# Day1 working lunch exercise

Name (Last, First):

You have 2 hours to complete this excercise. You may work together but each student should turn in their own copy of the exercise. We will grade on effort so please do your best to answer all the questions and work together!

Run code in the "terminal" and copy the command you ran and the output to this document. When finished save and submit it to canvas.

First, download this file containing the genome sequence of E. coli K12 using the `wget` command: https://github.com/doxeylab/learn-genomics-in-unix/raw/master/task1/e-coli-k12-genome.fasta.gz

## Questions:

1. Print out (in the shell) the first 5 lines of the file. Copy/paste them below.

Answer:

2. How many characters are in this file?

Answer:

3. How many lines are in the file?

Answer:

4. How many lines in the file contain the word “ATATATAT”?

Answer:

5. print file sizes rounded to a human-readable suffix (B, K, M etc) (hint: use the man page for ls!)

Answer:

6. get the ownership, size, and modification date for the file

Answer:

7. get the first 10 lines of the file and save them to a new file called “first10lines.txt”. Copy/paste the command you used to do this below.

Answer:

8. Print out the last 50 lines of the file to a new file called tail.txt. Paste the command that you used to do this into the answer space below. \_Do not paste the result into your assignment.\_

Answer:

9. What character (A, C, G, or T) is most common in tail.txt?

Answer:

10. How many lines in tail.txt contain the word “ATATATAT”?

Answer: