Introduction to Script Programming
Spring 2021 – Exam 2
April 27, 2021

1. Write a python script that asks the user to type a short DNA sequence (ACGT) (example ACTGGTCAGTGAC) and replaces all the "T" with "U" and print it out on the terminal.

2. Write a python script that takes as input two tab delimited text files and merge them together. The two files should have one common column based on which you will merge them. (names.txt and majors.txt)

   a. You should ask the user to enter the path to the first file and check if it exists and readable. If not, ask him to reenter it.
   b. Ask the user to enter the path to the second file and also check if it exists or not.
   c. Ask the user to enter the column title that needs to be used to merge the files (examples: Student_ID)
   d. Save the column names (header) of the first file in a list
   e. Save the column names (header) of the second file in a second list
   f. Check if the column name specified in part c. (Student_ID) is found in both lists. If not print out on the terminal that the column is not found and specify in which file it is not found.
   g. If the column is found in both files, create two dictionaries dict1 and dict2, one for each file, with the key being the value of the "Student_ID" (201909199) and the value the whole remaining columns for that row.
   h. Create a list, allKeys, that include all the Keys in both dictionaries combines, keys of dict1 and keys of dict2. Careful!!! Not all IDs are in both files!!!
   i. Create a new dictionary, mergedDict, with the keys being allKeys created in part h. and the values the concatenation of the value in dict1 and dict2.
   j. Print out the mergedDict and write it to a file called "mergedFiles.txt"
   k. Count the number of Ids in that are common to both files and the number unique in each file.
   l. Ask the user to enter the ID of one student and print out all the value of that ID in mergedDict.