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M.Sc. (BI) (Semester - 4th)

COMPUTATIONAL TECHNIQUES FOR GENOME ASSEMBLY & ANALYSIS (M.Sc. (BI) - 403)

Time : 03 Hours   Maximum Marks : 75

Instruction to Candidates:

1) Section - A is **compulsory.**

2) Attempt any **Nine** questions from Section - B.

Section - A

Q1)   (15 x 2 = 30)

a) What is Blast?

b) What is SRS?

c) Define Homology.

d) Give basic steps in phylogenetic analysis.

e) What is Dot Matrix method of sequence alignment?

f) Align the following sequence using BLOSUM 80
   Sequence #1: DALTNA
   Sequence #2: DLLVAQTNAMSDA
   Use gap penalty of – 5.

g) Give application of BioEdit.

h) Write any four molecular modeling programs of biochemical interest.

i) Write a short note on molecular Docking.

j) Draw a comparison between FASTA & BLAST algorithms.

k) Explain pattern recognition.

P.T.O.

l) What are the steps in profile searching?

m) Write briefly about dynamic programming algorithm.

n) What is Motifs?

o) Discuss Consensus Sequence.

Section - B

(9 x 5 = 45)

Q2) Draw an illustrated comparison between DOT matrix & dynamic programming method of sequence alignment.

Q3) What do you understand by Biological Databases? State its importance.

Q4) Discuss the steps used by BLAST algorithm.

Q5) Explain sequence alignment using Bayesian statistical methods.

Q6) Explain CpG Islands approach to identify the gene in contings.

Q7) Describe Heuristics methods of sequence alignment.

Q8) Compare and discuss PAM and BLOSUM matrices.

Q9) What are the major extensions of BLAST? Discuss the areas of application of these Programs.

Q10) Discuss the steps for constructing a profile HMM.

Q11) How can you find open reading frames (ORFs) in a gene DNA sequence?

Q12) What are the various "Wet-lab" techniques for gene prediction?

Q13) What are the recommended steps for a FASTA search?