Ahmedabad University

School of Arts and Sciences

BIO213 Bioinformatics

IMSc Programme
Mid Term Examination 2022 (Monsoon Semester)

Total Marks = 30 **Time – 1 hours 30 minutes**

Enrolment Number:..... **SET 1**
Date: 18-09-2022 (Exam date)
No. of printed pages: 1 (Pages of question paper)

Note: For problems 1 and 2, you should present your scoring/traceback matrices as well as the best alignment. For Problem 3 provide a screen shot of each step you performed. The screenshot should be of the whole screen with sufficient resolution read your results.

1) Find the best local alignment between sequences ATACTGGG and TGACTGAG and give us the total score of alignment. Here assume the scoring scheme is +1 for match, -1 for mismatch and -2 for an alignment with a gap.

2) Find the best global alignment between sequences ACTGATTCA and ACGCATCA and give us the total score of alignment. Use -2 as a gap penalty, -3 as a mismatch penalty, and 2 as the score for a match.

3) Find a novel gene using BLAST suite for the accession number NP_000389.1. You will need to the three step protocol discussed during the class to deduce a novel gene.

A BLAST hit is considered to be a novel gene hit if

(a) If you can get BLAST hit of the protein in the database after excluding the species corresponding to the accession number provided to you.
(b) If there is a match with >95% identity to a different species than the one you started with.
(c) Which other BLAST parameters did you check? What were the values of these parameters.
(d) Perform multiple sequence alignment of the bottom five of 500 BLAST hits.