

# Galaxy-Demo

## Galaxy

<http://galaxy/galaxy> (on the campus) or

<http://sequencing.csf.viennabiocenter.org/galaxy/> (outside of the campus)

**Homepage with workflows** based on Galaxy-tools:

<http://ngs.csf.ac.at/galaxydoc/>

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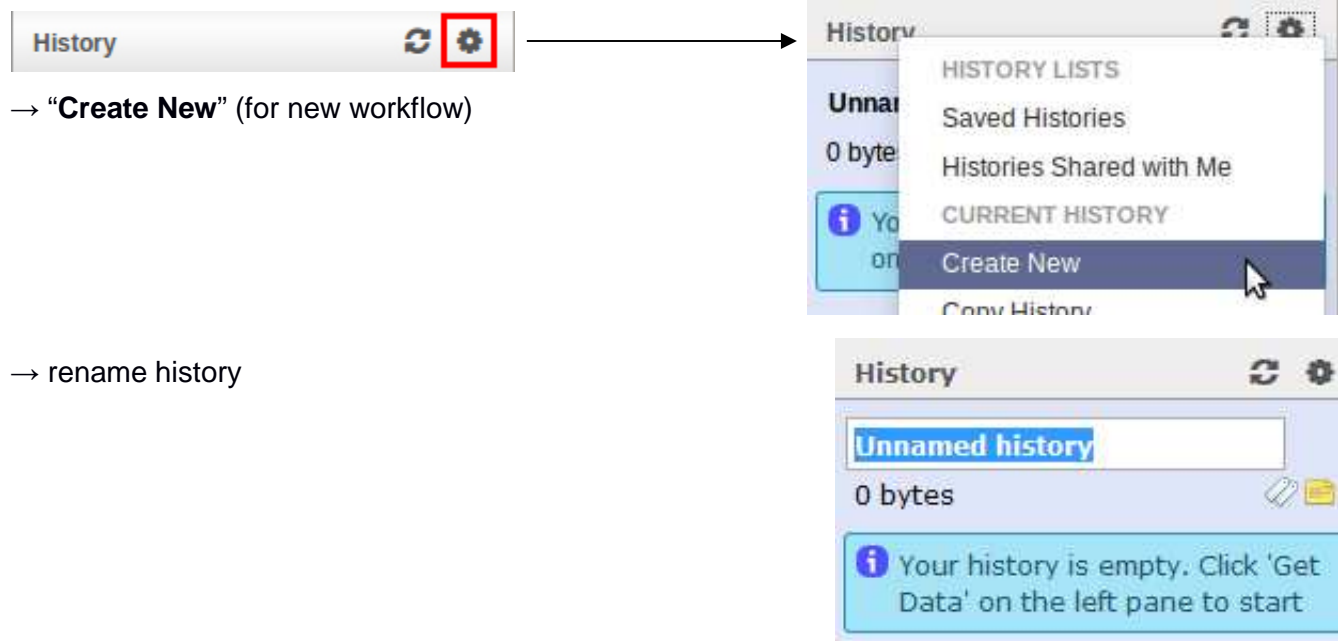
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## GALAXY

- Top menu:
  - **User** → **Login**
  - **Shared Data / Data Libraries** – annotation files
  - **Analyze Data**
- **Tools** (left)
- **History** (right) - results

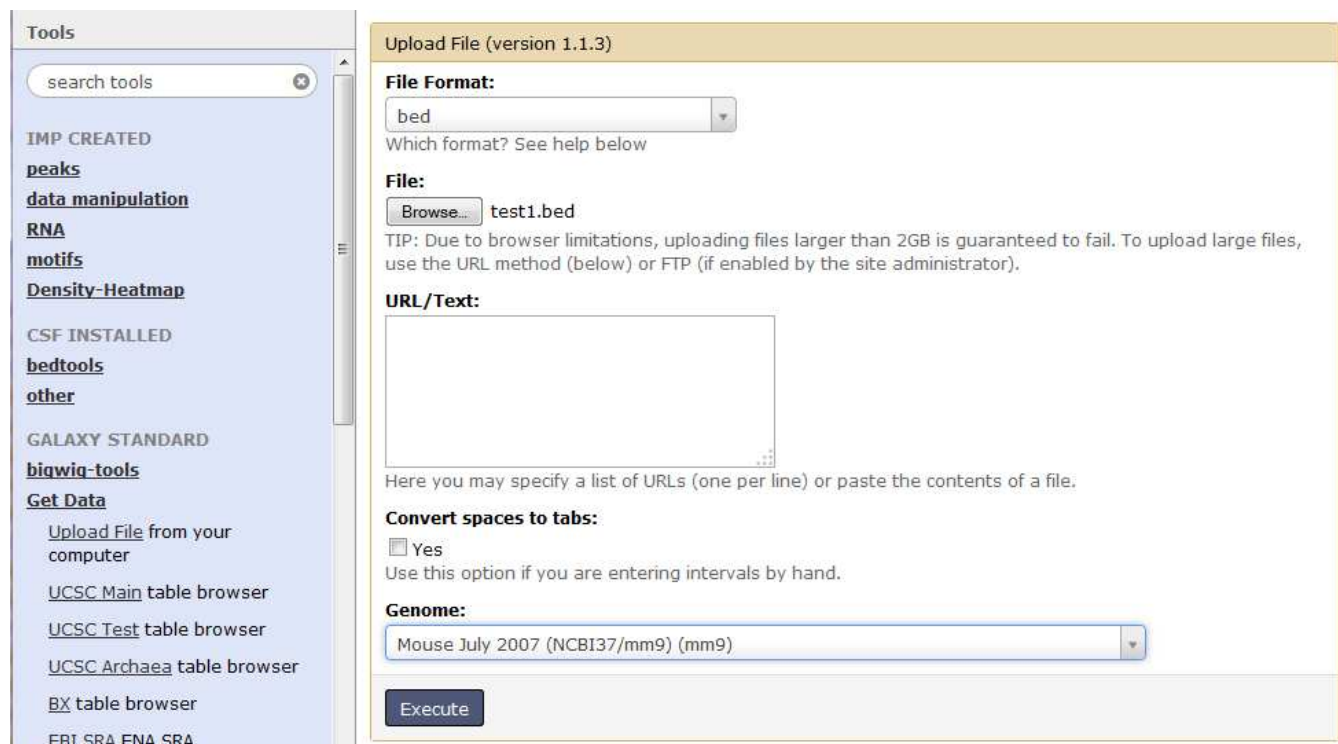
## Example 1:

→ History



→ rename history

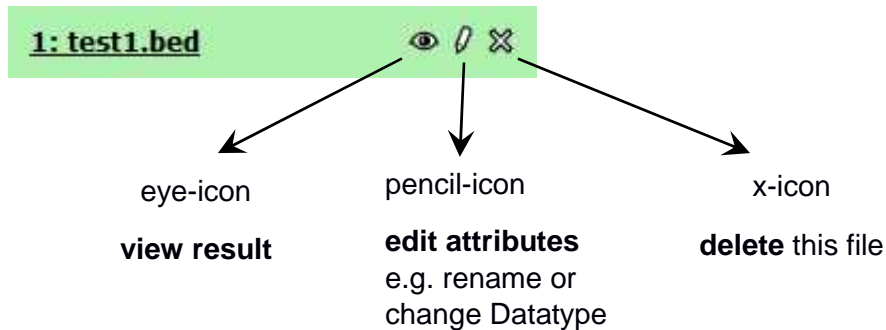
→ file < 2 GB from Computer → Tools: “Get Data/Upload file”




→ “Execute”

## History-result:

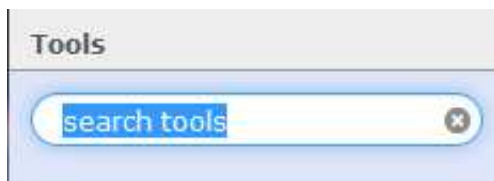
blue = uploading  
yellow = working  
green = ready



→ **file > 2 GB** => push from your **Queue**  
file appears in the new history → copy data to another → **History** -  - **Copy Datasets**

→ annotation files from **Shared Data / Data Libraries** → check a file → For selected datasets  
“Import to current history” → GO

## Example 2:



→ filter for reads on forward-Strand only




→ **Filter and sort / Filter:** c6=='+'

→ **Execute**





→ **History-colors:**

grey: tool is waiting to start  
yellow: tool is running  
green: result ready, went well - result can be viewed  
red: error

→ **result** in History panel:

**2: test1\_plus**   

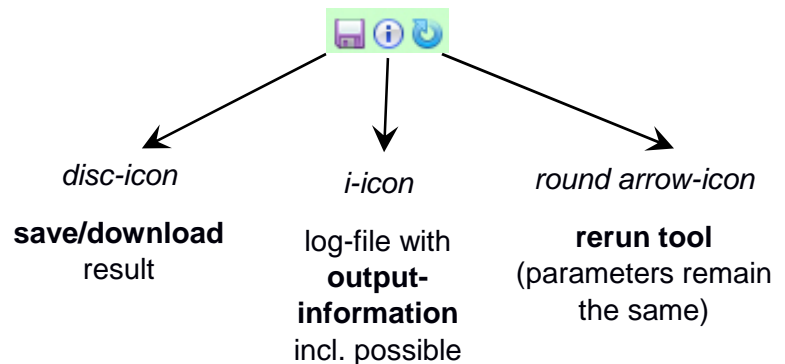
5,083 regions  
format: bed, database: mm9  
Filtering with c6=='+', kept 50.87% of 9992 valid lines (9992 total lines).

display at UCSC [main](#)  
display at UCSC [main](#)  
display in IGB [Local](#) [Web](#)




1.Chrom	2.Start	3.End	4.Name	5	6.Strand
chr1	4865506	4865556	0	0.0	+
chr1	5075377	5075427	0	0.0	+
chr1	5077434	5077484	0	0.0	+
chr1	5128062	5128087	0	0.0	+
chr1	5142381	5142431	0	0.0	+
chr1	6212055	6212104	0	0.0	+

→ Information on format, database, what was done, how many lines/regions






→ sneak preview of result

## Errors:

**18: Call MACS**   

**iteratively on data 3 and data 2: DatP Bed File**

tool error  
An error occurred with this dataset: *Unable to finish job*

bug-icon:  
**shows errors**

→ send history to Ido or Maggie:

**History** –  – “Share or Publish” – “Make History Accessible via Link” → copy link and send via email

### Example 3:

- use result for another tool
  - eventually rename file
  - select unique lines: **"data manipulation / Selects unique lines"**
  - **Execute**
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### Shared data/ Data Libraries:

- annotation files for different experiment-types

### History – most important menu items:

