

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

**BIO213 – Introduction to Quantitative Biology**

**ASSIGNMENT-1 (March 18, 2023)**

---

**Instructions:**

1. You are required to submit the assignments by next Sunday, 26 March 2023.
2. Use Python to write your program.
3. Compile everything into a single PDF. Use <roll no.-name> to label and save the file.
4. You are also required to submit a well commented working code.
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 given scoring scheme.

DNA sequences: (1) GATGCGCAG, (2) GGCAGTA

Scoring function: Match = +2, Mismatch = -3, 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.** Will changing the scoring scheme to [Match = +2, Mismatch = -1, Gap = -3] modify the results obtained in Question 1? If yes, show the results and justify the same. [10 marks]

**Question 3.** Compute the most optimal local alignment (using dynamic programming) for the same DNA sequences, and the scoring scheme provided in Question 2.

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

**Question 4.** What changes were required in the program in order to perform local rather than global pairwise sequence alignment? [5 marks]