

4/12/18 (M)

[This question paper contains 4 printed pages]

Your Roll No. :

Sl. No. of Q. Paper : **345** **I**

Unique Paper Code : 42167905

Name of the Course : **B.Sc.(Prog.) : DSE-1A**

Name of the Paper : Bioinformatics

Semester : V

Time : 3 Hours **Maximum Marks : 75**

Instructions for Candidates :

(a) Write your Roll No. on the top immediately on receipt of this question paper.

(b) Attempt **all** questions.

1. (a) Give the full form of any **five abbreviations :**

5

(i) NCBI

(ii) MEGA

(iii) PROSITE

(iv) CATH

P.T.O.

- (v) NDB
- (vi) EMBL
- (vii) DDBJ
- (viii) UNIPROT
- (ix) PHYLIP

(b) Match the following : 10

- | | |
|----------------|--|
| (i) CLUSTALX | (I) used pairwise alignment |
| (ii) PUBMED | (II) used for 3D structure prediction |
| (iii) GEO | (III) protein data bank |
| (iv) BLAST | (IV) Block substitution matrix |
| (v) PDB | (V) Genbank flat file format |
| (vi) FASTA | (VI) Data repository of gene expression data |
| (vii) TREEVIEW | (VII) Biomedical literature search |

- | | |
|---------------|---|
| (viii) BLOSUM | (VIII) basic local alignment search tools |
| (ix) MODELLER | (IX) used for phylogenetic analysis |
| (x) MODLOOP | (X) Used for multiple sequence alignment |

2. Describe any **three** from the following in brief :

5×3

- (a) Scoring matrix
- (b) SWISSPROT
- (c) PROTEOMICS
- (d) QSAR
- (e) Drug designing

3. Differentiate between the following with example (any **three**) :

5×3

- (a) Protein 2D and 3D structure
- (b) MEGA and Clustal W
- (c) Local and Global alignment
- (d) Phylogram and Dendrogram

4. Describe in detail (any two) : 7.5×2

(a) Classification scheme of Biological databases.

(b) Explain BLAST in detail with steps in the form of flow chart.

(c) Describe methods of Phylogeny.

5. (a) What is sequence alignment ? What are the methods of alignment ? 8

(b) Describe the role of bioinformatics in crop improvement. 7