1. Give the wget command to download the [Lab3 folder](#) on GitHub (found in Data/Lab3) to your computer. (The folder is on [Canvas](#) as well if you'd like to manually download it, but please give the command to download from GitHub. GitHub is weird with .tar.gz files, so use this link: [https://raw.githubusercontent.com/raw-lab/BINF2111/main/data/Lab3.tar.gz](#))

wget [https://raw.githubusercontent.com/raw-lab/BINF2111/main/data/Lab3.tar.gz](#)

2. Give the command to extract and unzip the Lab3 folder.

 tar -xzvf Lab3.tar.gz

3. Give the command to unzip lab3_EFMCounts.csv.gz (found in the Lab3 folder you just extracted/unzipped).

 gunzip lab3_EFMCounts.csv.gz

4. Use the printf command to answer the following questions in a text file. Each answer should be on a new line.

What is your name?
How are you doing today?
When is your birthday?
Is there anything you are still confused about?

printf 'My name is Laasya Machineni \nI'm doing good! \nMy birthday is February 4th \nI'm not currently confused about anything.'

5. Give the command to print all but the 3rd, 4th, and 5th columns of lab3_EFMCounts.csv into a new file.

cut -d',' -f3-5 --complement Lab3/lab3_EFMCounts.csv > newfile.csv

6. Give the command(s) to count the number of images that are of high quality in lab3_EFMCounts.csv. Hint: Image quality occurs in column 7.

cut -d',' -f7 Lab3/lab3_EFMCounts.csv | grep -c "high" outputs 19

7. Provide two unique commands to convert lab3_EFMCounts.csv to a TSV. Both commands cannot use the same base command (use sed & tr, sed & awk, etc. instead of sed & sed).

sed 's/,/\t/g' Lab3/lab3_EFMCounts.csv > Lab3/lab3_EFMCounts_sed.tsv

cat Lab3/lab3_EFMCounts.csv | tr ',' '\t' > Lab3/lab3_EFMCounts_tr.tsv

8. Using lab3_EFMCounts.csv OR the TSV you created in question 7, find the top 10 images with the highest counts. Hint: Counts are in column 6.
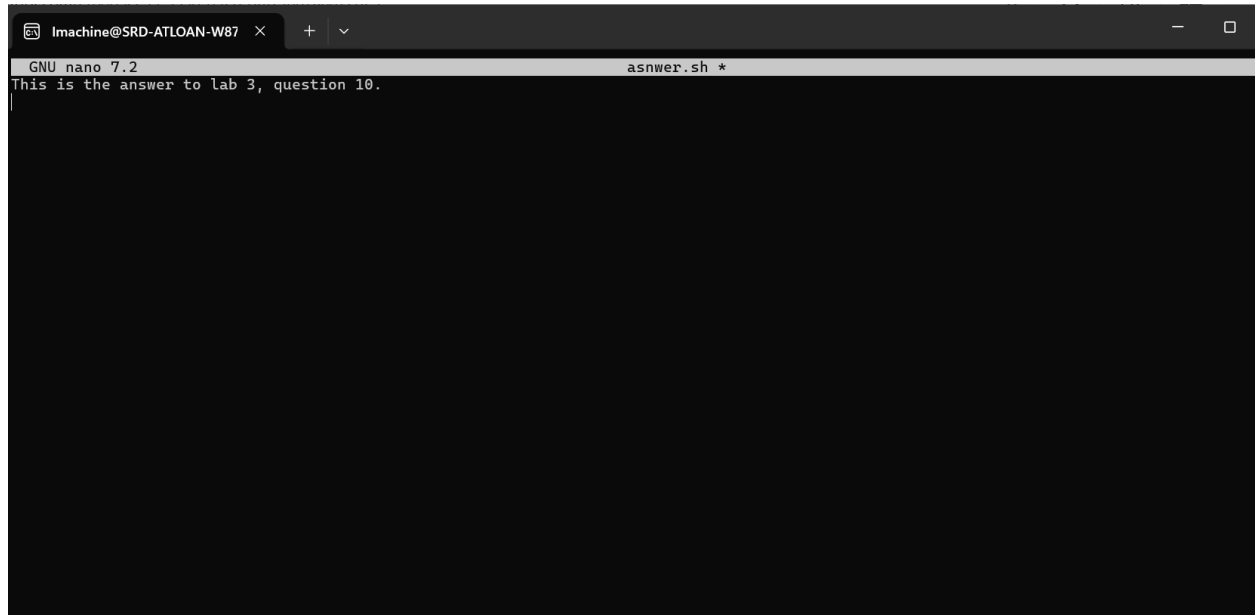
sort -t',' -k6,6nr Lab3/lab3_EFMCounts.csv | head -10

9. Give the command(s) to write a bash script that, when ran, will print out "Hello World". Be sure that the file ends in .sh!

echo -e '#!/bin/bash\necho "Hello World"' > hello.sh

bash hello.sh

10. Using any text editor, give the steps/commands to create a new file, write "This is the answer to lab 3, question 10.", and save and exit. You are not allowed to use printf or echo.

```
GNU nano 7.2                                        asnwer.sh *
This is the answer to lab 3, question 10.
|
```

nano answer.sh

This is the answer to lab 3, question 10.

BONUS I (2 pts): Find a way to convert lab3_EFMCounts.csv to SQL.

sed -n '1d; s/.*/INSERT INTO lab3_EFMCounts VALUES("&");/p' lab3_EFMCounts.csv | sed 's/,/","/g' > lab3_EFMCounts.sql

BONUS II (2 pts): Convert any nucleotide FASTA into amino acids using any command(s) you want.

grep -v '^>' input.fasta | tr -d '\n' | sed 's/.../&\n/g' | sed 's/ATG/M/g; s/TTT/F/g; s/TTC/F/g' | tr -d '\n'

I'm very confused about how to do this one.