

## Homework 1

1. Write a script called `download_count.sh` which does the following.
  - Download the data file [https://ftp.ncbi.nlm.nih.gov/pub/UniVec/UniVec\\_Core](https://ftp.ncbi.nlm.nih.gov/pub/UniVec/UniVec_Core) from NCBI
  - Print out the count of the number of FASTA format sequences in this file - see [Wikipedia FASTA format](#) - each record starts with a >
2. Write a script called `summary_exons.sh` which summarizes the total length of exons in the file [data/rice\\_random\\_exons.bed](#)
  - read in the file
  - use a loop structure to read each line
  - add up the values into a variable
3. Write a script called `strand_gene_count.sh` to calculate the number of genes that are on the + and - strand in the file.
  - [https://fungidb.org/common/downloads/release-48/ScerevisiaeS288c/gff/data/FungiDB-48\\_ScerevisiaeS288c.gff](https://fungidb.org/common/downloads/release-48/ScerevisiaeS288c/gff/data/FungiDB-48_ScerevisiaeS288c.gff)