Total number of printed pages–7

63/1 (SEM–5) DSE2/BOTHE5026

2024

BOTANY

Paper : BOTHE5026

(Bioinformatics)

Full Marks : 60

Pass Marks : 24

Time : Three hours

The figures in the margin indicate full marks for the questions.

1. Choose the correct option from the following : ***(any five)*** 1×5=5

   (a) In which year did the SWISSPROT protein sequence database begin?

      (i) 1988

      (ii) 1987

      (iii) 1986

      (iv) 1985

Contd.

(b) The human genome contains approximately ______.

(i) 3 billion base pairs

(ii) 4 billion base pairs

(iii) 5 billion base pairs

(iv) 6 billion base pairs

(c) Which of the following compounds has desirable properties to become a drug?

(i) Fit drug

(ii) Lead

(iii) Fit compound

(iv) All of the above

(d) Which of the following are not the application of bioinformatics?

(i) Drug designing

(ii) Data storage and management

(iii) Understand the relationships between organisms

(iv) None of the above

(e) A single piece of information in a database is called

(i) File

(ii) Field

(iii) Record

(iv) Data set

(f) Which of the following is a nucleotide sequence data base?

(i) EMBL

(ii) SWISS PROT

(iii) PROSITE

(iv) TrEMBL

(g) BLOSUM matrices are used for

(i) Multiple sequence Alignment

(ii) Pairwise sequence Alignment

(iii) Phylogenetic Analysis

(iv) All of the above

(h) Which of the following is not a variant of BLAST ?

(i) BLASTN

(ii) BLASTP

(iii) BLASTX

(iv) TBLASTNX

(i) Which one of the following best represent the central dogma of Bioinformatics ?

(i) Sequence–Structure–Function

(ii) DNA–RNA–Protein

(iii) Motifs–domains–Superfamilies

(iv) Data–Databanks–Data mining tools

(j) The numbers at the internal nodes of a phylogenetic tree indicate

(i) Number of times the OTUs were clustered together

(ii) Number of parsimony sites shared by OTUs

(iii) Number of mismatches shared by OTUs

(iv) Similarity score of OTUs that cluster together

2. Answer the following questions : ***(any five)*** 2×5=10

(a) Name *two* tools used in phylogenetic analysis.

(b) Define sequence alignment.

(c) What is data mining ?

(d) List *any two* protein database.

(e) Write different types of application of proteomics.

(f) Expand NCBI and QSAR.

(g) What is transgenic plant ? Give an example.

3. Answer ***any five*** of the following questions : 5×5=25

(a) What are the roles of bioinformatics in the field of medicine ?

(b) Describe the applications of microbial genome in crop improvement.

(c) Differentiate between sequence similarity and sequence homology.

(d) Explain PIR. Give an account on all the resources of PIR.

(e) Describe Nucleotide Database.

(f) Discuss the *three* methods used in construction of phylogenetic tree.

(g) Give an account on the organization of Databases of NCBI.

(h) Differentiate between Primary and Secondary database.

(i) What is the difference between PAM and BLOSUM ?

4. Answer ***any two*** of the following questions : 10×2=20

(a) What is DDBJ ? Give an account of various resources available at DDBJ. 2+8=10

(b) Define biological database. Briefly discuss the biological database retrieval system. 2+8=10

(c) Describe the word method for alignment of sequence. Mention the factors that affect the choice of template selection during homology modeling. 5+5=10

(d) What is bioinformatics ? Write a brief notes on different fields of bioinformatcies. 2+8=10
