxy Version 2.1.1)

9: Join two Datasets (Galaxy Version 2.1.1)

Saved Histories

The screenshot displays the Galaxy web interface. At the top, the navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Admin', 'Help', and 'User'. The main content area is titled 'Saved Histories' and contains a search bar and a table of saved history items. A dropdown menu is open over the table, showing options for 'Data Libraries', 'Histories', 'Workflows', 'Visualizations', and 'Pages'. A red arrow points to the 'Histories' option. On the right side, there is a 'History' panel with a search bar and a list of history items. A second red arrow points to this panel, with the text 'Special panel (next slide)' next to it.

Name	Items	Datasets	Size on Disk	Created	Last Updated	Status
Library test	14	14	96.2 GB	28 minutes ago	28 minutes ago	current history
Unnamed history	7	4 3	441.7 MB	4 hours ago	58 minutes ago	
imported: qiime test	49	6 5 19	1.2 GB	2 days ago	1 day ago	
imported: NOVOPlast error	201	23 166 11	1.8 GB	Apr 26, 2019	Sep 17, 2019	
vardictGATK HaplotypeCaller test	35	9 3 24 2	4.0 GB	Nov 21, 2018	Sep 04, 2019	
Tandem Repeats Merger - test	1041	76 2 526 683	Shared 2.0 GB	Dec 19, 2018	May 29, 2019	
Data managers and Genome indexes	498	118 18 280 50	54.9 GB	Oct 10, 2018	Apr 25, 2019	
imported: Lysak group tutorial - Ks	78	16 12 64	189.6 MB	Apr 17, 2019	Apr 17, 2019	
Lasyk group workshop (BLAST+R)	12	8 4	47.6 MB	Apr 17, 2019	Apr 17, 2019	
Lysak group test	96	28 29 46	198.7 KB	Apr 11, 2019	Apr 16, 2019	
test	38	20 2 16 6	191.2 MB	Jan 02, 2019	Feb 05, 2019	
Copy of 'kamila-dna-seq-sptal'	54	17 26 1	Shared 20.5 GB	Dec 03, 2018	Dec 12, 2018	
streika test	48	11 3 34	16.9 GB	Nov 25, 2018	Nov 28, 2018	
VEP test	22	7 2 13	25.3 KB	Nov 12, 2018	Nov 13, 2018	

For 0 selected items: [Rename](#) [Delete](#) [Delete Permanently](#) [Undelete](#)

Histories that have been deleted for more than a time period specified by the Galaxy administrator(s) may be permanently deleted.

Multi-history panel

The screenshot displays the Galaxy web interface with a multi-history panel. The top navigation bar includes the Galaxy logo, search bars for "search histories" and "search all datasets", and a "Create new" button. The main area is divided into five vertical panels, each representing a different history:

- Library test:** 14 shown, 96.15 GB. Lists datasets like "14: KD2_rep2_2.fastq", "13: KD2_rep2_1.fastq", etc.
- Unnamed history:** 4 shown, 441.74 MB. Contains a "Cutadapt on data 1: Read 1 Output" dataset with a detailed error message: "Fatal error: Exit code 1 () Traceback (most recent call last): File 'home/galaxy_new/dependencies/conda/.../import_(pkg_resources).run_script('qime=...'. File".
- Imported: qime test:** 11 shown, 1.15 GB. Contains error messages such as "49: Pick representative set of s equences on data 2 and data 1: Log error" and "48: Pick representative set of s equences on data 2 and data 1: Rep resentative sequences".
- Imported: NOVOPlast error:** 23 shown, 1.81 GB. Lists datasets like "201: NOVOPlasty on data 3, data 2, and data 1 (Option 4)", "200: NOVOPlasty on data 3, data 2, and data 1 (Option 3)", etc.
- vardict/GATK HaplotypeCaller test:** 12 shown, 4.03 GB. Lists datasets like "35: Tool for testing on data 21", "34: Generate GATK-sorted Picard indexes", etc.

Each panel includes a search bar, a "Switch to" dropdown, and a list of datasets with icons for viewing, deleting, and copying. The error messages in the "Unnamed history" and "Imported: qime test" panels are highlighted in red.

Multi-history panel - drag&drop copy Datasets

Galaxy

Analyze Data Workflow Visualize Shared Data Admin Help

search histories search all datasets

Current History

Library test
15 shown
96.15 GB
search datasets
Drag datasets here to copy them to the current history

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz

15: Cutadapt on data 1: Read 1 Output

14: KD2_rep2_2.fastq

13: KD2_rep2_1.fastq

12: KD2_rep1_2.fastq

11: KD2_rep1_1.fastq

10: KD1_rep2_2.fastq

9: KD1_rep2_1.fastq

Unnamed history
4 shown, 3 deleted
441.74 MB
search datasets

7: Cutadapt on data 1: Read 1 Output

3: ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/686/985/GCF_000686985.2_Bra_napus_v2.0_genomic.gff.gz

2: Pasted Entry

1: chrom_sizes test.fa

imported: qiime test
11 shown, 19 deleted
1.15 GB
search datasets

49: Pick representative set of sequences on data 2 and data 1: Log

error
An error occurred with this dataset:
Fatal error: Exit code 1 ()
Traceback (most recent call last):
File "/home/galaxy_new/dependencies/_conda/er...
__import__(pkg_resources).run_script('qiime==...
File

48: Pick representative set of sequences on data 2 and data 1: Representative sequences

47: Pick representative set of sequences on data 6 and data 2: Log

Visualization

Depends entirely on Dataset format

Using 83.2 GB

History refresh settings list

vardict/GATK HaplotypeCaller test

Found 3, [show deleted](#), [show hidden](#)

4.03 GB checkbox trash share

22: GATK - HaplotypeCaller on data 2 (log) eye trash share

21: GATK on data 2 (gVCF) eye trash share

2: xKD8500.sorted.mdup.bam eye trash share

bam

2.7 GB

format: **bam**, database: **hg19**

trash share

[display at UCSC main test](#)

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr21:33,031,597-33,041,570 9,974 bp.

chr21 (q22.11) 21p13 21p12 21p11.2 11p2 21q21.1 21q21.2 21q21.3 21q22.11 22q.2 21q22.3

Scale chr21: 33,033,000 33,034,000 33,035,000 2 kb hg19 33,036,000 33,037,000 33,038,000 33,039,000 33,040,000 33,041,000

0.sorted.mdup.bam xKD8500.sorted.mdup.bam

BC041449 (3) NCBI RefSeq genes, curated subset (NM_*, NR_*, NP_* or VP_*) - Annotation Release GCF_00001485.25_GRCh37.p13 (2017-04-15)

SOD1 Publications: Sequences in Scientific Articles

Sequences SIF

Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (578 donors)

NP00253.1 NP00254.0

100 Layered H3K27Ac H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

DNase Clusters DNase I Hypersensitivity Clusters in 125 cell types from ENCODE (US)

Txn Factor ChIP Transcription Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs

100 Vert. Cons. 100 vertebrates Basewise Conservation by PhyloP

Rhesus Mouse Dog Elephant Chicken X_Troops 10112 Zebra Finch Lamprey

Common SNPs (151) Simple Nucleotide Polymorphisms (dbSNP 151) Found in >= 1% of Samples

Repeating Elements by RepeatMasker

RepeatMasker

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

move start < 2.0 > move end

rch default tracks default order hide all manage custom tracks track hubs configure multi-region reverse resize

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Custom Tracks

xKD8500.sorted.mdup.bam

Mapping and Sequencing

Genes and Gene Predictions

UCSC Genes pack

NCBI RefSeq pack

Other RefSeq hide

AceView Genes hide

AUGUSTUS hide

CCDS hide