Program 3 Report

Objectives

The objectives of this program are to get more comfortable with string operations and manipulation in Python along with using conditional statements and loops to solve a simplified version of a real-world application.

Major Variables

* sequence – string input used for most of the program that is run.
* s – shortened variable used to manipulate the strings from sequence
* sq – function to determine length of the string given
* seq1 and seq2 – string inputs used to fulfill functions need more than one string.
* valid\_seq – function used to verify the validity of the DNA sequence given
* seq\_match – function used to verify if the correct part of the string match
* seq \_reverse – function used to reserve a given sequence string

The purpose of this code is to use the concepts of bioinformatics in computing simple operations involving DNA. Although the use of any such string would still bring out the same practical outcomes in the program. The first part of the code does the follow:

* Computes a mirror for the DNA returning the mirror component of each base
* Computing a “reverse” of the DNA sequence given
* Verifying the validity of the DNA string given
* Completing the task above for two DNA strings

The second part of the program does the following:

* Counts the total number of matches between two DNA strings
* Computes the length of the longest consecutive matches