## 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 you 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. <a href="https://github.com/raw-lab/BINF2111/blob/main/bin/argparse\_example.py">https://github.com/raw-lab/BINF2111/blob/main/bin/argparse\_example.py</a>

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 an assertions to test if each sequence starts with a methionine with a conditional of with a number of those that don't.

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

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Use the following assertions to test your function (part one): assert aa_function("MSRSLLRFLLFLLLLPPLP", "M") == 5 assert aa_function("MSRSLLRFLLFLLLLPPLP", "R") == 10 assert aa_function("MSRSLLRFLLFLLLLPPLP", "L") == 50 assert aa_function("MSRSLLRFLLFLLLLPPLP", "Y") == 0
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Use the following assertions to test your function (part two):

assert aa_function("MSRSLLRFLLFLLLLPPLP", ["M"]) == 5

assert aa_function("MSRSLLRFLLFLLLLPPLP", ['M', 'L']) == 55

assert aa_function("MSRSLLRFLLFLLLLPPLP", ['M', 'S', 'L'])) == 70

assert aa_function("MSRSLLRFLLFLLLLPPLP") == 65
```

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 read 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.