Exercises for Workshop W5a: RNA-seq I Analysis

**PRIOR TO CLASS:**

1. Make sure you have access to hoffman2. You can do this easily here: <https://www.hoffman2.idre.ucla.edu/Accounts/Requesting-an-account.html>
2. Once you have an account, we need a few software packages that are not available on hoffman2. I’ll provide step-by-step instructions.

First, we have to install FastQC:

* In your home directory, run the following command:

wget https://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc\_v0.11.9.zip --no-check-certificate

unzip fastqc\_v0.11.9.zip

To check if FastQC installed properly:

~/FastQC/fastqc --help

Next, we have to install trimmomatic:

wget http://www.usadellab.org/cms/uploads/supplementary/Trimmomatic/Trimmomatic-0.39.zip

unzip Trimmomatic-0.39.zip

To check if trimmomatic installed properly:

qrsh -l h\_rt=0:30:00,h\_data=5G

module load java

java -jar Trimmomatic-0.39/trimmomatic-0.39.jar

Lastly, we have to install Salmon:

wget https://github.com/COMBINE-lab/salmon/releases/download/v1.5.1/salmon-1.5.1\_linux\_x86\_64.tar.gz

tar xzvf salmon-1.5.1\_linux\_x86\_64.tar.gz

To check if Salmon installed properly:

salmon-1.5.1\_linux\_x86\_64/bin/salmon

Exercise 1

1A: Logging in (connected) to hoffman2

To log into the cluster, first open a terminal (Windows: PuTTY app, Mac OSX/Linux: Terminal app), and enter the following command:

ssh your\_username@hoffman2.idre.ucla.edu

Make sure you put in your own username here.

Important: Every time you connect to the Hoffman-2 cluster, you will initially have a session on the login node (login server). Because this computer is shared among all users and has limited computing resources, the first thing you should do after logging into the cluster is to ask for an interactive session on a worker node, by running the command:

qrsh -l h\_rt=2:00:00,h\_data=8G