

## Cluster Innovation Centre

Examination : End Semester Examination-May/June 2024  
Name of the Course : B.Tech. (Information Technology & Mathematical Innovations)  
Name of the Paper : *In Silico Biology*  
Paper Code : 3124002007  
Semester : IV

Duration: 2 hours

Maximum Marks: 60

### Instructions for Candidates

Attempt any four questions. Each question carries equal marks.

Q. 1. How is global alignment different from local alignment? Name the algorithms commonly used for alignment. Describe how modern genomics is dependent on bioinformatics? Also, discuss, how computational biology is defining recent biological advances. [3+2+5+5=15]

Q. 2. What are genomic and cDNA libraries? Also, discuss and compare gene expression databases, and gene function databases, giving one example of each. [8+7=15]

Q. 3. Write short notes for any three of the following: [15]  
(i). Motif and Promoter searches (ii). Phylogenetic analysis  
(iii). Gene Cards (iv). Scoring matrices

Q. 4. Discuss about various types of protein interactions and name at least one technique for detecting each type of interactions. Describe and compare BioGRID and STRING, especially in terms of their purpose, database and unique information these provide. [8+7=15]

Q. 5. Elaborate on scoring matrices and their significance in bioinformatics. How are these scoring matrices used to compare sequences and how does scoring matrices for nucleic acids and proteins differ? Explain the PAM and BLOSUM series in simple terms. [5+5+5=15]

Q. 6. Differentiate between any two of the following: [15]  
(i). Multiple sequence alignment and pairwise sequence alignment  
(ii). Morphological-based and Molecular-based phylogeny  
(iii). Primary and Secondary databases