Tuesday 19 Jan 2016

#set up folder structure on desktop (see my example for Bio343)

#log on using davidson##

w13426:~ user$ ssh -l user 192.112.102.21

submit password 4gcatRocks!

passwd (return and follow prompts)

#must have one cap letter, one number and one symbol

# Run this for each user’s home folder:

cd ..

chmod a+rx user

ls -al

cd user

# copy files into their folders, install Trimmomatic in bin folder, etc.

mkdir fastQCLiver # or fastQCintestine

cp -r ../campbell/fastQCLiver/ fastQCLiver # or fastQCintestine x 2

mkdir bin

cd bin

#do each line one at a time

wget <http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.32.zip>

unzip Trimmomatic-0.32.zip

rm Trimmomatic-0.32.zip

#now move from GCAT cluster to your local desktop

**#STEP 3: View fastQC reports on local machine**

#open new terminal window (local machine)

cd Desktop/Bio343/fastQC

scp -r user@192.112.102.21:/home/user/fastQCorgan/ .

#In finder, unzip all zip files

Go to each folder and open html file

Explore quality of reads for trimmomatic options