

# Gandhi Institute of Engineering and Technology University, Odisha, Gunupur (GIET University)



B. Tech (Sixth Semester - Regular) Examinations, April 2026

**23BBTPC36002 – Bioinformatics**

**(Biotechnology )**

Time: 3 hrs

Maximum: 60 Marks

(The figures in the right hand margin indicate marks)

## PART – A

(2 x 5 = 10 Marks)

Q.1. Answer **ALL** questions

- |                                                               |  | CO # | Blooms Level |
|---------------------------------------------------------------|--|------|--------------|
| a. Write the process of Entrez                                |  | CO1  | K1           |
| b. Expand KEGG. Write tis layer                               |  | CO2  | K1           |
| c. What is the difference between global and local alignment? |  | CO3  | K1           |
| d. Name the windows of Swiss PDB Viewer                       |  | CO5  | K1           |
| e. Write the flowchart of QSAR                                |  | CO5  | K1           |

## PART – B

(10 x 5 = 50 Marks)

Answer **ALL** the questions

- |                                                                                                                                                                                                                                                                                                                                                                                         |    | Marks | CO # | Blooms Level |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|-------|------|--------------|--|---|---|---|---|---|---|--|--|--|---|---|---|--|--|---|---|---|---|--|---|----|----|----|---|
| 2. a. Explain Swiss PDB database                                                                                                                                                                                                                                                                                                                                                        | 5  | CO1   | K1   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| b. Discuss the storing and retrieving method of NCBI database                                                                                                                                                                                                                                                                                                                           | 5  | CO1   | K1   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| (OR)                                                                                                                                                                                                                                                                                                                                                                                    |    |       |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| c. Explain SCOP and CATH                                                                                                                                                                                                                                                                                                                                                                | 5  | CO1   | K1   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| d. Discuss the metabolic pathway database                                                                                                                                                                                                                                                                                                                                               | 5  | CO1   | K1   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| 3.a. Find alignment score, optimal alignment and the signification of two sequence AAGATA and AATCTATA by using Dot matrix                                                                                                                                                                                                                                                              | 5  | CO2   | K2   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| b. Explain the option of BLAST and FASTA                                                                                                                                                                                                                                                                                                                                                | 5  | CO2   | K1   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| (OR)                                                                                                                                                                                                                                                                                                                                                                                    |    |       |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| c. Design a rooted phylogenetic tree of the given distance table by using UPGMA method                                                                                                                                                                                                                                                                                                  | 5  | CO3   | K2   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| <table border="1" style="margin-left: auto; margin-right: auto;"> <tr> <td></td><td>A</td><td>B</td><td>C</td><td>D</td></tr> <tr> <td>A</td><td>0</td><td></td><td></td><td></td></tr> <tr> <td>B</td><td>8</td><td>0</td><td></td><td></td></tr> <tr> <td>C</td><td>7</td><td>9</td><td>0</td><td></td></tr> <tr> <td>D</td><td>12</td><td>14</td><td>11</td><td>0</td></tr> </table> |    |       |      |              |  | A | B | C | D | A | 0 |  |  |  | B | 8 | 0 |  |  | C | 7 | 9 | 0 |  | D | 12 | 14 | 11 | 0 |
|                                                                                                                                                                                                                                                                                                                                                                                         | A  | B     | C    | D            |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| A                                                                                                                                                                                                                                                                                                                                                                                       | 0  |       |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| B                                                                                                                                                                                                                                                                                                                                                                                       | 8  | 0     |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| C                                                                                                                                                                                                                                                                                                                                                                                       | 7  | 9     | 0    |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| D                                                                                                                                                                                                                                                                                                                                                                                       | 12 | 14    | 11   | 0            |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| d. Design a Un- rooted phylogenetic tree of the given MSA By using NJ method                                                                                                                                                                                                                                                                                                            | 5  | CO3   | K2   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| CTGCGAGCCG<br>TTCTCGAAGC<br>GTACGGTGAG<br>CACGCCGCCG<br>GCGTTCTCAG                                                                                                                                                                                                                                                                                                                      |    |       |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| 4.a. Design a HMM of the given MSA                                                                                                                                                                                                                                                                                                                                                      | 5  | CO3   | K2   |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |
| VGA- -H<br>V - - -N<br>VEA- - D<br>VKG - - -<br>VYS - -T<br>FNA - - N<br>IAGADN                                                                                                                                                                                                                                                                                                         |    |       |      |              |  |   |   |   |   |   |   |  |  |  |   |   |   |  |  |   |   |   |   |  |   |    |    |    |   |

- b. If a protein contains a total of 1800 residues and 810 of them are in helix , considering the residue Ala among 300 residue 210 are in helix . What is the information content of Ala in helix. 5 CO4 K2
- (OR)
- c. Which two sequence are very closed to each other justify it by using Hamming distance method  
ADIKLAAIKL  
ADSKLAAIKA  
KILASDPQWE 5 CO4 K2
- d. Define Block and print. Find the BLOSUM value of all amino acid of the given block.  
AAI  
SAL  
TAL  
TAV  
AAL 5 CO5 K2
- 5.a. Explain the Naive String Matching Algorithm race the execution of the naive string matching algorithm for Text: AABAACAADAABAABA and Pattern: AABA 5 CO5 K2
- b. What is Motif? How motif are discovery by MEME algorithm 5 CO5 K2
- (OR)
- c. Make a PAM matrix of all amino acid of the given MSA  
GGGTCGGTAT  
ACTCCGGAAC  
TTCACGTTAC  
TTCTACAAGG  
ATTCCGTCAT 5 CO5 K2
- d. Write the computational procedure of Drug design 5 CO5 K2
- 6.a. What is protein Folding? Explain few method to estimate the protein stability 5 CO6 K1
- b. Explain the steps involve in Threading model 5 CO6 K1
- (OR)
- c. Explain MDS. Write the steps involve in AMBER package 5 CO6 K1
- d. Briefly explain QSAR and pharmacophore 5 CO6 K1

--- End of Paper ---