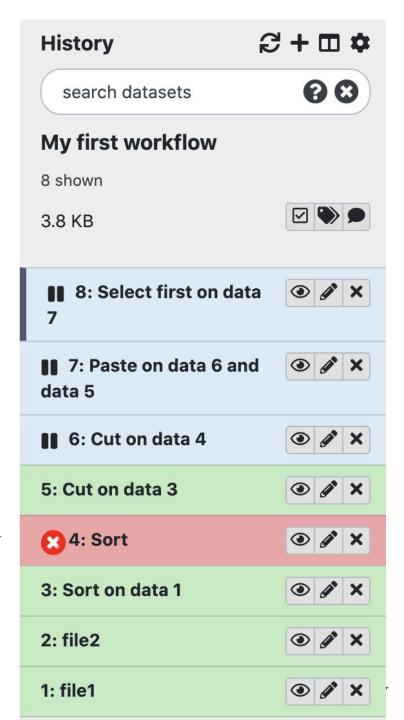
Report issues and how to get help

ELIXIR Norway, Norwegian e-infrastructure for Life Sciences and usegalaxy.no



When something goes wrong...

And we all know it does now and then.
What happens if we run "My first workflow" and forget to send in file 2?

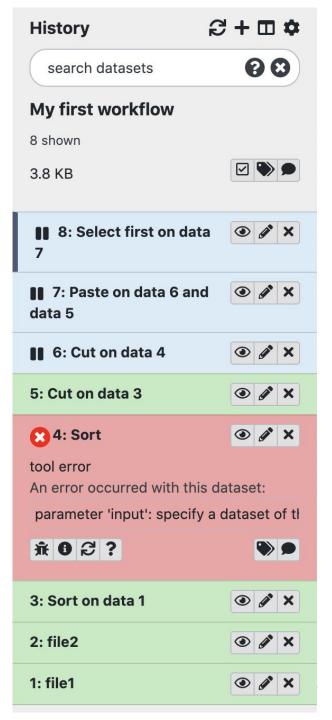


When something goes wrong...

Can we understand what's wrong based on the error message in the history?

parameter 'input': specify a dataset of the required format / build for parameter

So technically we get it from the error message. But what if we don't?



When something goes wrong...

Let's try to figure out what's wrong!

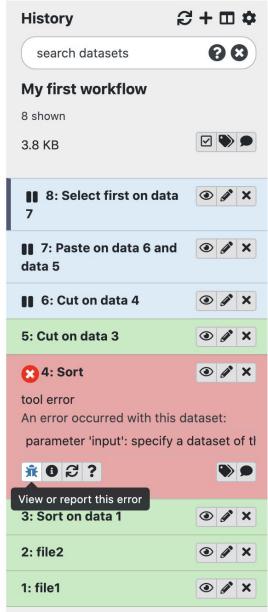
Sort					
Dataset Informatio	n				
Number:	48				
Name:	Sort				
Created:	Sun Mar 7	14:17:54 2021 (UTC)			
Filesize:	0 bytes				
Dbkey:	?				
Format:	data				
Job Information					
Galaxy Tool ID:		sort1			
Galaxy Tool Version:		1.1.0			
Tool Version:		None			
Tool Standard Output:		stdout			
Tool Standard Error:		stderr			
ool Exit Code:		None	None		
History Content API ID:	tory Content API ID:		300e5287c2c291cb		
Job API ID:	2698626f92a33abc				
History API ID:		544f4a5cb091a09c			
UUID:		05923272-f05d-4700-bb17-f331fbc6f60b			
Tool Parameters					
Input Parameter			Value		
Sort Dataset					
on column			2		
with flavor			Alphabetical sort		
everything in			Descending order		
Number of header lines to	skip		0		
Inheritance Chain					
		Sort			

2+11 **History** 88 search datasets My first workflow 8 shown 3.8 KB 8: Select first on data **◎** 🖋 × **◎** 🗳 × 7: Paste on data 6 and data 5 **③** Ø × 6: Cut on data 4 5: Cut on data 3 ① / X 2 4: Sort ① / X tool error An error occurred with this dataset: parameter 'input': specify a dataset of 1 View details **◎** 🖋 X 3: Sort on data 1 ① / × 2: file2 ① / X 1: file1

This should be an

indication in this case!

If everything is still wrong and horrible...



Dataset Error Report

An error occurred while running the tool sort1.

Troubleshooting

There are a number of helpful resources to self diagnose and correct problems. Start here: My job ended with an error. What can I do?

Issue Report

Report

Please provide detailed information on the activities leading to this issue:					





Job and Tool Error Help

Back to Support Hub

Related topics

■ Galaxy COMMUNITY HUB

- Tutorials
- Getting Inputs Right
- Extended Help for Differential Expression Analysis Tools
- Reporting Usage Issues or Software bugs
- Choices
- Ecosystem
- Galaxy Help
- Search all Prior Q&A and Galaxy Resources

Known Issues

- Galaxy
- Main https://usegalaxy.org
- Tools-devteam
- Tools-iuc

Job and Tool Error Help

So you started a job and it ended up failing. The result datasets are red in the history.

What to do? It depends on the failure type and where you are using Galaxy.

In a rush to solve the problem? The top reasons for failures are listed here. Also consider searching Known Issues and review the advanced troubleshooting help covered in Reporting Usage Issues or Software bugs (all linked above). Your problem may be something we are already working to correct or have exising prior Q and A, Galaxy help posts, documentation, and/or Galaxy tutorials that include a solution.

Query all Galaxy resources with the "Search Galaxy" box above

TIPS

- 1. The general troubleshooting help applies to most Galaxy servers/tools/functions.
- 2. The cluster error help is server specific for Galaxy Main at http://usegalaxy.org.
- 3. If working at a different public Galaxy server, contacting the admins directly to address server-related problems is often necessary. Each Galaxy is independently administered.

Job and Tool Error Help

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Determining the job failure type

Type: input problems

Type: cancelled by admin or a

cluster failure

Type: exceeds memory

allocation

Type: execution exceeds maximum allowed job run time

(walltime)

Type: ValueError: invalid literal

for int() with base 10

Type: Tool and software

problems



FAQ

Job and Tool Error Help

Galaxy Help Forum

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Galaxy Support

Quick Start

- NGS 101
- Tutorials
- Teaching with Galaxy
- Using Galaxy Choices
- Galaxy Project Highlights

Help Resources

- · Query all Galaxy resources with the search function in the top masthead
- Galaxy Help
- Chat
- Mailing Lists
- Video Help
- · Galaxy Biostars: retired Q&A archive

Using Galaxy FAQs

Basics

- Getting an account at Galaxy Main (http://usegalaxy.org)
- Loading Data
- Downloading Data
- Finding tools
- · Where is the tool help?
- · Job details: bug, info, and other useful dataset icons

Datasets and Histories

- · Understanding the Analysis History
- Managing Datasets
- · Datasets and how jobs execute
- . More about moving Datasets and Histories (external GVL blog)

Data Options

- Sharing and Publishing your work
- Data Privacy Features
- · Moving data between Galaxy servers (any!)

Help Guides

- · Why develop tools for Galaxy?
- Galaxy Tricks
- Commercial Galaxy Support

Troubleshooting

Account

- My history is missing! Good news, it probably isn't.
- A history was shared with me, where can I find it?
- The account usage quota seems incorrect
- Checking for active vs deleted vs permanently deleted (purged) datasets and histories
- Reset password or Change email, username, password

Unexpected results

- My job ended with an error. What can I do?
- Reporting Usage Issues or Software bugs
- Known Issues Galaxy
- Known Issues Main https://usegalaxy.org
- Known Issues Tools-devteam
- Known Issues Tools-iuc

Getting inputs right

- How to format fastq data for tools that require .fastqsanger format?
- Understanding compressed fastq data (fastq.gz)
- Reformatting fastq data loaded with NCBI SRA
- Format help for Tabular/BED/Interval Datasets
- Common datatypes explained
- The tool I'm using does not recognize any input datasets. Why?
- How do I find, adjust, and/or correct metadata?
- Tool error? Try Sorting Your Inputs
- Preparing and using a Custom Reference Genome or Build
- Mismatched Chromosome identifiers (and how to avoid them)
- Extended Help for Differential Expression Analysis Tools

Job and Tool Error Help

Galaxy Help Forum

FAQ

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■ ▼ Welcome to Galaxy Community Help For assistance with a specific Galaxy server please post into appropriate category.	= 😩	1	1.5k	Nov '18
Extract workflow with deleted intermediate steps: Freeing up quota space and saving prior work ■ workflow ■ history-download ■ workflow-extract ■ workflow-options ■ history-archive	B 🚳 🖄	3	11	1h
■ BWAMETH not working	S	0	9	2h
Mothur latest version	S	3	15	3h

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If everything is still wrong and horrible...





HELPDESK

Our **Helpdesk** is a nationally coordinated support centre for all types of bioinformatics related questions. We offer the following **types of support**:

- General advice and experimental design consultancy
- Programming and scripting assistance
- Data analysis
- Data management and storage

We have experience in most data types, such as:

- High-throughput sequence data (DNA / RNA)
- Proteomics data
- Chip-seq data
- Structural data

We have **expertise** in a wide range of biological and medical fields, including:

Genome and transcriptome assembly, Variant calling, Annotation, Gene expression, coding and noncoding, Methylation, Epigenetics, Statistical genomics, Network analysis, Metagenomics, Microbial genomics, Cancer, Health, Marine

Support models:

- Requests that can be solved within two working days or less are free of charge, provided that the platform has resources available
- For more comprehensive projects, an hourly rate applies
- Requests that require an effort beyond technical assistance/consultancy will be set up as a research collaboration. Funding for collaborative research performed by platform partners must be provided unless otherwise agreed. The result of joint research shall be published with joint authorship.

CONTACT US

contact@bioinfo.no



Don't worry, it'll all be alright:)

