

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2025

B. Tech-VIII Semester [All except Bio]

COURSE CODE (CREDITS): 21B1WBT833 (3)

MAX. MARKS: 35

COURSE NAME: Computational Biology for Engineers

MAX. TIME: 2 Hours

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Udayabhanu M

**Note:** (a) All questions are compulsory.

(b) The candidate is allowed to make Suitable numeric assumptions wherever required  
for solving problems

Q.No	Question	CO	Marks															
Q1	<p>Answer the following questions in context to multiple sequence alignment:</p> <p>a) Interpret the given multiple sequence alignment and write your inferences briefly.</p> <table> <tr> <td>S. scrofa</td> <td>MTELPAPLSYFQNAQMSEDNHVSNIWSSQNDSRERHEHSIERRRGNS</td> <td>60</td> </tr> <tr> <td>B. taurus</td> <td>MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDSRERHEHGNERRRGNTESVNENRAPSS</td> <td>60</td> </tr> <tr> <td>H. sapiens</td> <td>MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEH-HDRRSLGHPEPLSNGRPQGH</td> <td>59</td> </tr> <tr> <td>M. musculus</td> <td>MTEIPAPLSYFQNAQMSEDSHSSAIRSQNDSQERQQ-HDRQLDNPEPISNGRPQSH</td> <td>59</td> </tr> <tr> <td></td> <td>*****:*****:*****:*****:*****:*****:*****:*****:*****</td> <td></td> </tr> </table> <p>b) Calculate the sum of pairs for the given alignment:</p> <p style="text-align: center;"> <b>Seq1:</b> PKTV  <b>Seq2:</b> PKTV  <b>Seq3:</b> PKVV     </p> <p>c) Describe the progressive refinement approach for multiple sequence alignments?</p>	S. scrofa	MTELPAPLSYFQNAQMSEDNHVSNIWSSQNDSRERHEHSIERRRGNS	60	B. taurus	MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDSRERHEHGNERRRGNTESVNENRAPSS	60	H. sapiens	MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEH-HDRRSLGHPEPLSNGRPQGH	59	M. musculus	MTEIPAPLSYFQNAQMSEDSHSSAIRSQNDSQERQQ-HDRQLDNPEPISNGRPQSH	59		*****:*****:*****:*****:*****:*****:*****:*****:*****		3-5	3+3+4 =10
S. scrofa	MTELPAPLSYFQNAQMSEDNHVSNIWSSQNDSRERHEHSIERRRGNS	60																
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Q2	<p>Compare the given sequences using Needleman-Wunsch algorithm: Scoring scheme: Match = 1, Mismatch = -1, Gap = -2.</p> <p><b>Seq1:</b> ATTGC <b>Seq2:</b> AGGC</p>	3,4	5															
Q3.	<p>Short notes:</p> <ul style="list-style-type: none"> <li>a) Local vs. Global sequence alignment</li> <li>b) Homologous sequences</li> <li>c) Origination Vs. length gap penalty</li> <li>d) INSDC database</li> <li>e) Central dogma</li> </ul>	1-5	5															

Q4.	What is pharmacophore modeling? Explain its significance in drug discovery and describe the key features that constitute a pharmacophore model.	2,3	5
Q5.	Differentiate between High-Throughput Screening (HTS) and Virtual Screening (VS) in drug discovery. Discuss their methodologies, advantages, and limitations.	3,4	5
Q6.	What is molecular docking? Explain its role in drug discovery and discuss the process involved in the molecular docking.	4,5	5