Introduction to the ARIES webserver user-interface

Istituto Superiore di Sanita'

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

Tweets by @ARIES_GENOMICS

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...

Toward unrestricted use of public genomic data

View on Twitter

Embed

Please read our disclaimer before using ARIES.

The ARIES server will be down for maintenance from July 10th until July 13th

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, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Johns Hopkins University.

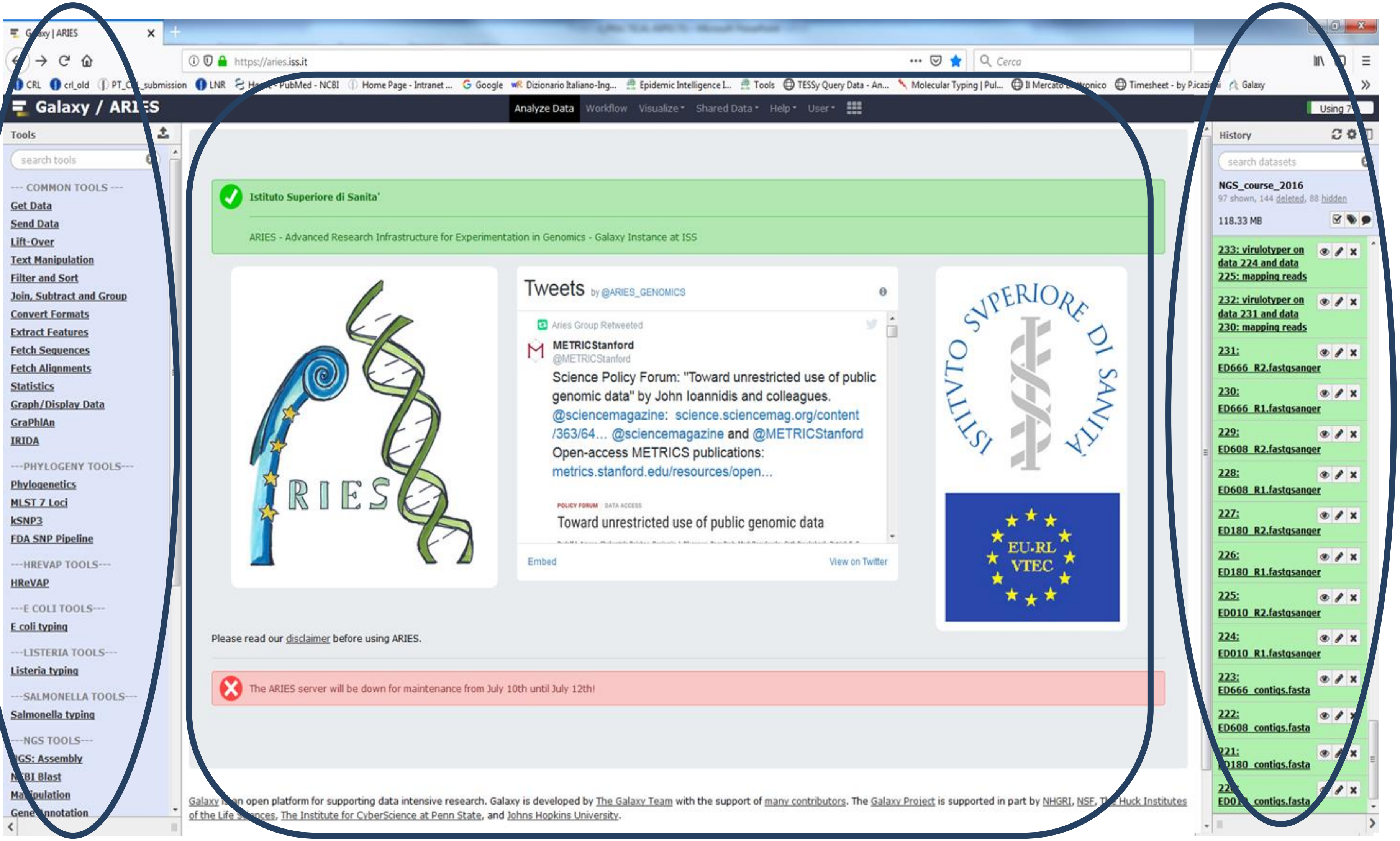
Antonella Maugliani

WGS course,
October 2020

TOOLS SECTION

MAIN WINDOW

HISTORY SECTION (UPLOAD & RESULTS)



Istituto Superiore di Sanita'

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

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...

Toward unrestricted use of public genomic data

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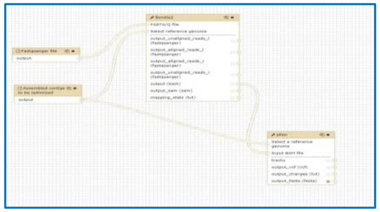
Is used for going back to home (main screen)

Workflow



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

Shared Data

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

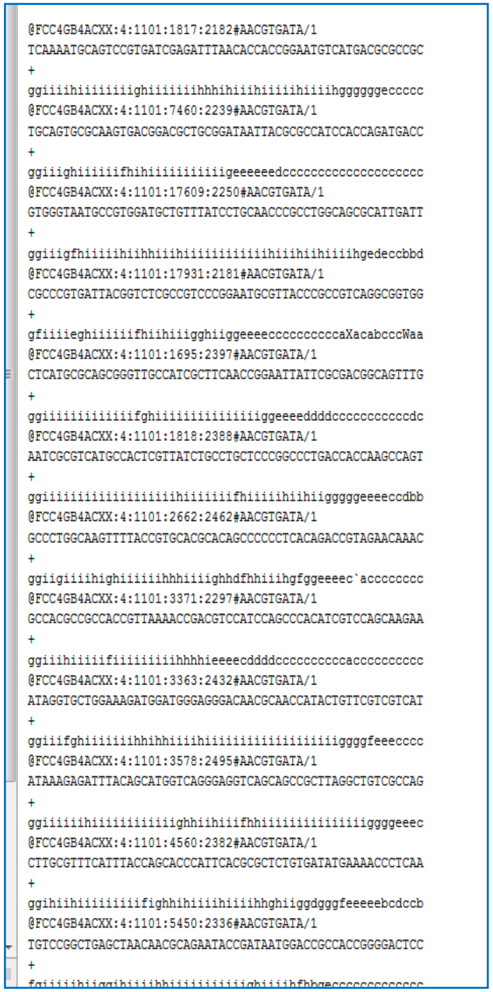
User

For login/logout

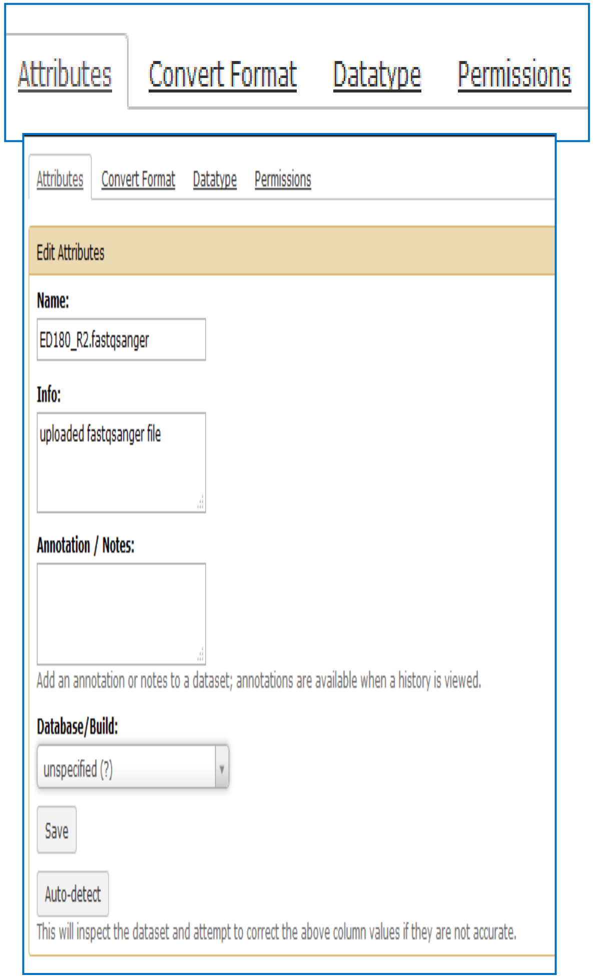
View data and analysis results

Edit attributes

delete



```
@FCC4GB4ACXX:4:1101:1817:2182#AACGTGATA/1
TCAAAATGCAGTCCGTGATCGAGATTTAACACCACCGGAATGTCATGACGCGCCGC
+
ggiiiihiiiiiiiighiiiiiiihhhihiiihiiiiihiiiihggggggeccccc
@FCC4GB4ACXX:4:1101:7460:2239#AACGTGATA/1
TGCAGTGCGCAAGTGACGGACGCTGCGGATAATTACGCGCCATCCACCAGATGACC
+
ggiiighiiiiiifhihiiiiiiiiiiigeeeeeedcccccccccccccccccccc
@FCC4GB4ACXX:4:1101:17609:2250#AACGTGATA/1
GTGGGTAATGCCGTGGATGCTGTTTATCCTGCAACCCGCCTGGCAGCGCATTGATT
+
ggiiigfhiiiiihiihhiiihiiiiiiiiiiiiihiiihiihiiiihgedeccbbd
@FCC4GB4ACXX:4:1101:17931:2181#AACGTGATA/1
CGCCCGTGATTACGGTCTCGCCGTCCCGGAATGCGTTACCCGCCGTCAGGCGGTGG
+
gfiiiieghiiiiiifhiihiiigghiiggeeeeccccccccccaXacabcccWaa
@FCC4GB4ACXX:4:1101:1695:2397#AACGTGATA/1
CTCATGCGCAGCGGGTTGCCATCGCTTCAACCGGAATTATTCGCGACGGCAGTTTG
+
ggiiiiiiiiiiiifghiiiiiiiiiiiiiiiggeeeeddddcccccccccccdc
@FCC4GB4ACXX:4:1101:1818:2388#AACGTGATA/1
AATCGCGTCATGCCACTCGTTATCTGCCTGCTCCCGGCCCTGACCACCAAGCCAGT
+
ggiiiiiiiiiiiiiiiiiiiiihiiiiiiiifhiiiiihiihiigggggeeeeccdbb
@FCC4GB4ACXX:4:1101:2662:2462#AACGTGATA/1
GCCCTGGCAAGTTTTACCGTGCACGCACAGCCCCCCTCACAGACCGTAGAACAAAC
+
ggiigiiiihighiiiiiihhhiiiighhdfhhiiihgfggeeeec`acccccccc
@FCC4GB4ACXX:4:1101:3371:2297#AACGTGATA/1
GCCACGCCGCCACCGTTAAAACCGACGTCCATCCAGCCCACATCGTCCAGCAAGAA
+
ggiiihiiiiifiiiiiiiiiihhhhieeeecddddcccccccccccaccccccccccc
@FCC4GB4ACXX:4:1101:3363:2432#AACGTGATA/1
ATAGGTGCTGGAAAGATGGATGGGAGGGACAACGCAACCATACTGTTCGTCGTCAT
+
ggiiifghiiiiiiihhihhiiiihiiiiiiiiiiiiiiiiiiiggggfeeecccc
@FCC4GB4ACXX:4:1101:3578:2495#AACGTGATA/1
ATAAAGAGATTTACAGCATGGTCAGGGAGGTCAGCAGCCGCTTAGGCTGTCGCCAG
+
ggiiiiiihiiiiiiiiiiiiighhiihiiifhhiiiiiiiiiiiiiiiiggggeeec
@FCC4GB4ACXX:4:1101:4560:2382#AACGTGATA/1
CTTGCGTTTCATTTACCAGCACCCATTCACGCGCTCTGTGATATGAAAACCCTCAA
+
ggihiihiiiiiiiiiifighhihiiiihiiiihhghiiggdgggfeeeeebcdccb
@FCC4GB4ACXX:4:1101:5450:2336#AACGTGATA/1
TGTCCGGCTGAGCTAACAACGCAGAATACCGATAATGGACCGCCACCGGGGACTCC
+
```



Name: ED180_R2.fastqsanger

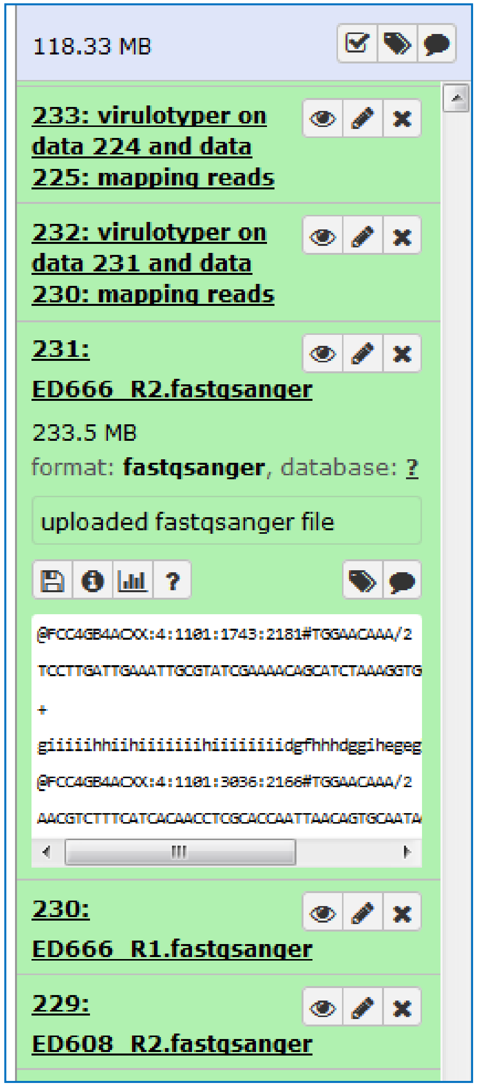
Info: uploaded fastqsanger file

Annotation / Notes:

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

Database/Build: unspecified (?)

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



118.33 MB

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

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

231: ED666_R2.fastqsanger

233.5 MB

format: **fastqsanger**, database: **?**

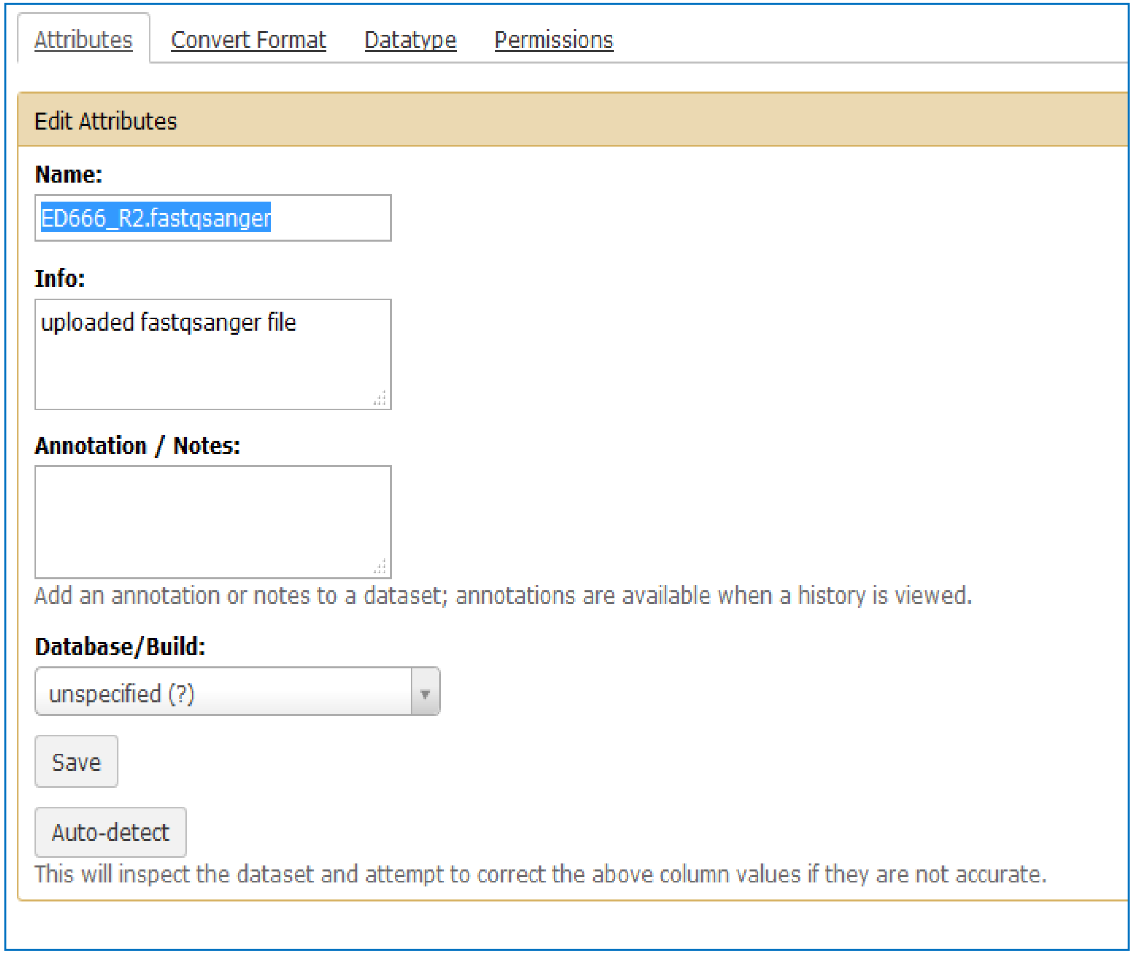
uploaded fastqsanger file

```
@FCC4GB4ACXX:4:1101:1743:2181#TGGAACAAA/2
TCCTTGATTGAAATTGCGTATCGAAAACAGCATCTAAAGGTG
+
giiiiihhiihiiiiiiihiiiiiiiiidgfhhhdggihegeg
@FCC4GB4ACXX:4:1101:3036:2166#TGGAACAAA/2
AACGTCTTTCATCACAACCTCGCACCAATTAACAGTGCAATA
```

230: ED666_R1.fastqsanger

229: ED608_R2.fastqsanger

Edit attributes



Edit Attributes

Name: ED666_R2.fastqsanger

Info: uploaded fastqsanger file

Annotation / Notes:

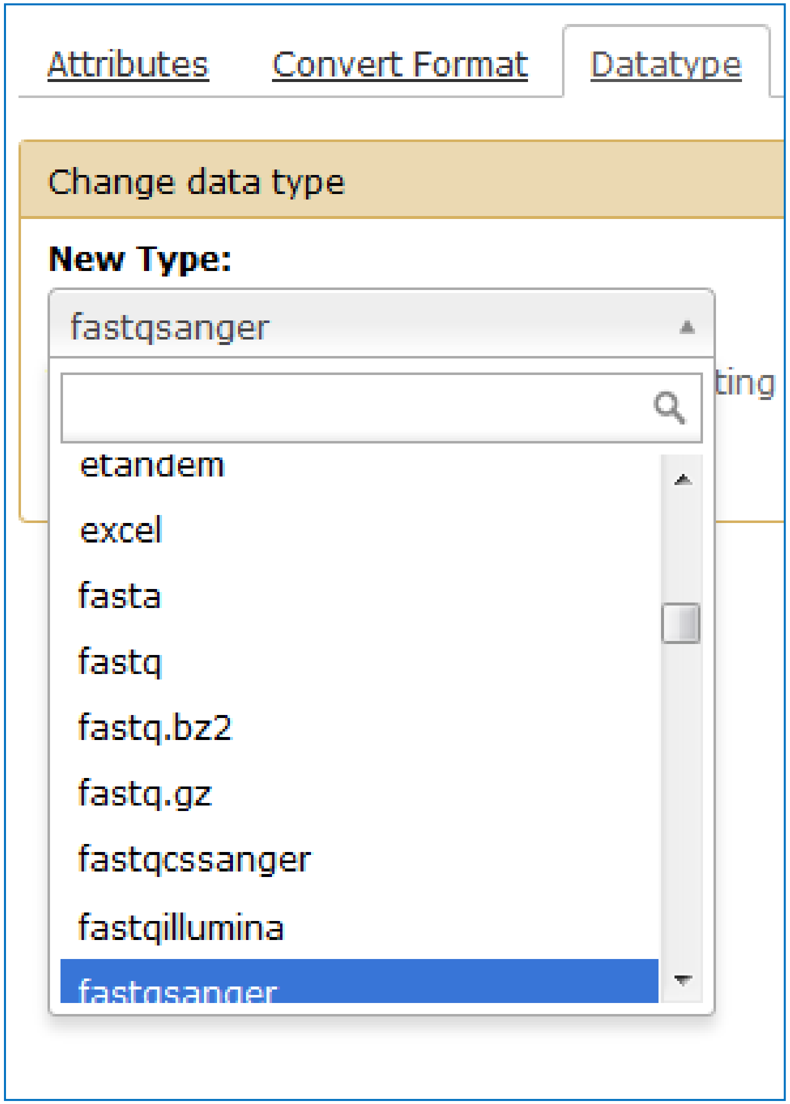
Add an annotation or notes to a dataset; annotations are available when a history is viewed.

Database/Build: unspecified (?)

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

IT CAN BE USED TO CHANGE THE FILE NAME

Edit attributes

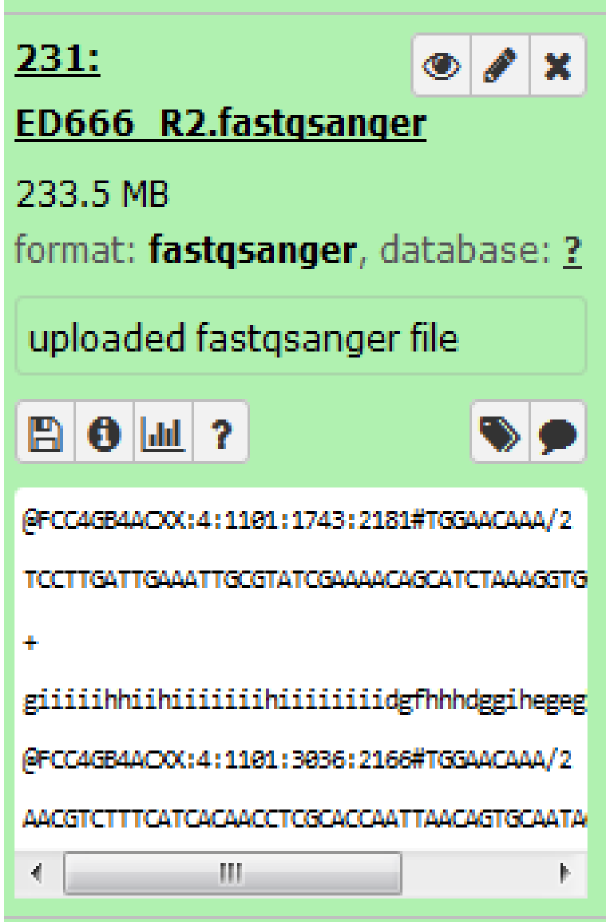


Change data type

New Type: fastqsanger

- ✓ **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



231: ED666_R2.fastqsanger

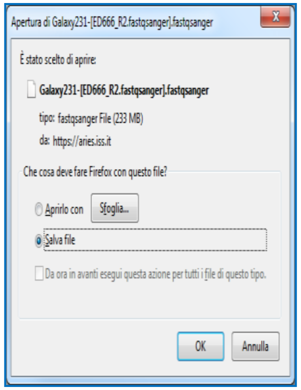
233.5 MB

format: **fastqsanger**, database: **?**

uploaded fastqsanger file

```
@FCC4GB4ACXX:4:1101:1743:2181#TGGAACAAA/2
TCCTTGATTGAAATTGCGTATCGAAAACAGCATCTAAAGGTG
+
giiiiihhiihiiiiiiihiiiiiiiidgfhhhdggihegeg
@FCC4GB4ACXX:4:1101:3036:2166#TGGAACAAA/2
AACGTCTTTCATCACAACCTCGCACCAATTAACAGTGCAATA
```

Download **View details** **Visualize in charts** **Tool Help**



Apertura di Galaxy231-[ED666_R2.fastqsanger].fastqsanger

È stato scelto di aprire:

Galaxy231-[ED666_R2.fastqsanger].fastqsanger

tipo: fastqsanger File (233 MB)

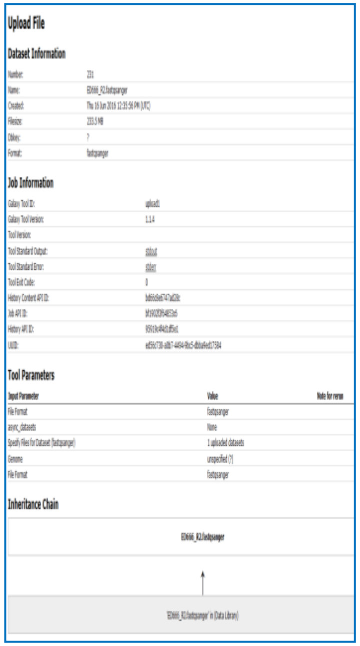
da: https://aries.iss.it

Che cosa deve fare Firefox con questo file?

○ Aprirlo con Sfoglia...

● Salva file

☐ Da ora in avanti esegui questa azione per tutti i file di questo tipo.



Upload File

Dataset Information

Number:	231
Name:	ED666_R2.fastqsanger
Created:	Thu 16 Jun 2016 12:35:56 PM (UTC)
Filesize:	233.5 MB
Dbkey:	?
Format:	fastqsanger

Job Information

Galaxy Tool ID:	upload1
Galaxy Tool Version:	1.1.4
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
History Content API ID:	[illegible]
Job API ID:	[illegible]
History API ID:	[illegible]
UUID:	[illegible]

Tool Parameters

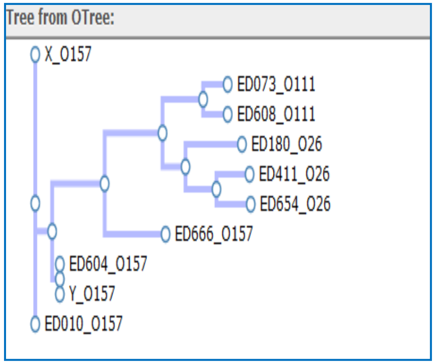
Input Parameter	Value	Note for rerun
File Format	fastqsanger	
async_datasets	None	
Specify Files for Dataset (fastqsanger)	1 uploaded datasets	
Genome	unspecified (?)	
File Format	fastqsanger	

Inheritance Chain

ED666_R2.fastqsanger

'ED666_R2.fastqsanger' in (Data Library)

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

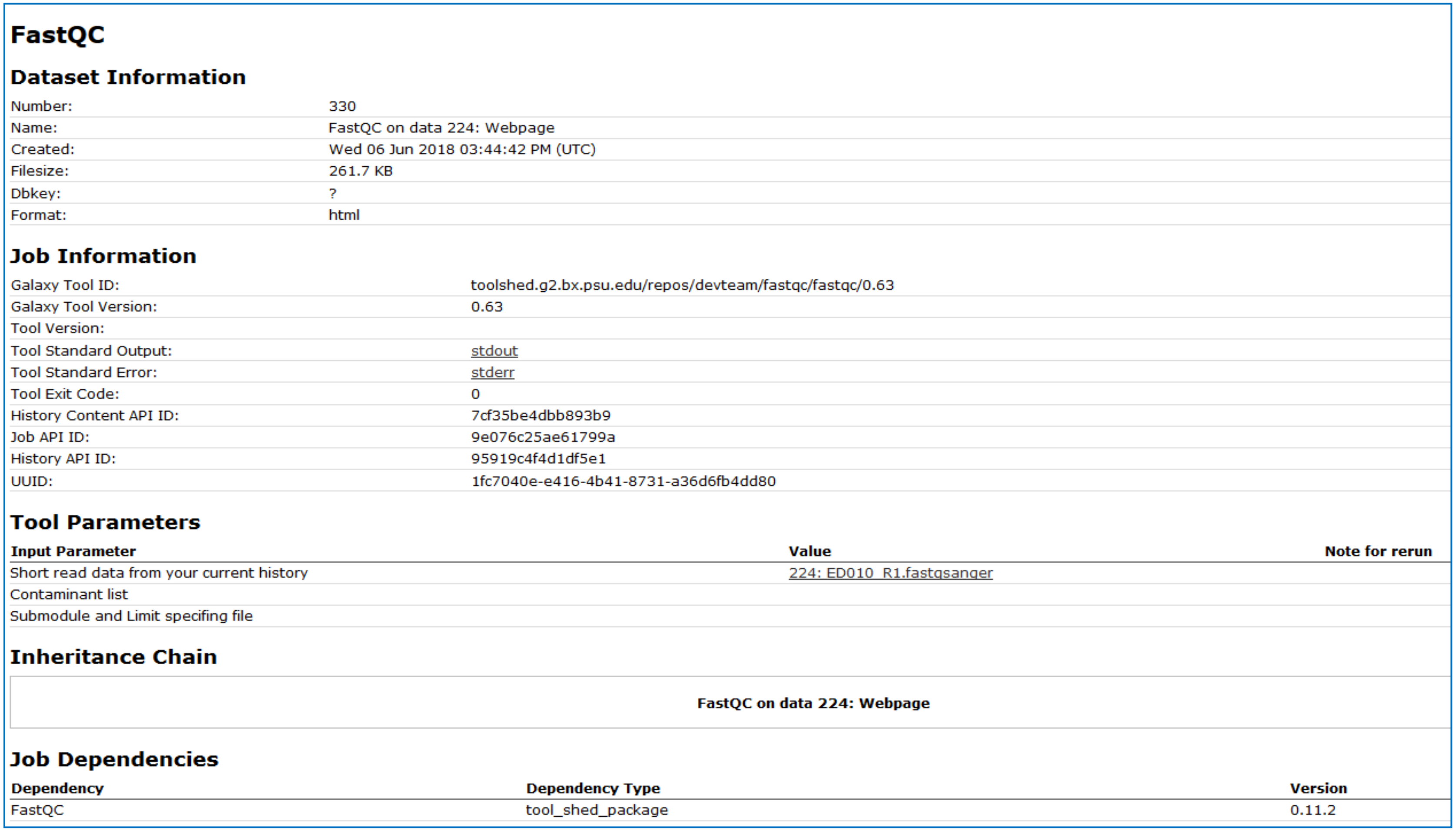


Tree from OTree:

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 specifing file		

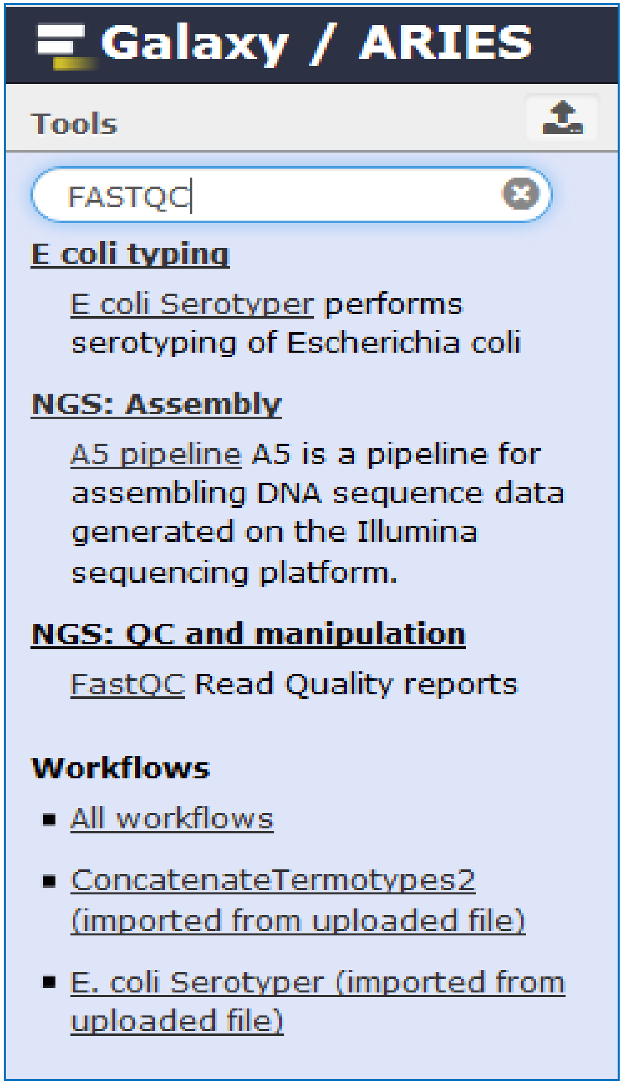
Inheritance Chain

FastQC on data 224: Webpage

Job Dependencies

Dependency	Dependency Type	Version
FastQC	tool_shed_package	0.11.2

HOW TO FIND THE TOOLS



Galaxy / ARIES

Tools

FASTQC

E coli typing

E coli Serotyper performs serotyping of Escherichia coli

NGS: Assembly

A5 pipeline A5 is a pipeline for assembling DNA sequence data generated on the Illumina sequencing platform.

NGS: QC and manipulation

FastQC Read Quality reports

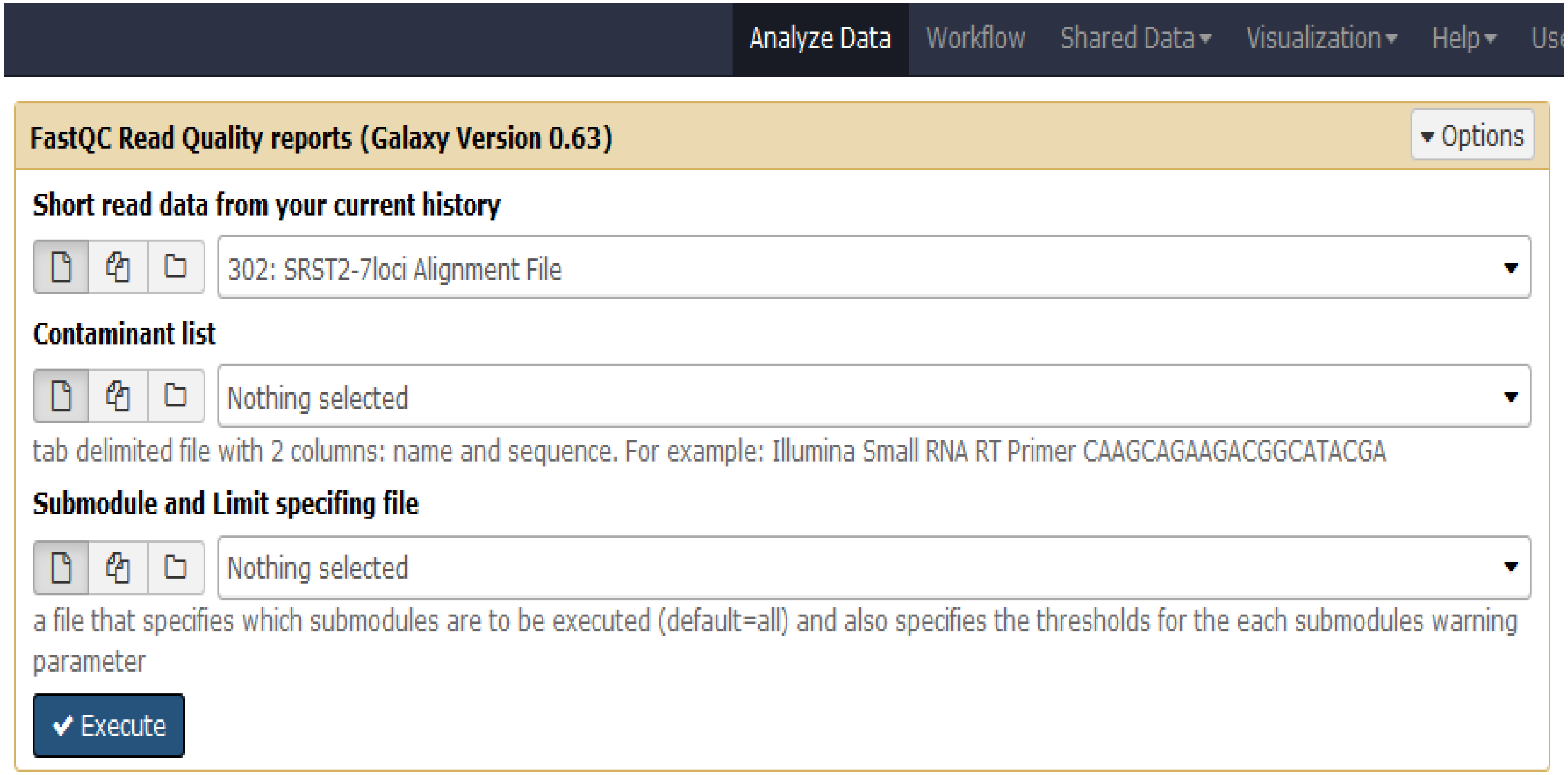
Workflows

- All workflows
- ConcatenateTermotypes2 (imported from uploaded file)
- 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)

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

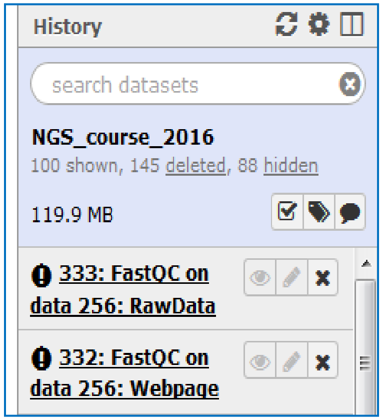
Submodule and Limit specifing file

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

THE COLOURS OF THE HISTORY WHEN YOU RUN THE TOOLS

GRAY



History

search datasets

NGS_course_2016

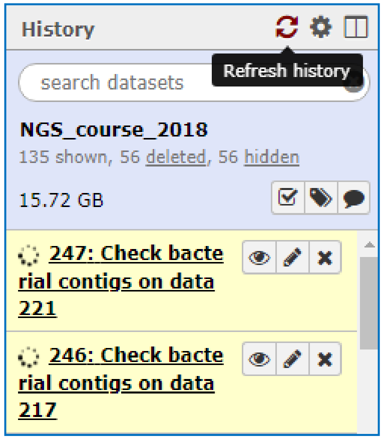
100 shown, 145 deleted, 88 hidden

119.9 MB

333: FastQC on data 256: RawData

332: FastQC on data 256: Webpage

YELLOW



History

Refresh history

search datasets

NGS_course_2018

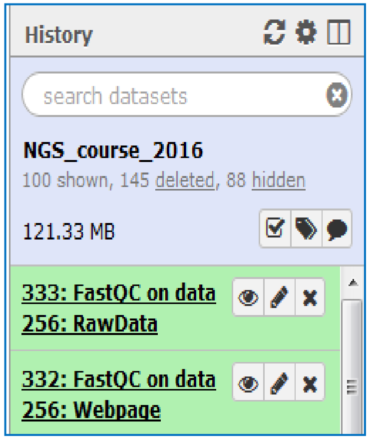
135 shown, 56 deleted, 56 hidden

15.72 GB

247: Check bacterial contigs on data 221

246: Check bacterial contigs on data 217

GREEN



History

search datasets

NGS_course_2016

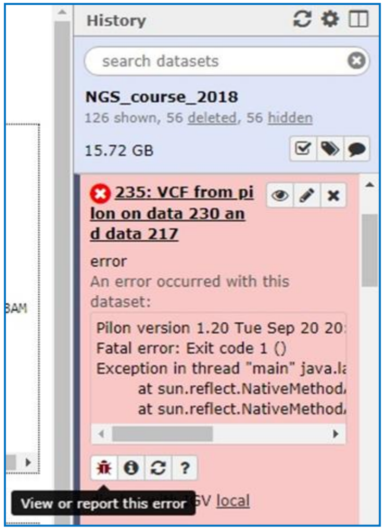
100 shown, 145 deleted, 88 hidden

121.33 MB

333: FastQC on data 256: RawData

332: FastQC on data 256: Webpage

RED



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:

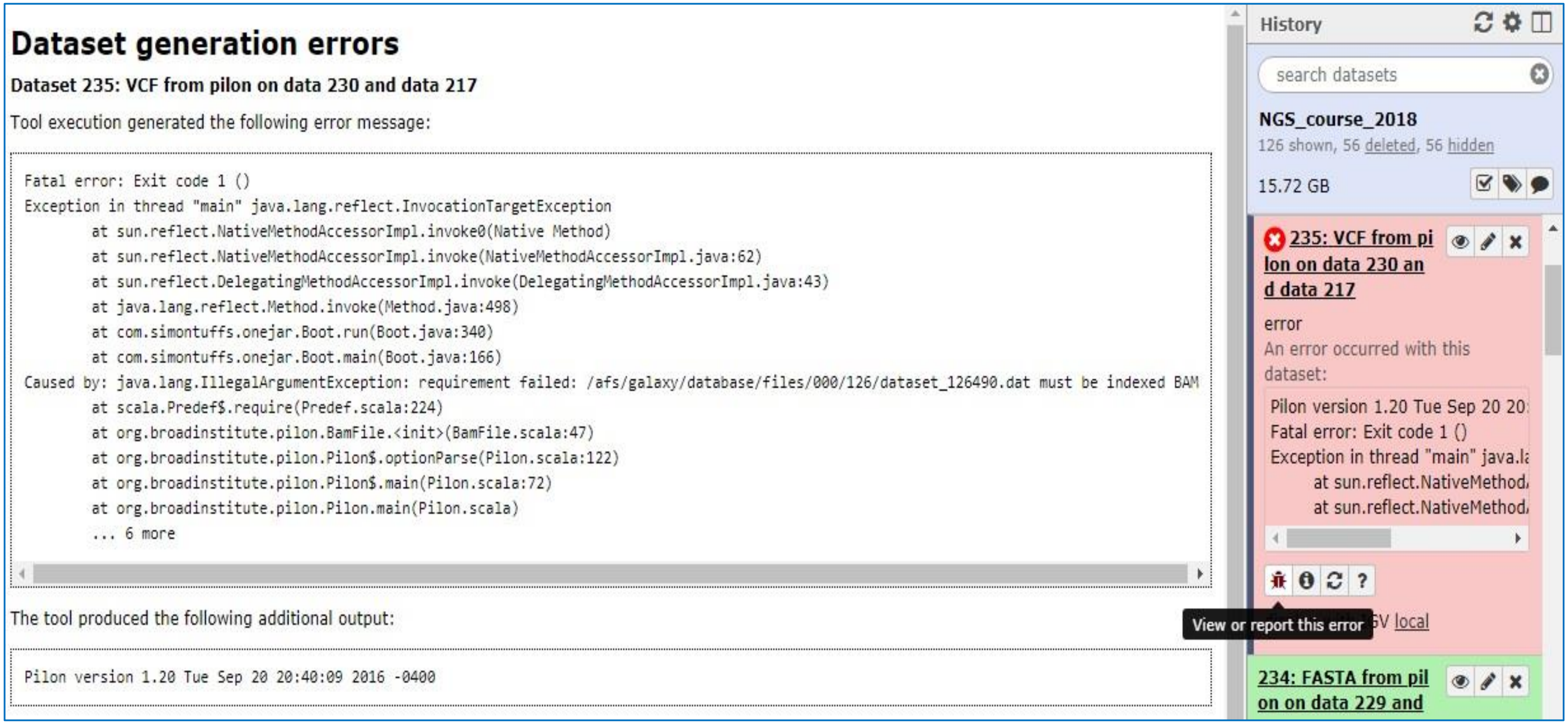
```
Pilon version 1.20 Tue Sep 20 20:
Fatal error: Exit code 1 ()
Exception in thread "main" java.l
        at sun.reflect.NativeMethod
        at sun.reflect.NativeMethod
```

View or report this error

local

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
```

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”