Name:

Enrolment No:

UPES
End Semester Examination, May 2025
Course: Computer Application and Bioinformatics **Semester: II**
Program: B.Sc. (Microbiology, Clinical Research, FN&D) **Duration: 3 Hours**
Course Code: HSCC1028 **Max. Marks: 100**

Instructions: The question paper comprises FOUR sections; all sections are compulsory.
Read the instructions given before each section carefully.

S. No.	**Section A** **Short answer questions/ MCQ/T&F** **(20Qx1.5M= 30 Marks)**	**Marks**	**COs**
Q 1	Which of the following is **NOT** an input device? a) Mouse b) Scanner c) Monitor d) Keyboard	**1.5**	**CO1**
Q 2	What is the primary function of an operating system? a) Creating graphics b) Managing hardware and software resources c) Typing documents d) Editing videos	**1.5**	**CO1**
Q 3	**True or False:** LAN covers a larger geographical area than WAN.	**1.5**	**CO1**
Q 4	HTTP is mainly used for: a) File transfer b) Email communication c) Webpage transmission d) Data encryption	**1.5**	**CO1**
Q 5	Expand BIOS.	**1.5**	**CO1**
Q 6	The application software 'Excel' is used mainly for: a) Image editing b) Data storage c) Spreadsheet tasks d) Web browsing	**1.5**	**CO1**
Q 7	Which is **NOT** a network device? a) Router b) Switch c) Monitor	**1.5**	**CO1**

	d) Access Point		
Q 8	Which file format is commonly used for representing nucleotide sequences? a) CSV b) FASTA c) XML d) DOC	**1.5**	**CO2**
Q 9	**Match the following:** GenBank - ________ SWISS-PROT - ________ PDB - ________ (Options: a) Protein sequences, b) Nucleotide sequences, c) 3D structures)	**1.5**	**CO2**
Q 10	**True or False:** BLAST is used for sequence alignment.	**1.5**	**CO3**
Q 11	What is the full form of PPI in databases?	**1.5**	**CO3**
Q 12	Identify the method used for global alignment: a) Smith-Waterman b) Needleman-Wunsch c) FASTA d) BLAST	**1.5**	**CO3**
Q 13	Which of the following predicts protein secondary structure? a) SWISS-MODEL b) DSSP c) STRING d) BLAST	**1.5**	**CO3**
Q 14	In bioinformatics, which alignment type allows gaps at the ends? a) Global Alignment b) Local Alignment c) Semi-global Alignment d) Dot Plot	**1.5**	**CO3**
Q 15	State the name of the database that provides metabolic pathway information.	**1.5**	**CO3**
Q 16	**True or False:** Homology modeling requires a template structure.	**1.5**	**CO4**
Q 17	Which tool is used for chemical structure databases? a) KEGG b) PubChem c) STRING d) PDB	**1.5**	**CO4**
Q 18	Which is an AI-based protein structure prediction tool? a) MODELLER b) RasMol c) AlphaFold d) DSSP	**1.5**	**CO4**

Q 19	**True or False:** The GOR method is used for tertiary structure prediction.	**1.5**	**CO4**
Q 20	State the name of one software used for protein structure visualization.	**1.5**	**CO4**
Section B **(4Qx5M=20 Marks)**			
Q 1	Differentiate between system software and application software with examples.	**5**	**CO1**
Q 2	Discuss primary and secondary biological databases with two examples each.	**5**	**CO2**
Q 3	Explain the concept of pairwise sequence alignment and mention any two methods used.	**5**	**CO3**
Q 4	Illustrate the steps involved in homology (comparative) modeling?	**5**	**CO4**
Section C **(2Qx15M=30 Marks)**			
Q 1	Describe the types of sequence alignment (Global, Local, Semi-global, Heuristic). Support your answer with examples and applications.	**6+3+6**	**CO3**
Q 2	Suppose you retrieved a protein sequence. Propose the steps and tools that you will apply to find a homologous protein structure and then predict the 3D structure using bioinformatics?	**5+5+5**	**CO4**
Section D **(2Qx10M=20 Marks)**			
Q 1	Explain the methods used for protein secondary structure prediction. Discuss Chou-Fasman and GOR methods in detail.	**5+5**	**CO4**
Q 2	Discuss the steps and tools involved in molecular docking in detail.	**5+5**	**CO5**