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🌐 Assembly Stats with MetaQuast

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Protocol status: Working

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Keywords: assembly stats with metaquast, assembly stat, various assembly statistics, metaquast app on the cyverse discovery environment, cyverse discovery environment, metaquast app, assembly, metaquast

Abstract

Calculate various assembly statistics using the MetaQuast app on the CyVerse Discovery Environment.

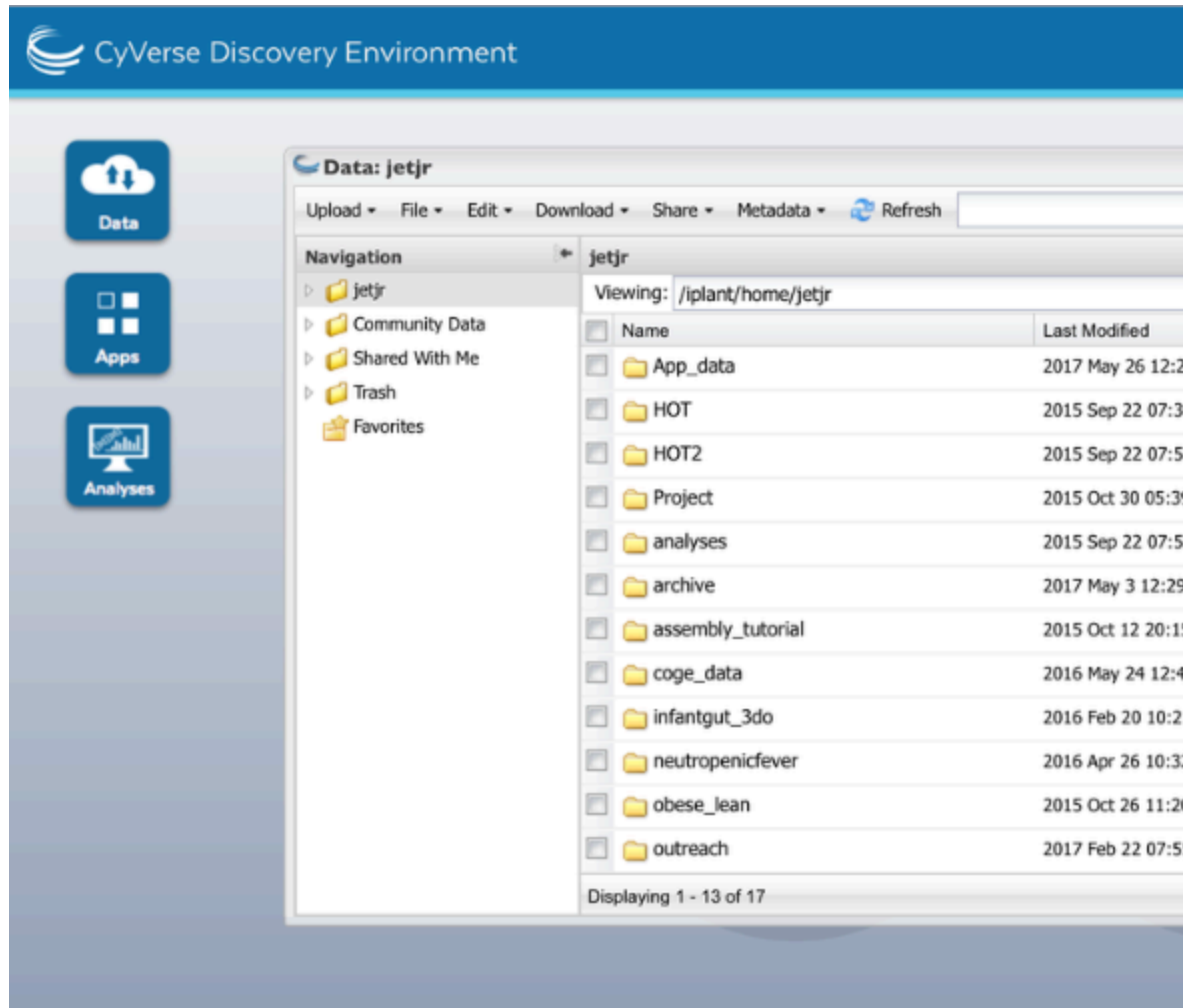
- 1 Go to <https://user.cyverse.org/>
<https://user.cyverse.org/>
- 2 Click "Sign Up" to create an account.
- 3 After account creation go back to <https://user.cyverse.org/> and login with your account.
<https://user.cyverse.org/>
- 4 Launch the discovery environment.



Discovery Environment

Use hundreds of bioinformatics apps and manage data in the interface

- 5 Click the "Data" button found on the left. Navigate to your user folder.



5

6 Click "Upload" > "Simple Upload From Desktop"

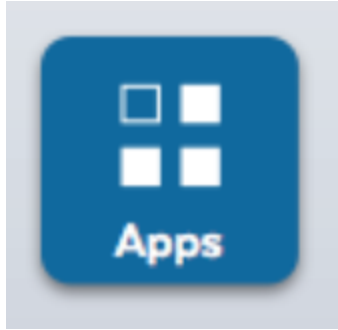
7 Upload your final.contigs.fa file generated from Megahit.

Note

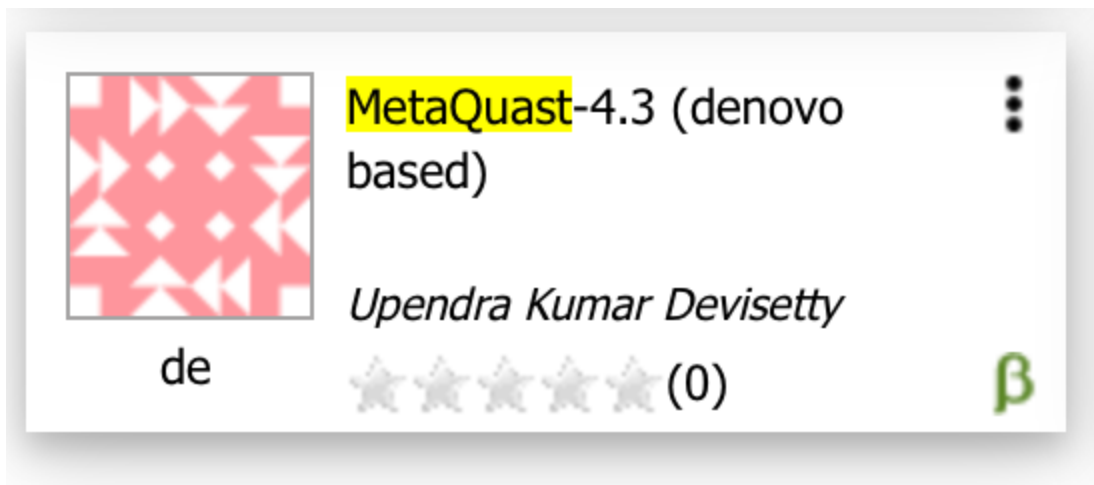
Important: You must scp your contigs to your local machine before you can upload.

```
$ scp  
username@sftp.hpc.arizona.edu:/rsgrps/bh_class/username/assembly/megahit-  
out/final.contigs.fa .
```

8 Once your upload is complete, click on the "Apps" button found on the left.



- 9 Search for "MetaQuast". Click on MetaQuast-4.3 (denovo based)



- 10 Under the "Fasta file(s)" tab, select the newly uploaded final.contigs.fa file. This is the only parameter that needs to change. Click "Launch Analysis".
- 11 Once MetaQuast is complete (email notification), navigate to the output found in the "analyses" folder in your data storage.
- 12 Download the "report.html" file found in the MegaQuast output folder.
- 13 Open the report.html file to see a summary of assembly statistics.