    (v) Accession number and version number

    (vi) GenBank and GenPept

4. (a) Give comparative account on Maximum parsimony, Maximum livelihood, Neighbour joining method of phylogenetic tree construction.   (9)

    (b) Expand BLAST. Discuss briefly about its different types.   (6)

5. (a) Define bioinformatics. Discuss the scope areas of bioinformatics in biology.   (6)

    (b) Give a comparative account on the various data submission and retrieval tools of NCBI and EMBL.   (9)

6. (a) What do you understand by computer-aided drug designing? Explain various phases of clinical trials?   (7)

    (b) Discuss different levels of protein structure and describe computational method of protein structure prediction.   (8)

[This question paper contains 4 printed pages.]

Your Roll No. ....

Sr. No. of Question Paper : 1526   C

Unique Paper Code   : 42167905

Name of the Paper   : Bioinformatics (DSE)

Name of the Course   : **B.Sc. Life Sciences III Year**

Semester   : V

Duration : 3 Hours   Maximum Marks : 75

Instructions for Candidates

1. Write your Roll No. on the top immediately on receipt of this question paper.

2. Attempt **five** questions in all.

3. Question number **1** is compulsory.

4. All parts of the questions must be answered together.

5. **All** questions carry equal marks.

1. (a) Define the following **(any five)** :   (1×5=5)

    (i) Expectation value (E value)

P.T.O.

   (ii) Node

   (iii) Proteomics

   (iv) Phylogenetic tree

   (v) Python

   (vi) Conserve sequence

   (vii) ORF

(b) Match the following :   (1×5=5)

Column A	Column B
(i) Margaret O. Dayhoff	BLAST
(ii) Stephen Altschul	Local sequence alignment
(iii) Needleman and Wiinsch	BLOSUM
(iv) Smith and Waterman	PAM
(v) Henikoff and Henikoff	Global sequence alignment

(c) Expand of the following (any five) :   (5×1=5)

   (i) CATH

   (ii) KEGG

   (iii) QSAR

   (iv) MIAME

   (v) OTU

   (vi) NIH

2.   Write short notes on (any three) :   (5×3=15)

   (i) Gene prediction methods

   (ii) Sequence file format

   (iii) Applications of bioinformatics in crop improvement

   (iv) Transcriptomics

3.   Differentiate between the following (any five) :

                                        (3×5=15)

   (i) Archival and derivative databases

   (ii) System biology and functional biology

   (iii) Bootstrap and Jackknife

   (iv) Local and global sequence alignment