Fill in with a list of commands

1. Write a python script (script that runs in terminal)! Provide the script! (2.5 pts)

The script must be able to provide two numbers in terminal, calculate the remainder post division, provide two conditionals on whether both numbers are divisible by 3, and print the number of times they are divisible by 3. Please write them as functions.

2. Write a python script (script that runs in terminal)! Provide the script! (2.5 pts)

The script must use argparse to load the CoV_Sprotein.faa file. Which the file is on canvas and github.

The argparse example is here on our class github.

https://github.com/raw-lab/BINF2111/blob/main/bin/argparse_example.py

Links to an external site.

As function(s) provide a length of each sequence within the file and the percentage of Methionine, Leucine, Arginine, and Tyrosine within each sequence. Use a conditional to test if each sequence starts with a methionine. Count the number of sequences that start with methionine, total sequences, and the sequences that dont start with methionine. Use an assert statement the validate the count of sequences that start with methionine.

3. Within the script it must contain a function that takes two arguments – a protein sequence and an amino acid residue code for Methionine, Leucine, Arginine, and Tyrosine. It must return the percentage of the protein that the amino acid makes up. Write as a function(s). Provide the script! (2.5 pts)

Use the following assertions to test your function (part one):

assert aa_function("MSRSLLRFLLFLLLPPLP", "M") == 5

assert aa_function("MSRSLLRFLLFLLLPPLP", "R") == 11

assert aa function("MSRSLLRFLLFLLLPPLP", "L") == 47

assert aa_function("MSRSLLRFLLFLLLPPLP", "Y") == 0

It must pass all these assertions.

4. From the AT content you did last week from argparse transform it into a function in a script you previously put together. One of the new outputs is to print out (from example2.fasta) all sequences with AT content less then 50%, then you must write a condition statement (ifelse) and for each sequence print whether the sequence is high (> 65% GC), medium (<65 to >45% AT), and low (0.45%). Write a python script (script that runs in terminal)! Provide the script! (2.5 pts). Please write them as functions.

BONUS (5 pts).

Access granted script. Using a conditional, function, and test with an assert statement.

Give a list of names that are preferred or access granted, if not that name access denied.