HW 2

Write a Perl program called score.pl that computes the number of correctly aligned residues in an alignment with respect to a given benchmark alignment. The program will take two inputs: (1) filename containing a "true" benchmark alignment of two proteins in FASTA format and (2) filename containing a computed alignment of the two proteins using an alignment program. Your program should output the number of residues "correctly" aligned residues in the computed alignment as a percentage of the length of the benchmark alignment.

Send your program as FirstnameLastnameScore.pl to usman@cs.njit.edu by Wednesday February 28th 1pm.