

ARIES WEB INTERFACE

TOOLS SECTION

MAIN WINDOW

HISTORY SECTION (UPLOAD & RESULTS)

Galaxy / ARIES

Analyze Data Workflow Shared Data Visualization Help User

Using %

Tools

search 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
- GraphAn
- Phylogenetics

---HREVAP TOOLS---

HReVAP

---NGS TOOLS---

- E coli typing
- NGS: Assembly
- NCBI Blast
- Manipulation
- Gene Annotation
- FASTA/FASTQ manipulation
- NGS: Mapping
- NGS: SAM Tools
- NGS: BED Tools
- NGS: RNA Analysis
- NGS: QC and manipulation

---METAGENOMICS TOOLS---

- MetaGenomics
- Commet
- QIIME
- IRIDA

Workflows

Istituto Superiore di Sanita'

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

Tweets by @ARIES_GENOMICS

Aries Group Retweeted

Genomics Education
@genomicsedu

Do you know the ins and outs of whole genome sequencing and NGS technology? Whatever your background, sign up now for our free online course in September to learn more about them and how they're used in healthcare: socs.in/Q2lri #genomics #genomes100k

Embed View on Twitter

Wonderful course!
Something that

ISTITUTO SUPERIORE DI SANITA'

EU.RL VTEC

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

FTP is now available for data upload at ariesftp.iss.it (explicit FTP over TLS)

Take an interactive tour: [Galaxy UI](#) [History](#) [Scratchbook](#)

History

search datasets

NGS_course_2016
97 shown, 144 deleted, 88 hidden
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
- 230: ED666_R1.fastqsanger
- 229: ED608_R2.fastqsanger
- 228: ED608_R1.fastqsanger
- 227: ED180_R2.fastqsanger
- 226: ED180_R1.fastqsanger
- 225: ED010_R2.fastqsanger
- 224: ED010_R1.fastqsanger
- 223: ED666_contigs.fasta
- 222: ED608_contigs.fasta
- 221: ED180_contigs.fasta
- 220: ED010_contigs.fasta

View data

Edit attributes

delete

```
@FCC4GB4ACXX:4:1101:1817:2182#AACGTGATA/1
TCAAAAATGCAGTCCGATCGAGATTAAACACCACCAGGATGTCATGACGCGCCGC
+
ggiiihiiiiiihghiiiiiihhhhiiiiiihiiiihggggggcccccc
@FCC4GB4ACXX:4:1101:7460:2239#AACGTGATA/1
TGCAGTGCAGGTCAGCGGCTGCGGATAATTACGGCCATCCACAGATGACC
+
ggiihghiiiiiihfhiiiiiiiiiieeeeeccccccccccccccccccc
@FCC4GB4ACXX:4:1101:17609:2250#AACGTGATA/1
GTGGTAATGCGGTGGATGCTGTATTATCTGCAACCOCCTGGCGCGCATTGATT
+
ggiiigfhiiiiifhiiiiiiiiiieeeeeccccccccccccccccccc
@FCC4GB4ACXX:4:1101:17931:2181#AACGTGATA/1
CGCGCGTGAATACGGTCTCGCGTCCCGGAATGCGTACCOCCTGAGCGGTTGG
+
gfiieeehiiiiifhiiiiigghiiieeeeecccccccccccacacbccWaa
@FCC4GB4ACXX:4:1101:1695:2397#AACGTGATA/1
CTCATGCGCAGCGGGTGCACATCGCTTCAACCGGAATTATCGGACGGCAGTTT
+
ggiiiiiiiiiiiiifghiiiiiiiiiiiggeeeedddccccccccccc
@FCC4GB4ACXX:4:1101:1818:2389#AACGTGATA/1
AATGCGTCATGCCACTGCTTCTGCTGCTCCCGGCTGACCCACCAAGCCAGT
+
ggiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiggggggcccccb
@FCC4GB4ACXX:4:1101:2662:2462#AACGTGATA/1
GCCCTGGCAAGTTTACCGTGCACGACAGCCCTCACAGCCGTAGAACAAAC
+
ggiiigiiiihghiiiiiihhhhiiiiigghdfhiiiihgfggeeeec' acccccccc
@FCC4GB4ACXX:4:1101:3371:2297#AACGTGATA/1
GCCACGCCACCACCTTAAAAACGAGCTCCATCCAGCCCATGCTCCAGCAAGA
+
ggiiihiiiiifiiiiiiiiihhhieeeeeccccccccccccccccccc
@FCC4GB4ACXX:4:1101:3363:2432#AACGTGATA/1
ATAGGTGCTGGAAAGATGGATGGAGGGAACAACGCAACATCTGCTGCTCAT
+
ggiiiifghiiiiiihhhhiiiiiiiiiiiiiiiiiiiiiiiggggfcccccc
@FCC4GB4ACXX:4:1101:3578:2495#AACGTGATA/1
ATAAAGAGATTACAGCATGGTCAGGAGGTCAGGAGCCCTTAGCTGTCGCCAG
+
ggiiiiihihiiiiiiiiiiiiiiigghiihiiiiiiiiiiiiiiiggggeeeec
@FCC4GB4ACXX:4:1101:4560:2382#AACGTGATA/1
CTTGCCTTCATTACAGCACCCATTACGCCCTCTGTGATATGAAAACCTCAA
+
gghiihiiiiiiiiifghiiiiiiiiiihhghiiigddgggfeeeeccccb
@FCC4GB4ACXX:4:1101:5450:2336#AACGTGATA/1
TGTCCGGCTGAGCTACRACGAGATACCGGATATGGACCACCAGGGGACTCC
+
fziiiihiigiiiihiiiiiiiiiiiiiiiiiihghiiifhbcccccccccccccc
```

Attributes Convert Format Datatype Permissions

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.

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: ?

```
@FCC4GB4A0OX:4:1101:1743:2181#TGSAACAAA/2
TCCTTGATTGAAATTGCSTATCGSAAAACAGCATCTAAAGSTG
+
giiiiihiiiiiiiiiiiiiiiiiiiiidgfhhhdggihegeg
@FCC4GB4A0OX:4:1101:3036:2166#TGSAACAAA/2
AACGTCTTTCATCACAACTCGCACCAATTAACAGTGAATA
```

230: ED666 R1.fastqsanger

229: ED608 R2.fastqsanger



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:

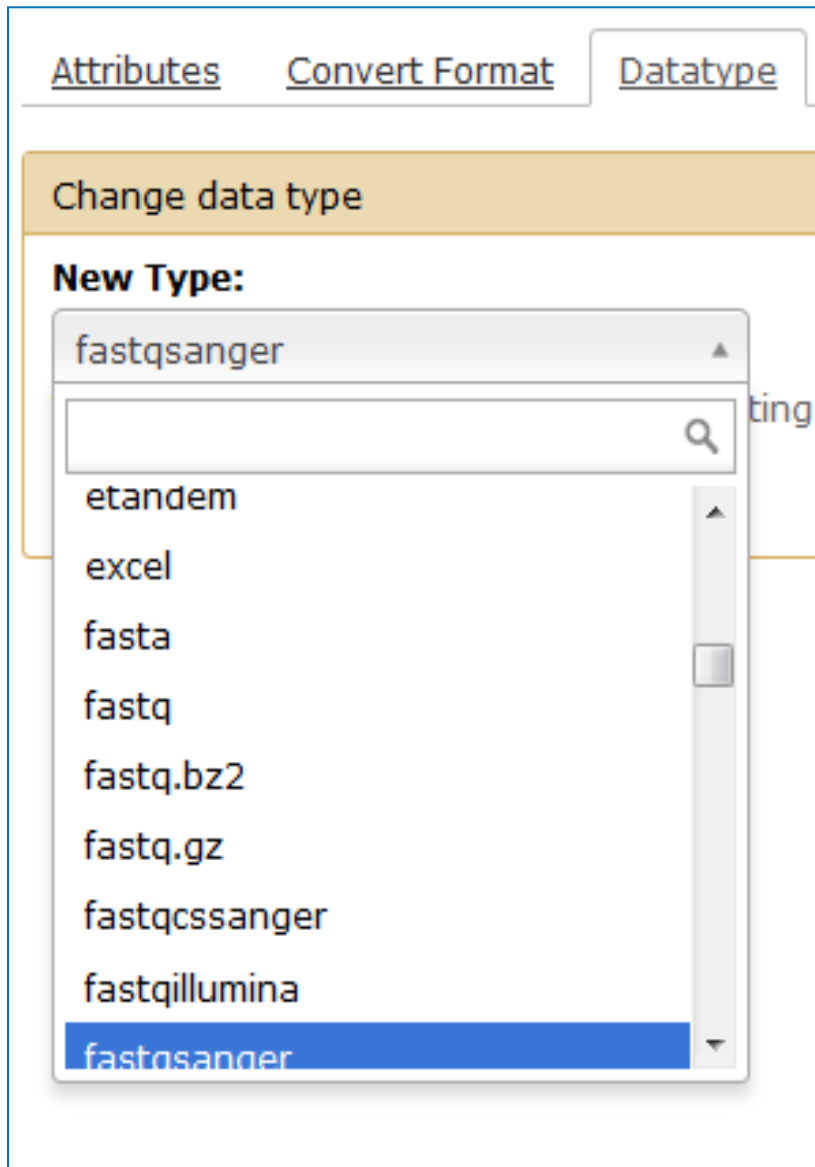
This will inspect the dataset and attempt to correct the above column values if they are not accurate.

Attributes

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



Edit attributes



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**

FILES DETAILS FROM THE HISTORY

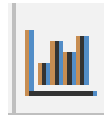
Download



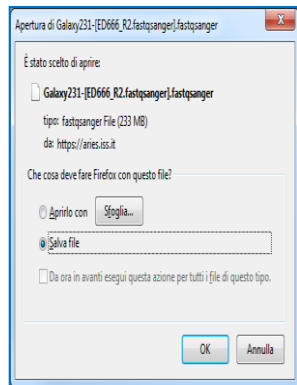
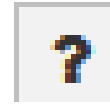
View details



Visualize in charts



Tool Help



Upload File

Dataset Information

Number:	231
Name:	ED666_R2.fastqsanger
Created:	Thu 10 Jun 2010 12:29:54 PM (UTC)
Filesize:	233.5 MB
Owner:	?
Format:	fastqsanger

Job Information

Galaxy Tool ID:	upload
Galaxy Tool Version:	1.14
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Tool Exit Code:	0
History Command #1 ID:	9d50d6747a26e
Job ABI ID:	9f02094626e
History #1 ID:	9f01a4626e
UUID:	ed6673a-487-449-84c-d846ed2704

Tool Parameters

Input Parameter	Value	Note for user
File Format:	fastqsanger	
allow_overwrite:	True	
Upload Files to Dataset (fastqsanger):	1 uploaded datasets	
Genome:	unspecified (*)	
File Format:	fastqsanger	

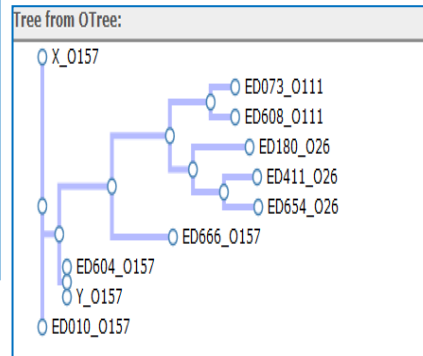
Inheritance Chain

ED666_R2.fastqsanger

↑

ED666_R2.fastqsanger in Data Library

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



231:

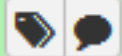
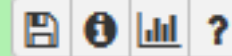


ED666_R2.fastqsanger

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
AACGTCTTTTCATCACAACCTCGACCAATTAACAGTGCAATA
```

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		

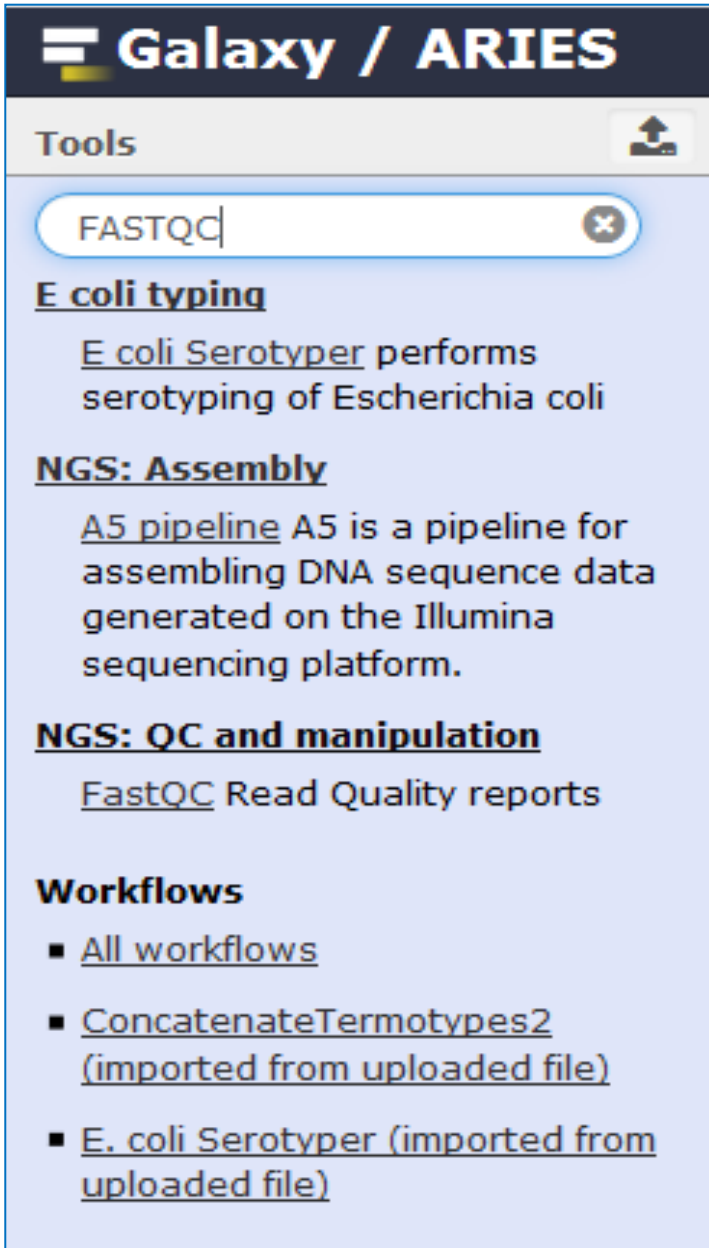
Inheritance Chain

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 dark header with the text "Galaxy / ARIES" and a hamburger menu icon. Below the header is a light gray bar labeled "Tools" with an upload icon. A search bar contains the text "FASTQC" and a close button. The search results are displayed in a light blue box and are organized into several sections:

- 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...

Analyze Data

Workflow

Shared Data ▾

Visualization ▾

Help ▾

Use

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

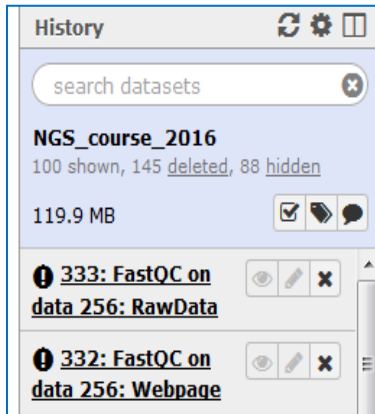
   Nothing selected ▾

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

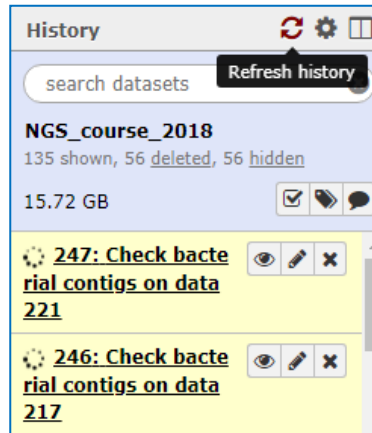
✓ Execute

THE COLOURS OF THE HISTORY WHEN YOU RUN THE TOOLS

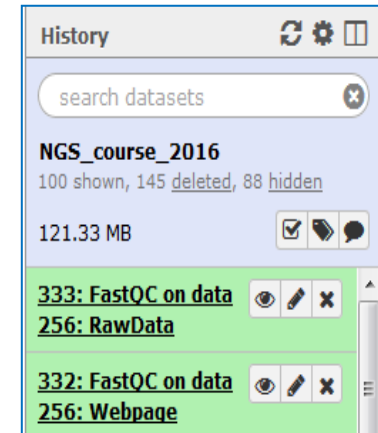
GRAY



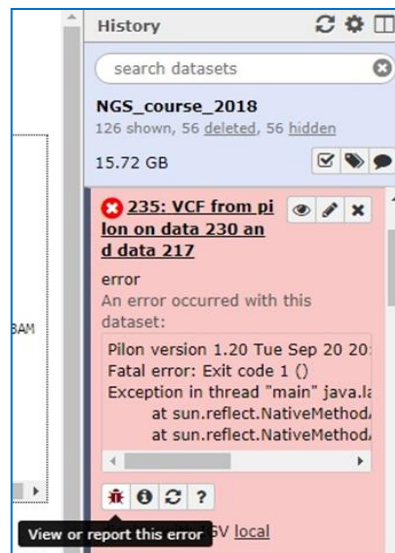
YELLOW



GREEN



RED





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)
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
```

View or report this error [local](#)

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”

