

Fill in with a list of commands

1. Write a python script (script that runs in terminal)! Provide the script! (5 pts)

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. Use argparse for parameters where you can give a file (e.g., example2.fasta) or give it a protein sequence of your choice (e.g., MMLLLYWW)

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
```

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.

2. 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! (5 pts)