Fill in with a list of commands

1. Write a bash script that prints any range of lines you give it from a file.

For example, bash script.sh file.tsv (prints lines 2 to 5). Place code here and make an executable script.

2. Oh NO! You tried to saved your file from a text editor and it got corrupted (Corrupted.fq) You must now find where the file is corrupted by looking at what is missing in the file?

Check against MultiN.fastq

Write a command or script (better) to find the corrupted lines then print their line numbers.

Describe what is messing in those lines?

3. Write a bash script or command to find sequences with >4 N's in the sequence (MultiN.fastq), have it print the header of the sequence and the sequence itself.

4. Write a bash script that count the number of ATG (starts), Serine (S), Arginine (R), and TAA, TAG, TGA (stops) from the example2.fasta file then converts them into amino acid M, S, R, and * for TAA, TAG, TGA for stop codon.

Remember that ATG encodes for methonine so the only count the from the beginning of the sequence or the end for the stops. Serine and Arginine can be throughout the sequence.

5. Write a bash script that tells me my username, current directory, the location of our desktop directory, and the date/time

BONUS 1 (3pts):

Write a bash script that converts this into a tsv file (specific files and all files)?

With this file:
Rat,steven,bear,Xi
Olf,thor,flower,Ton
Lazy,aaron,larry,jose
old,thor,flower,Ton

BONUS 2 (3pts):

Write a bash script that prints all the lengths of the sequences (MultiN.fastq)
For example, seq 1 – 101 etc. Place code here and make an executable script.

EXTRA BONUS (5 pts):

Convert all of example2.fasta into it's amino acids using any command(s) you want?

- Script here