Fill in with a list of commands

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

Using this input protein = 'vlspadknvww'

a) It must convert from lower to upper case.

b) Count the number of valine

c) Count the number of tryptophan

d) Count the length of the sequence

e) Count the number of polar neutral side-chains

f) Replaces all tryptophans with glycine

g) Prints them in a final list in terminal or output

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

Using this input sequence = GAATTCAGTAGATAGTAAGGAATTCTATGTATGTAGGCGCGCGTGCGCGTGCGCGGAATTC

a) Count the number of AT repeats

b) Count the number of GC repeats

c) Prints the complement of this sequence

d) Count the number of EcoR1 sites (G*AATTC)

e) Prints the three sequences post EcoRI cutting

f) Counts AT and GC content

g) Replaces all T with U and prints sequence

g) Prints them in a final list in terminal or output