

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

**BIO213 – Introduction to Quantitative Biology**

**ASSIGNMENT-1**

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**Instructions:**

1. You are required to submit the assignments by next Saturday, 13 February 2021.
2. Use Python or R to write your program.
3. Name the file you submit as [Roll no.]-[python/R]. For example, 2019227-python or 2019227-R.
4. You also have to submit well commented code that you will write to solve the following problems.
5. Requests for extension of submission deadline will not be entertained.

The aim is to use dynamic programming for finding the best local and global alignment for the given DNA sequences, their corresponding alignment scores, and possibility of multiple optimal alignments.

**Question 1.** Find the best **global alignment** between the following DNA sequences using dynamic programming and the provided scoring scheme.

DNA sequences:	Scoring function:
1. ATCAGAGTA	Match = +2
2. TTCAGTA	Mismatch = -1
	Gap = -1

- a) Provide the generated dynamic programming matrix. [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 dynamic programming matrix. [5 marks]
- b) Provide the best alignment obtained with its corresponding score. [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 the above questions? If yes, comment on the same. [10 marks]