UF HPC Training
Working with NGS data
October 8, 2012

Fastq filtering example

1. Copy the file sample submission script to your scratch directory
    a. Login: `ssh user@submit.hpc.ufl.edu`
    b. cd to /scratch: `cd /scratch/hpc/user/`
    c. Copy file: `cp /project/bio/training/2012-10-08/sickle_demo.pbs .`
2. Edit sickle_demo.pbs to add you e-mail
    a. `nano sickle_demo.pbs`
3. Submit this file and check out the results

Fastq filtering demo from Galaxy dataset
1. The example script is in the training directory, called sickle_demo_galaxy.pbs
2. To get the path of a Galaxy dataset, click the ⓘ icon.
3.

Tool: FASTQ Groomer	
Name:	FASTQ Groomer on data 2
Created:	Oct 08, 2012
Filesize:	376.9 MB
Dbkey:	?
Format:	fastqsanger
Tool Version:	
Tool Standard Output:	stdout
Tool Standard Error:	stderr
Full Path:	/galaxy/run/prod/database/files/025/dataset_25369.dat

See http://wiki.hpc.ufl.edu/doc/Galaxy_Data_Import for information on getting data back into Galaxy. This is the same method used for scp/sftp upload.