**Q**. What does the star character accomplish here? Ask Barry, or your class neighbor, if you are not sure!

The star character stands for the wild card for all the files that end with faa.gz

**Q**. How many sequences are in this mouse.1.protein.faa file? Hint: Try using **grep** to figure this out…

grep musculus mouse.1.protein.faa | wc -l

There are 67876 sequences in mouse1 file.

**Q.** What happens if you run the above command without the > mm-first.fa part?

Will print out the first 11 lines of the file.

head -11 mouse.1.protein.faa

**Q.** What happens if you were to use two ‘>’ symbols (i.e. >> mm-first.fa)?

will append the first 11 lines of the file at the end of the mm-first.fa file.

**Q.** How would you determine how many sequences are in the mm-second.fa file?

grep musculus mm-second.fa | wc -l

**Q**. Note the addition of the -r option here: What is it’s purpose? Also what about the \*, what is it’s purpose here?

The purpose of -r is to recursively copy all the files in the directory, and \* is the wildcard symbol, indicating that all the files in the work directory should be copied.

scp -i /c/BIMM143/week4/Bimm143\_Ruby\_Fa21/class13/bioinfo\_Tianru.pem ubuntu@ec2-35-86-84-179.us-west-2.compute.amazonaws.com:~/work/\* ./aws