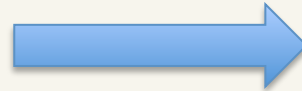


Getting data into Galaxy

Tools

- [BEDTools](#)
- [Get Data](#)
- [ENCODE Tools](#)
- [Lift-Over](#)
- [Text Manipulation](#)
- [Filter and Sort](#)
- [Join, Subtract and Group](#)
- [Convert Formats](#)
- [Extract Features](#)



Tools

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 - [BioMart Central server](#)
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Getting data into Galaxy

Galaxy / UIUC

Analyze Data Workflow Shared Data Visualization Help User

Using 57.2 Gb

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- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
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- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+

Upload File (version 1.1.3)

File Format:
Auto-detect
Which format? See help below

File:
Choose File no file selected
TIP: Due to browser limitations, uploading files larger than 2GB is guaranteed to fail. To upload large files, use the URL method (below) or FTP (if enabled by the site administrator).

URL/Text:

Here you may specify a list of URLs (one per line) or paste the contents of a file.

Files uploaded via FTP:

File	Size	Date
Your FTP upload directory contains no files.		

This Galaxy server allows you to upload files via FTP. To upload some files, log in to the FTP server at biocluster.igb.illinois.edu using your Galaxy credentials (email address and password).

Convert spaces to tabs:
 Yes
Use this option if you are entering intervals by hand.

Genome:
----- Additional Species Are Below -----

Execute

History

Unnamed history 0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

- Click “Choose File”, and proceed to pick your file from your computer.
- Click Execute to start the upload
- **2Gb file size limit**

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- This is generally not advisable, since usually files are very large; you can paste small files in.

Getting data into Galaxy

The screenshot shows the Galaxy / UIUC interface with the 'Upload File (version 1.1.3)' tool selected. The left sidebar contains a 'Tools' menu with categories like 'BEDTools', 'Get Data', 'ENCODE Tools', etc. The 'Upload File' tool interface includes a 'File Format' dropdown set to 'Auto-detect', a 'File' section with a 'Choose File' button, and a 'URL/Text' input area. A table titled 'Files uploaded via FTP:' is empty, with columns for 'File', 'Size', and 'Date'. Below the table, there is a checkbox for 'Convert spaces to tabs:' and a 'Genome:' dropdown menu. An 'Execute' button is at the bottom of the tool interface. A red circle highlights the 'Upload File from your computer' option in the 'Get Data' section of the sidebar. Another red circle highlights the 'Files uploaded via FTP:' table and its associated text.

Galaxy / UIUC

Analyze Data Workflow Shared Data Visualization Help User Using 57.2 Gb

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History

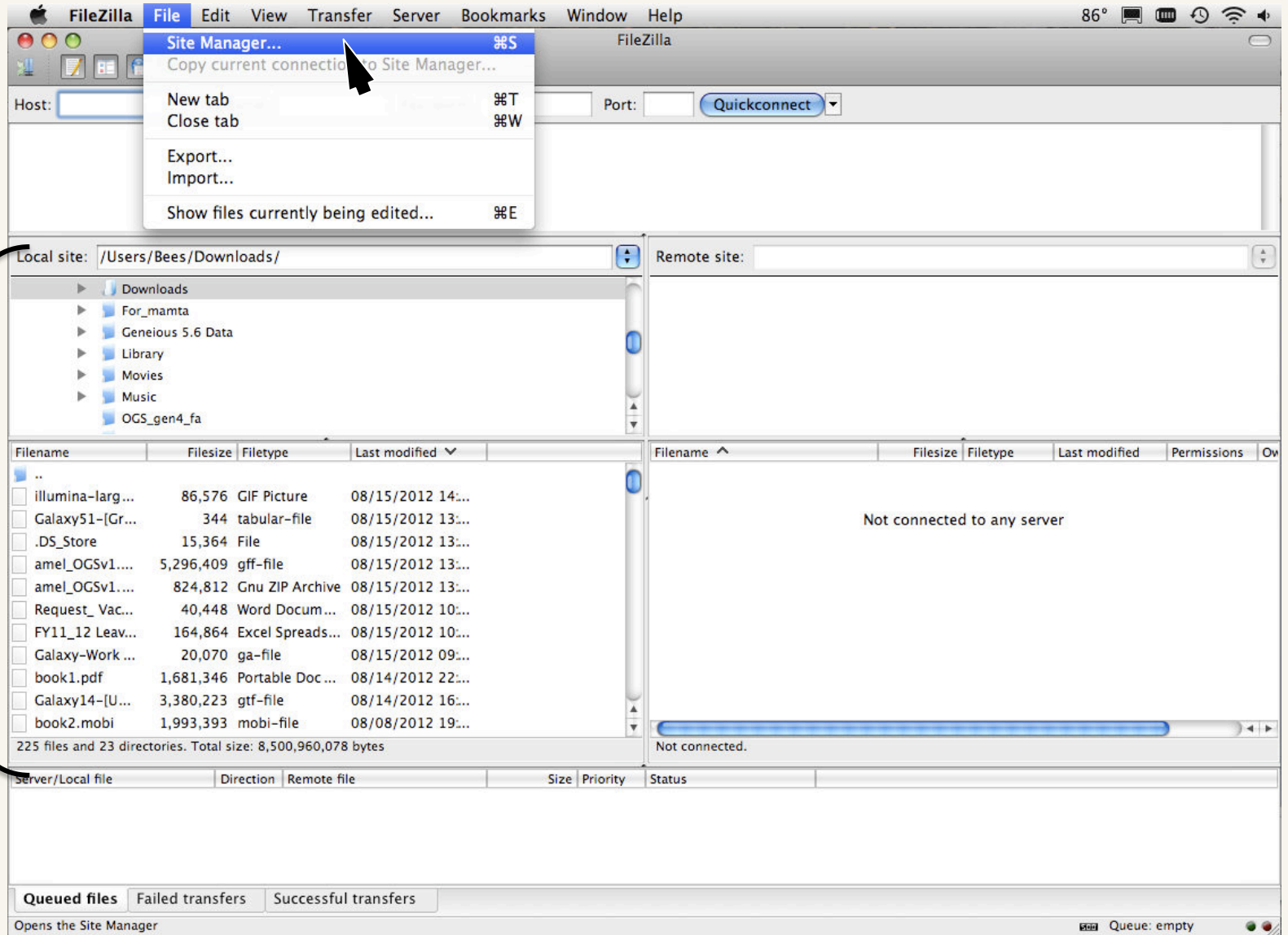
Unnamed history 0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

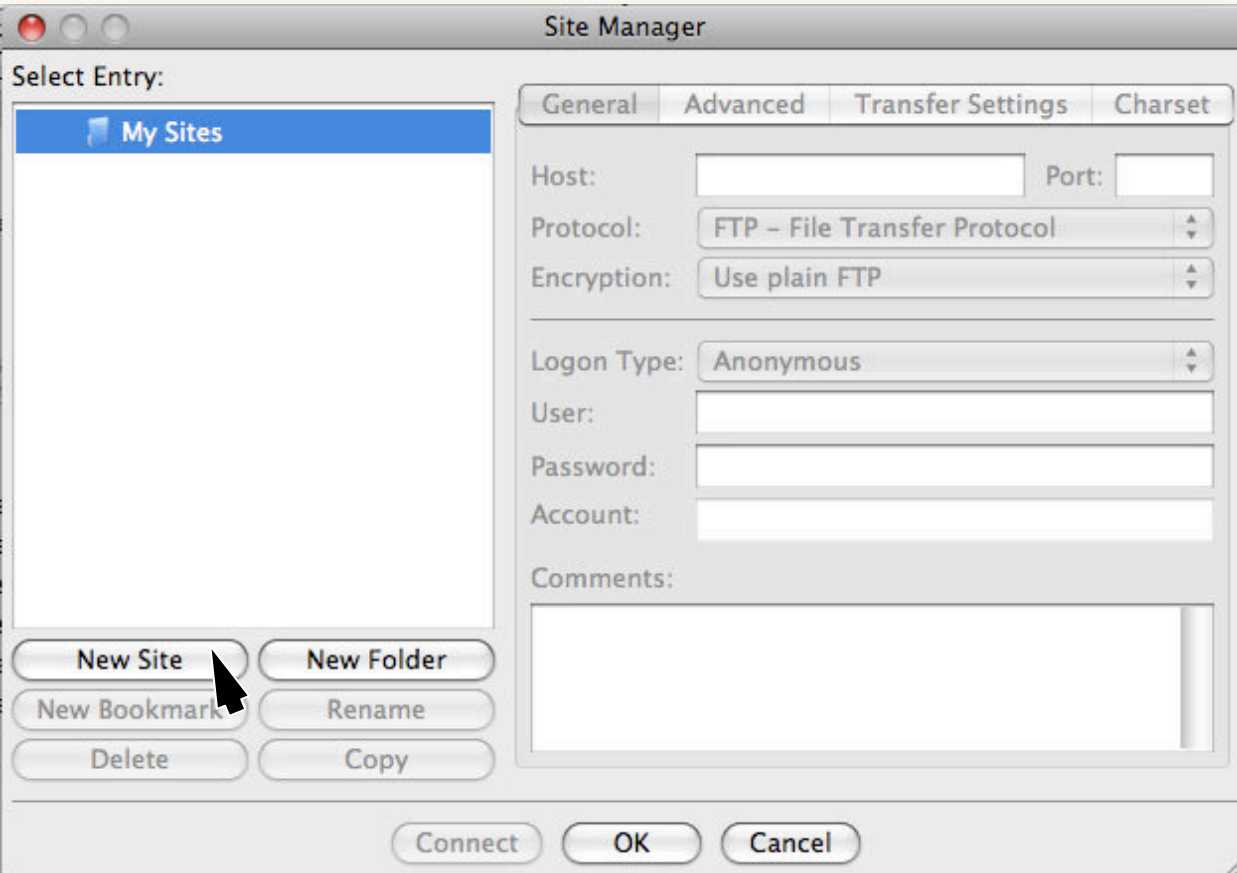
- You can upload files (SFTP) using an FTP client like Filezilla, Cyberduck, Fugu

Getting data into Galaxy

Directory structure of your current computer

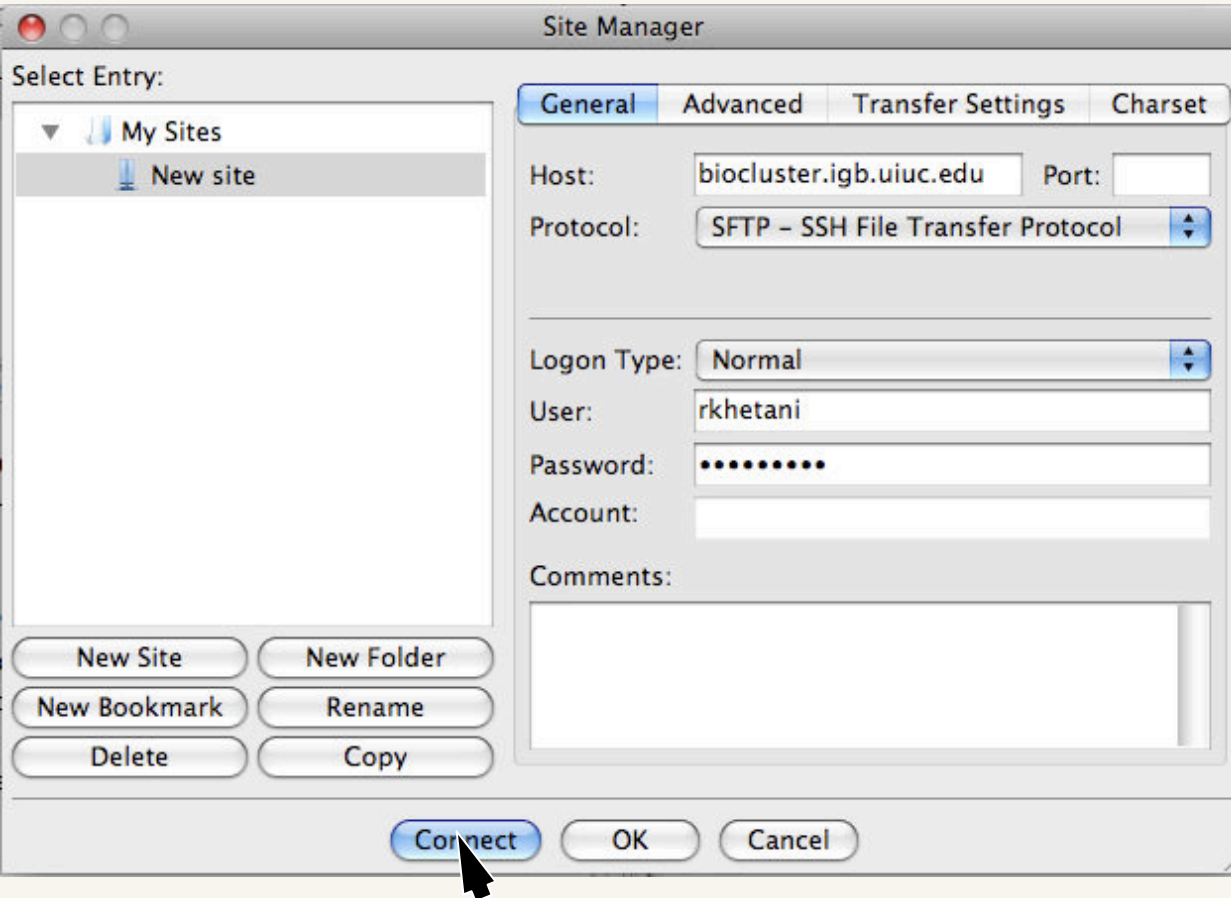


Getting data into Galaxy



- Add a new site

Getting data into Galaxy



- In the “Host:” field type biocluster.igb.uiuc.edu
- Leave “Port:” empty
- Make sure you select SFTP from the “Protocol:” pull-down menu
- Change “Logon Type:” to Normal
- Enter your galaxy username and password
- Leave “Account:” empty
- Click Connect

Getting data into Galaxy

Host: Username: Password: Port: Quickconnect

Command: ls
Status: Listing directory /home/n-z/rkhetani
Status: Calculating timezone offset of server...
Command: mtime ".ssh"
Response: 1343749064
Status: Timezone offsets: Server: -18000 seconds. Local: -18000 seconds. Difference: 0 seconds.
Status: Directory listing successful

Local site: /Users/Bees/Downloads/ Remote site: /home/n-z/rkhetani

Filename	Filesize	Filetype	Last modified
..			
illumina-larg...	86,576	GIF Picture	08/15/2012 14:...
Galaxy51-(Gr...	344	tabular-file	08/15/2012 13:...
.DS_Store	15,364	File	08/15/2012 13:...
ameI_OGSv1....	5,296,409	gff-file	08/15/2012 13:...
ameI_OGSv1....	824,812	Gnu ZIP Archive	08/15/2012 13:...
Request_ Vac...	40,448	Word Docum...	08/15/2012 10:...
FY11_12 Leav...	164,864	Excel Spreads...	08/15/2012 10:...
Galaxy-Work ...	20,070	ga-file	08/15/2012 09:...
book1.pdf	1,681,346	Portable Doc ...	08/14/2012 22:...
Galaxy14-(U...	3,380,223	gtf-file	08/14/2012 16:...
book2.mobi	1,993,393	mobi-file	08/08/2012 19:...

Filename	Filesize	Filetype	Last modified	Permissions
Galaxy_tutorial		Directory	08/15/2012...	drwxrwxr-x
Homo_sapiens		Directory	08/08/2012...	drwxrwxr-x
Nurse-For		Directory	08/10/2012...	drwxrwxr-x
bio		Directory	02/13/2012	drwxr-xr-x
bowtie_test		Directory	08/08/2012...	drwxrwxr-x
control-thrombin-500K		Directory	08/14/2012...	drwxrwxr-x
expt-thrombin-500K		Directory	08/14/2012...	drwxrwxr-x
galaxy-upload		Directory	02/08/2012	lrwxrwxrwx
lh3-seqtk-771d60b		Directory	07/31/2012...	drwxr-xr-x
no_backup		Directory	07/26/2012...	drwxr-xr-x
sceman		Directory	08/14/2012...	drwxrwxr-x

- You will see that both sides of the split windows will fill up
- Click on the “galaxy-upload” directory
- Drag and drop files from your folder into the galaxy-upload folder

Getting data into Galaxy

Galaxy / UIUC

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Genome:
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Execute

History

Unnamed history 0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

- If you click on “Upload File” again, the file you transferred will appear in the area that was previously empty.
- This is the best way to get large files into galaxy