**RNASeq Workshop**

November 5-7, 2020 Florida International University

November 12-14, 2020 University of Puerto Rico

November 19-21, 2020 University of Puerto Rico

**Linux Practice Material**

**For all the exercises given below please write down in a word document all the commands, and where appropriate, the outputs that you have received to execute the tasks listed.**

**Exercise 1:**

Please list all the steps you followed to login to the HPC cluster at FIU. For each step write the command and the parameters used. For windows users who use MobaXterm please provide screenshot of the MobaXterm window where you enter the login details.

**Exercise 2:**

After you login to your home directory, create a directory with name “Test\_project”. Inside this directory create three sub directories with names (***without quotes***): “test\_data”, “test\_results” and “test\_src”. Inside each of these three sub directories create a directory with name “temp” and three text files with names: <DirectoryName>\_file1.txt, <DirectoryName>\_file2.txt and <DirectoryName>\_file3.txt

**Exercise 3:**

Go into each of the three sub directories created in Exercise 2 and run a command that

1. lists the directory you are in
2. lists all the contents of the directory
3. lists all the contents of the directory with detailed information about each file. How do you differentiate a file from a directory using the information listed?
4. lists all the contents of the directory with detailed information about each file sorted by file modification time
5. lists all the contents of the directory with detailed information about each file in a human readable file sizes format
6. lists all the contents of the directory including all the hidden files

**Exercise 4:**

Change permissions for the test\_src directory created in Exercise 2 so that only the owner has read, write and execute permissions. Change permissions for the test\_results directory so that only owner and group has read and write permissions.

**Exercise 5:**

Go to test\_data directory and create a text file using nano. Copy paste the following text and save the file with name “test\_dataset.txt”. Within the saved file using the nano editor please make the following changes. For the lines that begin with “@” symbol please delete all the characters in that line and replace them with the text: “sequence header”. Please write down all the commands (or steps) that you have used for creating the file and for modifying the text in the saved file.

@V300017787L4C002R0061184898/1

GTTCATTGCATTATTTAATAATATCCCGGTGTTTTCGCTGACTACTCCGCTTCCGAAATAGAAATTAATAGTACTAGTAGCTGATACTGCATCTCCATTT

+

FFFGGFAFGGEGDGFFEG@GEFFFFGGFGGGEFFGGGGFBFFGEFEGFAFFFGGGEGFB?GEFGGGEFGAGGFGFDEGAGFFF?GAGFGGFBGGFGFGFF

@V300017787L4C002R0061184920/1

CTTTATTAGAGCGCCACAATCTTTCCATACCATTACGATGTAAAGCCATTCGAGTAAGTTCAGAAAAACTTTCACGAATATTAAAATCACAGAGAGGTGA

+

F6CCDFF'BF0??8FAB=F;BF@FE0DG1FD8DCEF0FFEDFBCE=GDBFB<=F&:@G5FF@DF8F;FEFGFFE<F?CGGC>DEGEFDDCEGFF=07DF8

@V300017787L4C002R0061184952/1

ATGAGATAGGAAATCAAAGGGTATCTACAACAGCACGTATTATTCATGGAATAATTATAGTTTTTATTTTAATTTCTATAATATTAGCTATAGCAAATGT

+

?FFDFEFCFEEFFFFFEFF?FEFFFFFEF@FFEFFFFBFFFFFFFFFFDEFFFFFEFFFFEEFEBFDEFFCFFFFFFFFFFEFFFDFEFDAFC?FFFFF=

**Exercise 6:**

Please type a command on your terminal so that you print the first 6 lines of the file you have saved in the previous exercise.

What command(s) you would use to browse the entire content of the file?

Please type a command on your terminal so that you print all the lines that contain “@” in the test\_dataset.txt file

Please type a command on your terminal so that you print total number of lines that contain “@” in the test\_dataset.txt file

**Exercise 7:**

Using any Linux editor, create a file with the following text with file name “samples.txt” and sort the file in reverse order (alphanumerically). Type a command to print the first two characters before the first “-” symbol, for each line of the samples.txt file.

C4-45-2

C4-45-3

C4-45-4

T3-45-1

T3-45-2

T3-45-4

**Exercise 8:**

Copy the samples.txt file created in the previous exercise to test\_results directory.

Move the samples.txt file from the test\_results directory to test\_src directory.

**Exercise 9:**

Go to test\_src directory and within that directory create a bash script to run fastqc program. Enter parameters to run the fastqc program so that it lists only the help menu and exit.

**Exercise 10:**

Go to the home directory and create a tar gzip file of the test\_project directory that was created earlier. Create a directory with name “Backup” within your home directory and copy the tar gzipped file that you just created to the “Backup” directory. Within the “Backup” directory untar and unzip the file.

**Exercise 11:**

Please download the tar gzipped file that was created in the previous exercise on to your laptop. Please upload any small text file (with size <1Mb) from your laptop to your home directory in the HPC cluster.