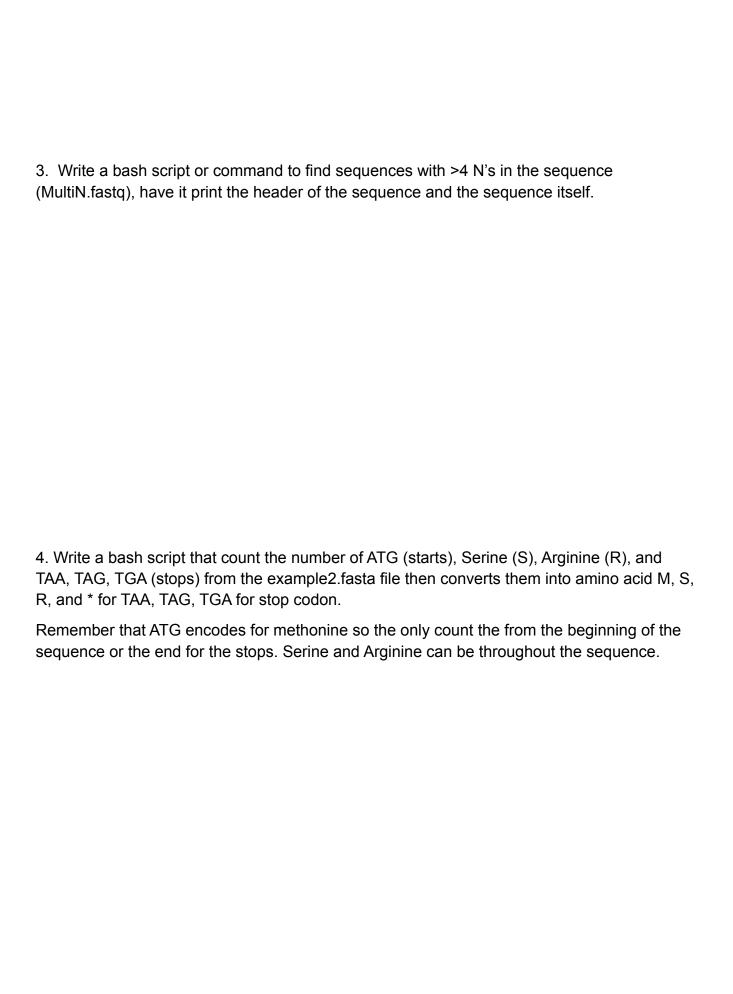
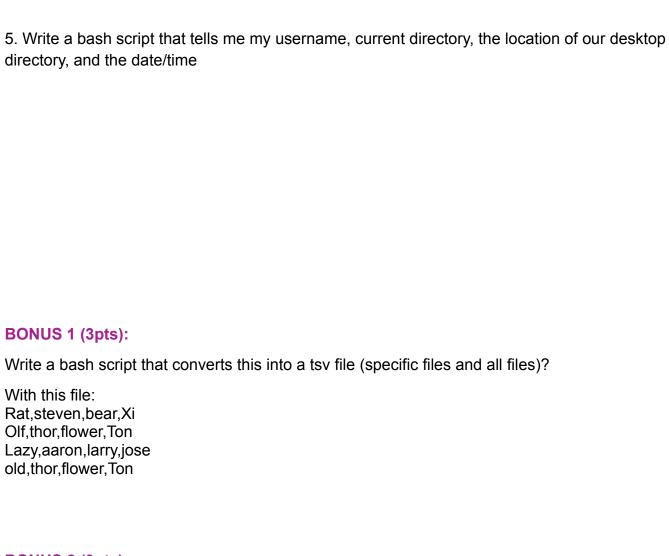
Fill in with a list of commands

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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?





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