UNIX Review & Class Prep

1. Create a new folder for the class titled "BEDtools"

2. Move to this directory and download the course materials from the course website/provided link using wget.

3. Unzip the course materials

4. How many files are in this folder?

5. How many lines does the file `ChIPseq_ATF1_K562.narrowPeak` have?

6. What is the first line of the file `Gencode.chr15.bed`?

Exercise Set #1

1. How many individual reads are in the file `RNAseq_K562_chr22.bam`?

2. How many individual splicing events are in the data?

3. How many read pairs are there? (use the pre-sorted file `RNAseq_K562_chr22.sorted.bam`)