

Total No. of Pages :02

Total No. of Questions : 09

B.Tech.(BT) (2012 to 2017) (Sem.-5)

BIOINFORMATICS

Subject Code : BTBT-505

M.Code : 70506

Time : 3 Hrs.

Max. Marks : 60

INSTRUCTIONS TO CANDIDATES :

1. **SECTION-A is COMPULSORY consisting of TEN questions carrying TWO marks each.**
2. **SECTION-B contains FIVE questions carrying FIVE marks each and students have to attempt any FOUR questions.**
3. **SECTION-C contains THREE questions carrying TEN marks each and students have to attempt any TWO questions.**

SECTION-A

1. Answer briefly :

- Sequence similarity vs. sequence identity
- EMBL
- Global alignment
- Affine gap penalties
- BIT score
- Rasmol
- COGS
- Bootstrap
- Entrez
- Phylogram

SECTION-B

2. Write about the CATH database.
3. Describe the GOR method of protein secondary structure prediction.
4. Explain Smith-Waterman algorithm.
5. Describe any one multiple sequence alignment tool.
6. Differentiate between PAM and BLOSUM scoring matrices.

SECTION-C

7. Blast is used for database searching. Describe the BLAST algorithm and BLAST output.
8. Describe different bioinformatics methods of gene prediction. How prokaryotic gene prediction tool is different from eukaryotic gene prediction tool?
9. Write the application of phylogenetic tree constructions. Construct the tree based on given matrix using UPGMA method.

	A	B	C	D
A	0			
B	7	0		
C	6	8	0	
D	11	13	10	0

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.