



# *Report issues and how to get help*

*ELIXIR Norway, Norwegian e-infrastructure for Life Sciences and [usegalaxy.no](http://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?

The screenshot shows a 'History' panel with a search bar and a list of workflow steps. The steps are numbered 1 through 8. Step 4, 'Sort', is highlighted in red and has a red 'x' icon, indicating it failed. Step 8, 'Select first on data', is highlighted in blue and has a blue bar on its left side, indicating it is the current step. Steps 1-3 and 5-7 are highlighted in green. Each step has icons for view, edit, and delete. A blue arrow points from the text on the left to the failed step 4.

Step	Name	Status
1	file1	Success
2	file2	Success
3	Sort on data 1	Success
4	Sort	Failed
5	Cut on data 3	Success
6	Cut on data 4	Success
7	Paste on data 6 and data 5	Success
8	Select first on data 7	Success

# 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?

**History**

search datasets

**My first workflow**

8 shown

3.8 KB

**8: Select first on data 7**

**7: Paste on data 6 and data 5**

**6: Cut on data 4**

**5: Cut on data 3**

**4: Sort**

tool error  
An error occurred with this dataset:  
parameter 'input': specify a dataset of tl

**3: Sort on data 1**

**2: file2**

**1: file1**

# When something goes wrong..

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

### Sort

#### Dataset Information

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:	<a href="#">stdout</a>
Tool Standard Error:	<a href="#">stderr</a>
Tool Exit Code:	None
History 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
------

This should be an indication in this case!

### History

search datasets





#### My first workflow



8 shown

3.8 KB

- 8: Select first on data 7
- 7: Paste on data 6 and data 5
- 6: Cut on data 4
- 5: Cut on data 3
- 4: Sort**  
tool error  
An error occurred with this dataset:  
parameter 'input': specify a dataset of 1
- 3: Sort on data 1
- 2: file2
- 1: file1




# If everything is still wrong and horrible..




**History**    




search datasets  




**My first workflow**




8 shown




3.8 KB   

**8: Select first on data 7**   







**7: Paste on data 6 and data 5**   

**6: Cut on data 4**   




**5: Cut on data 3**   




**✘ 4: Sort**   




tool error  
An error occurred with this dataset:  
parameter 'input': specify a dataset of tl

**View or report this error**

**3: Sort on data 1**   

**2: file2**   

**1: file1**   

## 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

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

 Report





## Job and Tool Error Help

[Back to Support Hub](#)

### Related topics

- [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](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 existing 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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### TIPS

#### 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

Galaxy Help Forum

## Job and Tool Error Help

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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](#)



FAQ

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Topic		Replies	Views	Activity
<p><b>🚫 March 2021 Galaxy News</b></p> <p>■ jobs ■ events ■ news ■ platforms ■ community</p> <p>Hello all, It is a very busy time in the Galaxy. 2021 is young, but we have already had two large training events, including the largest Galaxy event ever - the GTN Smörgåsbord (with an amazing 1100+ people registered).... read more</p>		1	18	1d
<p><b>🔒 🚫 Troubleshooting resources for errors or unexpected results</b></p> <p>usegalaxy.org support</p> <p>Check to see if there is a known usegalaxy.* server issue. Server Status: <a href="https://status.galaxyproject.org/">https://status.galaxyproject.org/</a> If the server was down when you first ran your job, try a rerun once back up. A rerun can also eliminate tra... read more</p>		1	3.2k	Nov '18
<p><b>🔒 🚫 Welcome to Galaxy Community Help</b></p> <p>For assistance with a specific Galaxy server please post into appropriate category.</p>		1	1.5k	Nov '18
<p><b>Extract workflow with deleted intermediate steps: Freeing up quota space and saving prior work</b></p> <p>■ workflow ■ history-download ■ workflow-extract ■ workflow-options ■ history-archive</p>		3	11	1h
<p><b>🔒 BWAMETH not working</b></p>		0	9	2h
<p><b>Mothur latest version</b></p>		3	15	3h

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# If everything is still wrong and horrible..

## MENU

Agreement

## 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](mailto:contact@bioinfo.no)

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

