

Summer 2020

Unix/Linux for Informatic Analysis

https://github.com/sabrsyed/InformaticsTools_2020

Week 1

- Unix Primer for Biologists: Chapters U1 – U16
 - Learn how to use UNIX/Linux
- Logging in to the Cluster
 - Learn to navigate the Cluster
- Powerpoint Presentation: learn the technology behind genome sequencing, what does ChIP-Seq data look like
- Pipeline for ChIP alignment
- IGV and UCSC for viewing .bedgraph and .bam files

Tasks:

Install IGV and view Mtf1 ChIP-Seq .bedgraph files

Identify modules available on Cottontail

Week 2

- Unix Primer for Biologists: Chapters U17 – U34
 - Learn how to use UNIX/Linux
- GEO Omnibus for publicly available datasets
- <https://www.ebi.ac.uk/ena> for FASTQ files
- Filezilla
 - Uploading files to the Cluster
- Powerpoint Presentation: RNA-Sequencing, what does RNA-Seq data look like
- Pipeline for RNA-Seq alignment

Optional Exercise:

https://github.com/sabrsyed/InformaticsTools_2020/blob/master/01_Unix_QuickReview_ProblemSet.md