Steps:

1. ask user for DNA sequence [tip: use function *input()*]

2. compute statistics [tip: use function *count()*]

3. print results

4. define dictionary with restriction enzymes [tip: see class slides #17]

5. ask user for restriction enzyme [tip: use this as the *key* to the dictionary defined in step 4]

6. test if the DNA sequence contains the restriction site [tip: use the operator *in* and take a peek at slide #17]

Algorithm 1 Assigment 1 pseudocode

1: $DNA \leftarrow userinput$
2: $numberA \leftarrow Count"A"inDNA$
3: Print $numberA$
4: $numberC \leftarrow Count"C"inDNA$
5: Print $numberC$
6: $numberG \leftarrow Count"G"inDNA$
7: Print $numberG$
8: $numberT \leftarrow Count"T"inDNA$
9: Print $numberT$
10: $REdic \leftarrow "EcoRI" : "GAATTC", "BamHI" : "GGATCC", "HindIII" : "AAGCTT", "NotI" : "GC$
11: $Enz \leftarrow userinput$
12: $Cut \leftarrow REdic[Enz]inDNA$
13: Print Cut