Roll No:

# BTECH

## (SEM. VI) THEORY EXAMINATION 2025-26

## BIOINFORMATICS -II

**TIME: 3 HRS** **M.MARKS: 70**

**Note:** Attempt all Sections. In case of any missing data; choose suitably.

## SECTION A

**1. Attempt *all* questions in brief.** **02 x 7 = 14**

| Q no. | Question | CO | Level |
|---|---|---|---|
| a. | State the difference between orthologs and paralogs in homology detection. | 1 | K1 |
| b. | Name the secondary and tertiary structure prediction challenges in proteins. | 1 | K1 |
| c. | List down any two tools used for RNA structure prediction. | 2 | K1 |
| d. | Draw any 4 RNA secondary structures and write their features. | 2 | K2 |
| e. | Define simulated annealing. | 3 | K1 |
| f. | Explain force field in molecular modeling. | 4 | K3 |
| g. | Paraphrase simulation in bioinformatics. | 4 | K2 |

## SECTION B

**2. Attempt any *three* of the following:** **07 x 3 = 21**

| | | | |
|---|---|---|---|
| a. | Compare template-based (homology modeling) vs. ab initio methods for tertiary protein structure prediction; analyze strengths and weaknesses. | 1 | K4 |
| b. | Extend a detailed note on RNA secondary structure prediction. Explain any one method in detail. | 2 | K2,K3 |
| c. | Summarize clustering. Extend a detailed note on Genetic algorithms and its applications. | 3 | K3,K4 |
| d. | What do you understand by potential energy calculation? Add a note on molecular modeling. | 4 | K2 |
| e. | Evaluate the importance of QSAR, ADME, and Lipinski's rule in drug development. | 5 | K5 |

## SECTION C

**3. Attempt any *one* part of the following:** **07 x 1 = 07**

| | | | |
|---|---|---|---|
| a. | List down the features of Next Generation Sequencing Technique. Extend a detailed note on pyro sequencing. | 1 | K2 |
| b. | Compare prediction based on self-complementary regions versus most probable structure (partition function); analyze why the latter provides base-pair probabilities for a microRNA precursor. | 2 | K4 |

**4. Attempt any *one* part of the following:** **07 x 1 = 07**

| | | | |
|---|---|---|---|
| a. | Select a case study and explain the mechanism for gene expression analysis using microarray technology. | 1 | K6 |
| b. | Design a workflow combining sequence covariance with MFE for predicting a viral RNA genome structure. | 2 | K4,K5 |

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**5. Attempt any *one* part of the following:** **07 x 1 = 07**

| | | | |
|---|---|---|---|
| a. | Compare how Artificial Neural Networks use backpropagation for protein structure prediction versus Hidden Markov Models for gene finding | 3 | K4 |
| b. | Summarize Continuous, Discrete-event and Hybrid simulation techniques. Also add examples for each of them. | 4 | K2,K3 |

**6. Attempt any *one* part of the following:** **07 x 1 = 07**

| | | | |
|---|---|---|---|
| a. | Differentiate between ligand-based and structure-based drug designing approaches. Also describe techniques for managing large biological document collections. | 5 | K4 |
| b. | Compare and contrast between parametric and non-parametric test. Support your answer with examples. | 3 | K4,K5 |

**7. Attempt any *one* part of the following:** **07 x 1 = 07**

| | | | |
|---|---|---|---|
| a. | Apply the steps involved in in silico drug designing to outline how a potential drug candidate is identified. | 5 | K3 |
| b. | "Force fields and computational simulation techniques are fundamental tools in molecular modeling." Analyze the role of differential equation solvers, parameter estimation, and sensitivity analysis in simulation studies. Also evaluate their importance in accurate modeling of real-world systems. | 4 | K5,K6 |