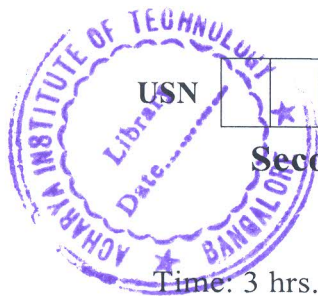


# CBCS SCHEME



18BBT22

Second Semester M.Tech. Degree Examination, June/July 2019  
**Advanced Bioinformatics**

Time: 3 hrs.

Max. Marks: 100

Note: Answer any FIVE full questions, choosing ONE full question from each module.

### Module-1

- 1 a. Explain the levels of Protein structure. (10 Marks)  
b. Summarize the goals and potential benefits of Human Genome Project. (10 Marks)

OR

- 2 a. Outline the DNA sequencing method by Sanger method and list the limitations. (10 Marks)  
b. Write the steps of Central dogma. (05 Marks)  
c. Comment on the necessity of mapping the genes in each chromosome. (05 Marks)

### Module-2

- 3 a. Classify the biological databases with suitable example. (10 Marks)  
b. Outline the schematic of a typical progressive alignment procedure for multiple sequence alignment. (10 Marks)

OR

- 4 a. List the challenges of Biological databases. (05 Marks)  
b. State Markov model. Draw a simplified HMM involving two inter connected Markov chains with observed states and common "begin" and "end" states. (07 Marks)  
c. Explain the steps involved in Viterbi algorithm. (08 Marks)

### Module-3

- 5 a. Discuss the steps involved in modeling a 3 – D structure of protein for which experimental 3D structure is not available in PDB. (10 Marks)  
b. Draw the schematic representation of structure – based drug design and list the limitations. (10 Marks)

OR

- 6 a. Expand ADMET and comment on the necessity of performing ADMET analysis in virtual screening. (08 Marks)  
b. What are Transmembrane proteins? With example, explain how these protein play role in disease. (08 Marks)  
c. List the limitations and advantages of Insilico drug design. (04 Marks)

### Module-4

- 7 a. Write the PERL code to convert DNA to protein. (10 Marks)  
b. List the key features of Discovery studio. (05 Marks)  
c. Highlight the application of Quantum mechanism. (05 Marks)

OR

- 8 a. List the advantages and benefits of working with PERL. (08 Marks)  
b. Classify the methods for virtual screening of compounds. (12 Marks)

Important Note : 1. On completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages.  
2. Any revealing of identification, appeal to evaluator and/or equations written eg, 42+8 = 50, will be treated as malpractice.

**Module-5**

- 9 a. Write the steps in pharmacophore generation. (06 Marks)  
b. List the unique features of MODELER for protein modeling. (06 Marks)  
c. Explain the concept and method of simulating a protein – drug interaction. (08 Marks)

**OR**

- 10 a. Explain Fragment – based drug design approach. (10 Marks)  
b. Explain CHARMM. Outline general CHARMM project. (10 Marks)

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