Summer 2020

Unix/Linux for Informatic Analysis
https://github.com/sabrsyed/InformaticsTools_2020

Week 3

- Unix Problem Set Q&A
- Review ChIP-Seq and RNA-Seq pipelines

- Loading files to the cluster using FileZilla and rsync

- On the ghpcc06 cluster, read criteria for running bowtie2, picard, samtools, etc.
- See sample bsub commands for running each module
- Look at bowtie2 output files
- Use IGV to view .bam and .bed files

Tasks:
Create lab schedule for using the ghpcc06 cluster
Explore the cluster and examine modules and tools for data analysis that are available
Upload Fastq files to ghpcc06 cluster

Week 4

- On the ghpcc06 cluster, read criteria for running macs, rsem-calculate-expression, etc.
- running rsem-calculate-expression on the cluster
  https://bioinfo.umassmed.edu/index.php?p=33
- Look at macs2 and RSEM output files
- RNA-Seq – Look at RSEM output files
- See sample bsub commands for rsem-calculate-expression

Tasks:
Create lab schedule for using the ghpcc06 cluster
Explore the cluster and examine modules and tools for data analysis that are available
Upload Fastq files to ghpcc06 cluster