BNFO 240 HW 1

Write a Perl program computes the optimal alignment of two sequences from a FASTA formatted file called "dna.fasta". Your program should use a match score of 3, mismatch score of -1, and gap penalty of -3. Your program should save the optimal alignment and the optimal score to a file called "alignment.txt".

This program is due Wednesday February 7th by 1pm. Send the .pl as an attachment to usman@cs.njit.edu. Collaboration is allowed but you must write the final program on your own and by yourself.