

Indraprastha Institute of Information Technology Delhi (IIITD)
Department of Computational Biotechnology

BIO213 – Introduction to Quantitative Biology

ASSIGNMENT-1 (February 18, 2022)

Instructions:

1. You are required to submit the assignments by next Sunday, 27 February 2021.
2. Use Python to write your program.
3. Use your Roll no. and name to save the file.
4. You have to submit well commented scripts, and a PDF file with all the properly labelled answers.
5. Requests for extension of submission deadline will not be entertained.

The objective of this assignment is to learn the implementation of dynamic programming for finding the best local and global alignments for the given DNA sequences.

Question 1. Compute global alignment between the following DNA sequences using dynamic programming and the scoring scheme given below.

DNA sequences: (1) ATCAGAGTA, (2) TTCAGTA
Scoring function: Match = +2, Mismatch = -1, Gap = -1

- a) Provide the bidimensional array obtained for computing the optimal alignment. [5 marks]
- b) Is there more than one possibility of optimally aligning the given sequences? [5 marks]
- c) If yes, show all the optimal alignments with their scores. If no, provide the best alignment obtained with its corresponding score. [10 marks]

Question 2. Using the sequences and scoring scheme provided in Question 1, compute the most optimal local alignment using dynamic programming.

- a) Provide the generated bidimensional array. [5 marks]
- b) Provide all the alignments obtained with their corresponding scores. [10 marks]

Question 3. What changes were required in the program in order to perform local rather than global pairwise sequence alignment? [5 marks]

Question 4. Will changing the scoring scheme to *Match* = +2, *Mismatch* = -1, *Gap* = -2 modify the results obtained in Question 1 and 2 above? If yes, show the results and justify the same. [10 marks]