CBCS SCHEME

USN | | | | | | | | | | |

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)**

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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