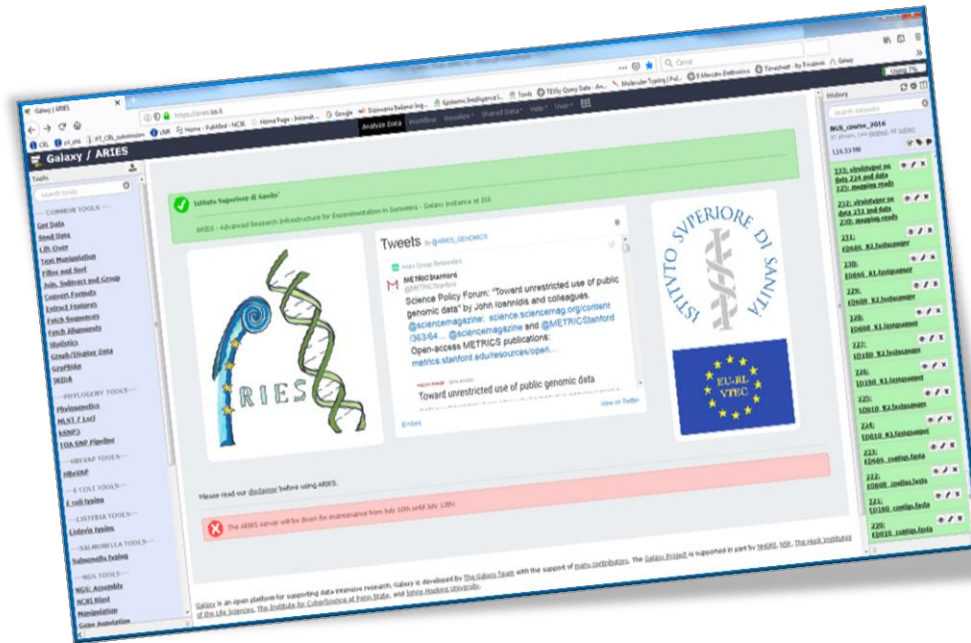


Introduction to the ARIES webserver user-interface



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Bioinformatics training,
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TOOLS SECTION

MAIN WINDOW

HISTORY SECTION (UPLOAD & RESULTS)

Galaxy / ARIES

Tools

- COMMON TOOLS
- Get Data
- Send Data
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Statistics
- Graph/Display Data
- GraphLAN
- IRIDA
- PHYLOGENY TOOLS
- Phylogenetics
- MLST 7 Loci
- kSNP3
- FDA SNP Pipeline
- HREVP TOOLS
- HReVAP
- E COLI TOOLS
- E coli typing
- LISTERIA TOOLS
- Listeria typing
- SALMONELLA TOOLS
- Salmonella typing
- NGS TOOLS
- GS: Assembly
- NCBI Blast
- Manipulation
- Gene annotation

Istituto Superiore di Sanità

ARIES - Advanced Research Infrastructure for Experimentation in Genomics - Galaxy Instance at ISS

Tweets by @ARIES_GENOMICS

METRICStanford @METRICStanford

Science Policy Forum: "Toward unrestricted use of public genomic data" by John Ioannidis and colleagues. @sciencemagazine: science.sciencemag.org/content/363/64... @sciencemagazine and @METRICStanford Open-access METRICS publications: metrics.stanford.edu/resources/open...

POLICY FORUM DATA ACCESS

Toward unrestricted use of public genomic data

Please read our [disclaimer](#) before using ARIES.

The ARIES server will be down for maintenance from July 10th until July 12th!

History

NGS_course_2016

233: virulotyper on data 224 and data 225: mapping reads

232: virulotyper on data 231 and data 230: mapping reads

231: ED666_R2.fastasanger

230: ED666_R1.fastasanger

229: ED608_R2.fastasanger

228: ED608_R1.fastasanger

227: ED180_R2.fastasanger

226: ED180_R1.fastasanger

225: ED010_R2.fastasanger

224: ED010_R1.fastasanger

223: ED666_contigs.fasta

222: ED608_contigs.fasta

221: ED180_contigs.fasta

220: ED010_contigs.fasta

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



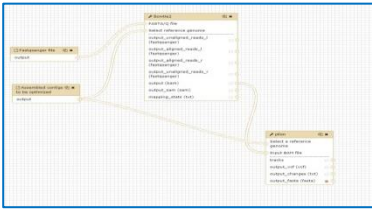
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Is used for going back to home (main screen)

Workflow




Can be used for a customized pipeline, by selecting specific tools

Shared Data



Can be used for share data libraries, histories, workflows, visualizations, pages

User



For login/logout



Edit attributes

Attributes Convert Format Datatype Permissions

Edit Attributes

Name:

Info:

Annotation / Notes:

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

Database/Build:

This will inspect the dataset and attempt to correct the above column values if they are not accurate.

Attributes

**IT CAN BE USED TO
CHANGE THE FILE
NAME**



Edit attributes

Attributes Convert Format Datatype

Change data type

New Type:

fastqsanger

etandem

excel

fasta

fastq

fastq.bz2

fastq.gz

fastqc ssanger

fastqillumina

fastqsanger

Datatype

- ✓ **SPECIFY THE DATA FORMAT**
- ✓ **All NGS platforms produce data in the same .fastq format, using the same ASCII code for PHRED scores (.fastqsanger).**
- ✓ **However, some tools require the use with declared data type .fastqsanger**
- ✓ **ALWAYS SET THE DATATYPE OF SEQUENCING READS FILES AS .fastqsanger**
- ✓ **E.g. from «.txt» to «.tabular»**

FILES DETAILS FROM THE HISTORY

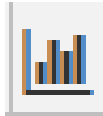
Download



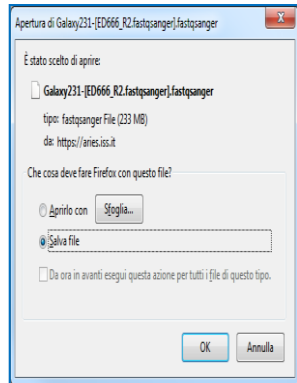
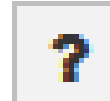
View details



Visualize in charts



Tool Help



Upload File

Dataset Information

Number:	231
Name:	ED666_R2.fastqsanger
Created:	Thu 10 Jun 2015 12:35:54 (UTC)
Release:	2015-10
Owner:	?
Format:	fastqsanger

Job Information

Galaxy Tool ID:	galaxytool
Galaxy Tool Version:	1.14
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
History Command #1 ID:	galaxytool-galaxy
Job #1 ID:	91020946230
History #1 ID:	91020946230
UUID:	ed6666-487-444-8c4-dba4edc734

Tool Parameters

Input Parameter	Value	Help/Source
File Format:	fastqsanger	
auto_stats:	None	
Split Files by Dataset (fastqsanger):	1 split(s) dataset	
Genome:	unspecified(?)	
File Format:	fastqsanger	

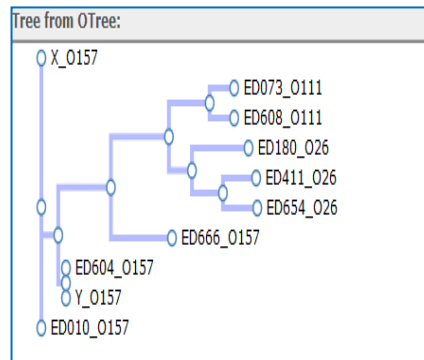
Inheritance Chain

ED666_R2.fastqsanger

↑

ED666_R2.fastqsanger (Data Store)

IN CASE OF THE USE OF TOOLS FOR SOME GRAFIC VISUALIZATION (TREES)



231:

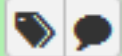


ED666_R2.fastqsanger

233.5 MB

format: **fastqsanger**, database: ?

uploaded fastqsanger file



```

@FCC4GB4AOX:4:1101:1743:2181#TGGAACAAA/2
TCCTTGATTGAAATTGCGTATCGAAAAACAGCATCTAAAGGTG
+
giiiiihhiiiiiiiiiiiiiiiiidgFhhhdggihegeg
@FCC4GB4AOX:4:1101:3036:2166#TGGAACAAA/2
AACGTCTTTCATCACAACCTCGCACCAATTAACAGTGCAATA
  
```

Edit dataset tags

Edit dataset annotation



View details



FOR THE DATA OBTAINED AS RESULTS OF TOOLS, YOU CAN SEE THE INFORMATION OF THE INPUT DATA, OF THE PROGRAM USED AND ALL THE DETAILS OF THE ANALISYS PERFORMED

FastQC

Dataset Information

Number:	330
Name:	FastQC on data 224: Webpage
Created:	Wed 06 Jun 2018 03:44:42 PM (UTC)
Filesize:	261.7 KB
Dbkey:	?
Format:	html

Job Information

Galaxy Tool ID:	toolshed.g2.bx.psu.edu/repos/devteam/fastqc/fastqc/0.63
Galaxy Tool Version:	0.63
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
History Content API ID:	7cf35be4dbb893b9
Job API ID:	9e076c25ae61799a
History API ID:	95919c4f4d1df5e1
UUID:	1fc7040e-e416-4b41-8731-a36d6fb4dd80

Tool Parameters

Input Parameter	Value	Note for rerun
Short read data from your current history	224: ED010_R1.fastqsanger	
Contaminant list		
Submodule and Limit specifying file		

Inheritance Chain

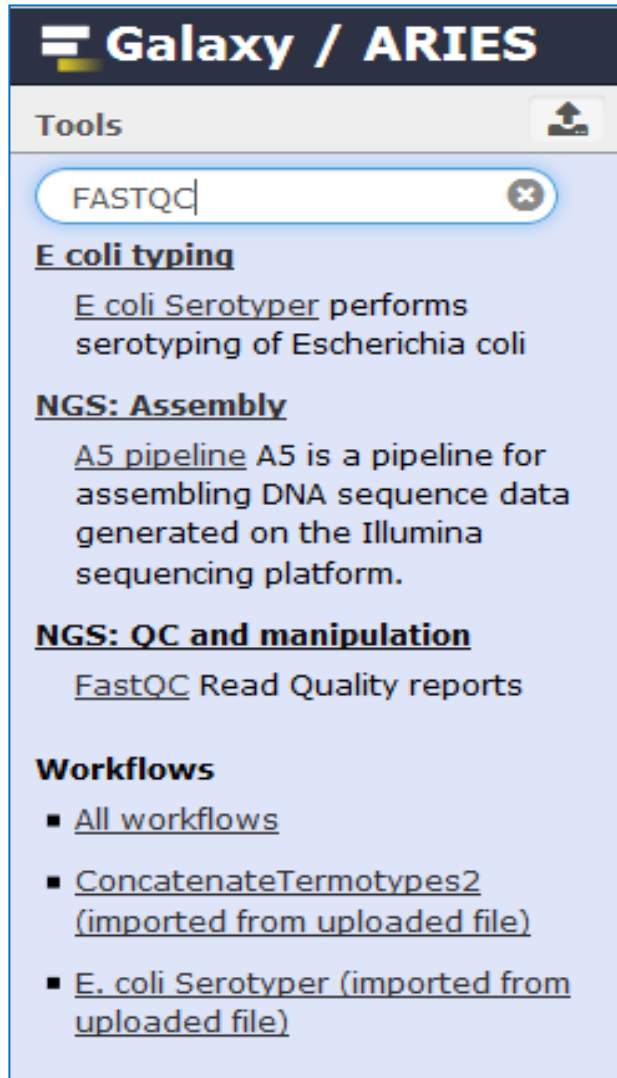
FastQC on data 224: Webpage

Job Dependencies

Dependency	Dependency Type	Version
FastQC	tool_shed_package	0.11.2



HOW TO FIND THE TOOLS



The screenshot shows the Galaxy / ARIES interface. At the top, there is a header with the text "Galaxy / ARIES" and a hamburger menu icon. Below the header is a "Tools" section with a search bar containing the text "FASTQC". The search results are categorized into several sections: "E coli typing" with a link to "E coli Serotyper" (described as performing serotyping of Escherichia coli), "NGS: Assembly" with a link to "A5 pipeline" (described as a pipeline for assembling DNA sequence data generated on the Illumina sequencing platform), "NGS: QC and manipulation" with a link to "FastQC" (described as Read Quality reports), and "Workflows" with a list of three items: "All workflows", "ConcatenateTermotypes2 (imported from uploaded file)", and "E. coli Serotyper (imported from uploaded file)".

In the tool section, you can select the tool needed by typing the name of the tool in the search section

**In the main window you will see the window for selecting the files to be analyzed by the chosen tool (scroll from the menu or type the correct name of the file uploaded in the history).
Once all the fields have been filled, click on Execute and check the colours in the history window...**

FastQC Read Quality reports (Galaxy Version 0.63) Options

Short read data from your current history

302: SRST2-7loci Alignment File

Contaminant list

Nothing selected

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

Submodule and Limit specifying file

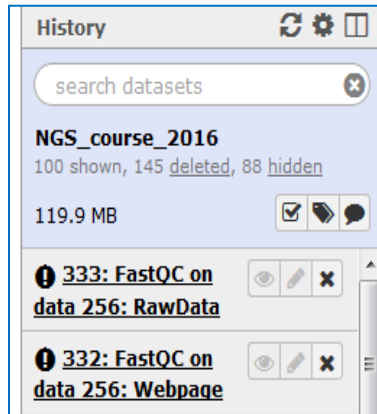
Nothing selected

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

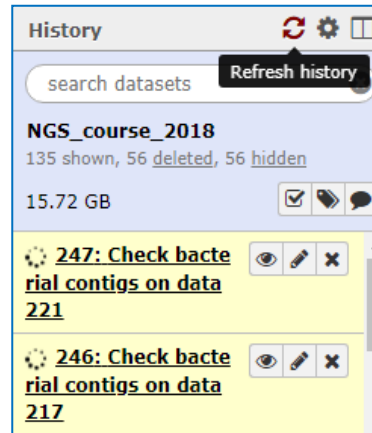
Execute

THE COLOURS OF THE HISTORY WHEN YOU RUN THE TOOLS

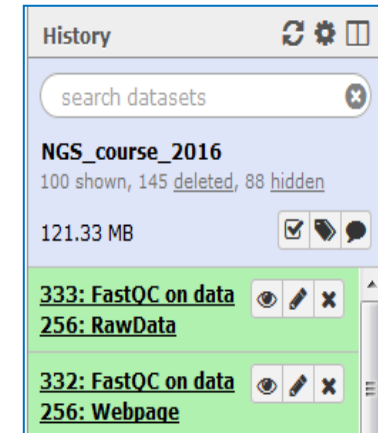
GRAY



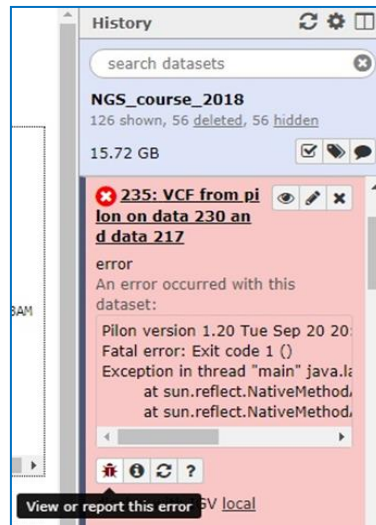
YELLOW



GREEN



RED



In the HISTORY section, you can select the FILE needed by typing the name of the FILE in the search section



View or report this error

Dataset generation errors

Dataset 235: VCF from pilon on data 230 and data 217

Tool execution generated the following error message:

```
Fatal error: Exit code 1 ()
Exception in thread "main" java.lang.reflect.InvocationTargetException
    at sun.reflect.NativeMethodAccessorImpl.invoke0(Native Method)
    at sun.reflect.NativeMethodAccessorImpl.invoke(NativeMethodAccessorImpl.java:62)
    at sun.reflect.DelegatingMethodAccessorImpl.invoke(DelegatingMethodAccessorImpl.java:43)
    at java.lang.reflect.Method.invoke(Method.java:498)
    at com.simontuffs.onejar.Boot.run(Boot.java:340)
    at com.simontuffs.onejar.Boot.main(Boot.java:166)
Caused by: java.lang.IllegalArgumentException: requirement failed: /afs/galaxy/database/files/000/126/dataset_126490.dat must be indexed BAM
    at scala.Predef$.require(Predef.scala:224)
    at org.broadinstitute.pilon.BamFile.<init>(BamFile.scala:47)
    at org.broadinstitute.pilon.Pilon$.optionParse(Pilon.scala:122)
    at org.broadinstitute.pilon.Pilon$.main(Pilon.scala:72)
    at org.broadinstitute.pilon.Pilon.main(Pilon.scala)
    ... 6 more
```

The tool produced the following additional output:

```
Pilon version 1.20 Tue Sep 20 20:40:09 2016 -0400
```

History

search datasets

NGS_course_2018

126 shown, 56 deleted, 56 hidden

15.72 GB

235: VCF from pilon on data 230 and data 217

error

An error occurred with this dataset:

```
Pilon version 1.20 Tue Sep 20 20:40:09 2016 -0400
Fatal error: Exit code 1 ()
Exception in thread "main" java.lang.reflect.InvocationTargetException
    at sun.reflect.NativeMethodAccessorImpl.invoke0(Native Method)
    at sun.reflect.NativeMethodAccessorImpl.invoke(NativeMethodAccessorImpl.java:62)
    at sun.reflect.DelegatingMethodAccessorImpl.invoke(DelegatingMethodAccessorImpl.java:43)
    at java.lang.reflect.Method.invoke(Method.java:498)
    at com.simontuffs.onejar.Boot.run(Boot.java:340)
    at com.simontuffs.onejar.Boot.main(Boot.java:166)
```

View or report this error

234: FASTA from pilon on data 229 and data 217

Click on «View or report this error» and copy the text from the main window, then past and send the text to **aries@iss.it**

or

“Report this error to the local Galaxy administrators”



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hands
on



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