CSE 4065 – Computational Genomics

Programming Assignment # 2

DUE TO: 28/12/2022 - 23:55

In this assignment, you are going to implement dynamic pairwise sequence alignment algorithm. You will use your program to align DNA sequences. DNA sequences will be read from your input file. You will use gap and mismatch penalties, match scores while performing alignment. Your program will find the optimum alignment between the given sequences using the following scores.

Default values for scores are as follows:
- match score: +3
- mismatch score: -1
- affine gap penalty: gap opening penalty: -1, gap extension penalty: -0.5

You will be given 5 test sequences and find the optimum alignment for these sequences. Your program will give the optimum alignment and its score as an output.

You will write a report including the alignments for the 5 test sequences with their scores. (You can put screenshots from your program outputs) Your report will also contain the detailed information about your implementation.

Notes:
- No late homework will be accepted!
- In case of any form of copying and cheating on solutions, all parties/groups will get ZERO grade. You should submit your own work.

What to submit?

A soft copy of your *source codes* which are extensively commented and appropriately structured and a *project report* should be submitted through Canvas.

All files should be submitted as **one zip** file.