



Instructions to Upload Data into Galaxy via HiPerGator Server

There are a couple different ways to upload data into the local Galaxy instance hosted by HiPerGator at the University of Florida (UF). Data upload sizes may range from a single or a few files to many.

- Data upload from local computer – You can use the “Get Data – Upload File” tool in Galaxy to upload files from your local computer. This is convenient when working with a small set of files located on your local computer.
- Data upload from HiPerGator – It is required to upload large datasets into Galaxy from HiPerGator, as opposed from your local computer. This has the advantage that all of this data movement is not burdening your Institution’s network. You need to know a few bash commands on the command-line prior to using the “Get Data – Upload File” tool for the upload. This data upload method also allows you to upload data into Galaxy directly from BaseSpace, using the BaseSpace command-line interface (CLI) on HiPerGator, thus preventing the need for unnecessary downloads to your local computer. (See the separate information sheet, “Instructions to Install and Configure BaseSpace CLI”, to learn how to transfer data directly from BaseSpace to HiPerGator).

Below are step-by-step instructions to upload data from your state group directories on HiPerGator into Galaxy.

1. Login to HiPerGator via Putty or a terminal. You will be in your home directory (/home/<user>).
2. Create your Galaxy upload directory. (Don’t include the \$ sign).
 - a. Note – You only have to do this step once, the first time you ever upload data to Galaxy via HiPerGator.

```
$ mkdir /ufrc/apps/galaxy/incoming/<your email address in galaxy>
#For example: mkdir /ufrc/apps/galaxy/incoming/sarah.schmedes@flhealth.gov

$ ls /ufrc/apps/galaxy/incoming/<your email address in galaxy>
#If you see “your email address”, then your new directory was successfully created.
```



3. Navigate (change directories) to your Galaxy upload directory.

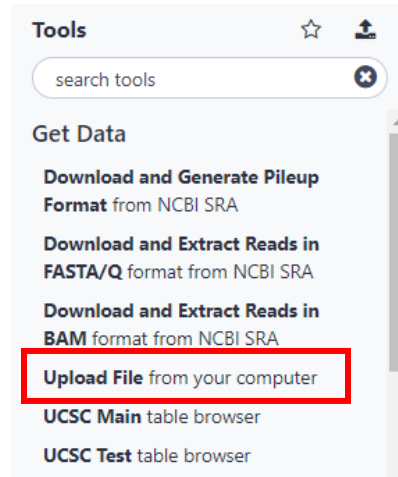
```
$ cd /ufrc/apps/galaxy/incoming/<your email address in galaxy>
```

4. Copy the data you want to upload to Galaxy into your Galaxy upload directory.

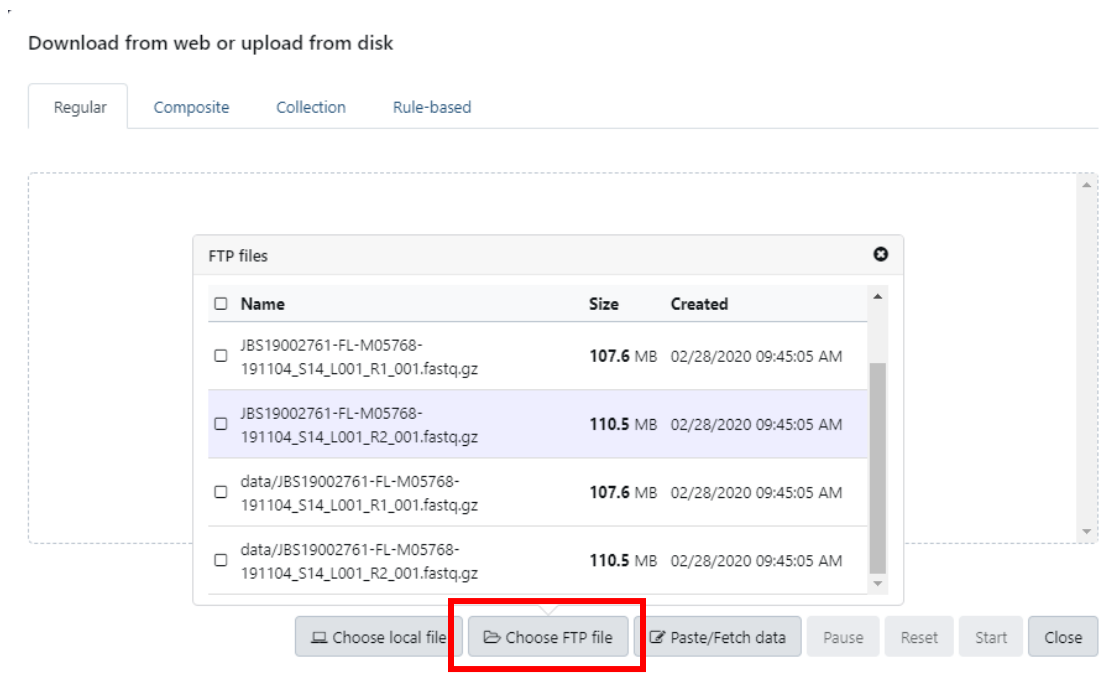
```
$ cp /path/to/my/data/sample_1.fastq.gz .  
#This will copy a single fastq file, one at a time.  
  
or  
  
$ cp /path/to/my/data/sample_*.fastq.gz .  
#Use the * (wild card) symbol if you have paired-end data files in the same  
#directory. This will copy your R1 and R2 files at the sample time.  
  
Or  
  
$ cp /path/to/my/data/*.fastq.gz .  
#This will copy all files with .fastq.gz extension in this directory to your  
#current directory (Galaxy upload directory).  
  
$ ls  
#Do you see your files? If so, you copied them successfully.
```

5. Once you have finished copying all data into your Galaxy upload directory, login to Galaxy at <https://galaxy.rc.ufl.edu/login>.
 - a. Note – Your data is not uploaded into Galaxy yet. The data files have just been copied into a directory that you can access directly from Galaxy.
 - b. Note – Also, your Galaxy upload directory is temporary storage and will be cleared out periodically by HiPerGator staff. Do not use this directory as long-term data storage.

6. Click on the “Get Data – Upload File” tool.



7. Click “Choose FTP file”. You will see a list of the data files located in your Galaxy upload directory. Select the samples you want to upload and click “Start”.
- Note – It may take up to 15 minutes for your samples to appear in the list. (I’ve never had a delay, but it’s a possibility).





8. Your data will now start uploading into Galaxy.

For more information about using the UF local Galaxy instance on HiPerGator, please see <https://help.rc.ufl.edu/doc/Galaxy>.