# Command Line for Data Filtering Exercises

**Before you begin, copy “example.tsv” from “penelopeprime” to your home directory and then open Terminal. Alternatively, you can download the example file from:**  
<https://funcgen2019.buschlab.org/downloads/command-line/example.tsv>

1. Using the awk and wc commands (and a pipe), find out how many genes are significantly differentially expressed (i.e. adjusted p-value < 0.05).
2. Using the cut command, make a new file that just contains the Ensembl ID, the adjusted p-value, the log2 fold change and the gene name and description.
3. Search for all the genes whose name begins with “si:”. How many are there?
4. How many genes have a biotype of “protein\_coding”?
5. Using just the awk command, make a new file that contains the Ensembl ID, gene name, chromosome and strand (in that order) for all the genes on the reverse strand.
6. Use the man command to find out about the more command. What option do you need to use with more to see line numbers in the example.tsv file?
7. Use the sort command to order the file by chromosome. Does the order of the non-numeric “chromosomes” make sense? Try using the -V option of sort, instead of -g. Is the order now better? (The -V option is technically for sorting version numbers, but it’s also really useful for sorting chromosome names!)
8. How many genes are between 10,000,000 bp and 20,000,000 bp on chromosome 1?