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63/1 (SEM-5) DSE2/BOTHE5026

2023

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) The alignment method suitable for finding out conserved pattern in DNA or protein sequences is

(i) multiple sequence alignment

(ii) pairwise alignment

(iii) global alignment

(iv) local alignment

Contd.

- (b) The Homology and similarity tool is
- (i) BLAST
 - (ii) EMBOSS
 - (iii) PROSPECT
 - (iv) RasMol
- (c) STAG is maintained by
- (i) Brookhaven laboratory
 - (ii) DNA database of Japan (DDBJ)
 - (iii) European Molecular Biology Laboratory (EMBL)
 - (iv) National Centre for Biotechnology Information (NCBI)
- (d) Which of the following tools is used for the identification of motifs ?
- (i) BLAST
 - (ii) COPIA
 - (iii) PROSPECT
 - (iv) Pattern hunter

- (e) The identification of drugs through the genomic study is called
- (i) Genomics
 - (ii) Pharmacogenetics
 - (iii) Pharmacogenomics
 - (iv) Cheminformatics
- (f) The search and retrieval tool of NCBI is
- (i) SAKURA
 - (ii) SRS
 - (iii) Sequin
 - (iv) Entrez
- (g) Sequence alignment helps scientists
- (i) to trace out evolutionary relationships
 - (ii) to infer the functions of newly synthesized genes
 - (iii) to predict new members of gene families
 - (iv) All of the above

- (h) Which of the following is not a benefit or a factual of FASTA over BLAST ?
- (i) FASTA scans smaller window sizes
 - (ii) it gives more sensitive results
 - (iii) it gives less sensitive results
 - (iv) it gives results with a better coverage rate for homologs
- (i) Which of the following is the first completed and published gene sequence ?
- (i) $O \times 174$
 - (ii) T4 phage
 - (iii) M13 phage
 - (iv) Lambda phage
- (j) The first bacterial genome to be sequenced a mild human pathogen which is
- (i) Hemophilus influenzae
 - (ii) Lactobacillus
 - (iii) Vibrio cholerae
 - (iv) Clostridium botulinum

2. Answer the following questions : **(any five)**
2×5=10
- (a) What is local alignment ?
 - (b) Differentiate between global alignment and local alignment.
 - (c) Expand BLOSUM.
 - (d) Write *any two* uses of GenBank.
 - (e) Why is bioinformatics called “In silico biology” ?
 - (f) Write *two* bio-medical applications of bioinformatics.
 - (g) Define genomics and proteomics.
3. Answer **any five** of the following questions :
5×5=25
- (a) What is SWISS-PORT protein sequence database ? How is it used ?
 - (b) Write the characteristics of good database.
 - (c) Explain DDBJ.
 - (d) Write on database retrieval tools.
 - (e) How do SCOP and CATH classify proteins ?
 - (f) Write on phylogenetic tree.

- (g) Write on microbial genome application.
- (h) Explain submission of nucleotide sequence in data bank.
- (i) Give a brief account of bioremediation.

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

(a) Define genomics. Describe the applications of microbial genome in crop improvement and environment.

2+(4+4)=10

(b) What is NCBI? Mention briefly various tools of NCBI. Discuss the organization of Databases of NCBI.

2+2+6=10

(c) Discuss the role of bioinformatics in the field of agriculture and medicine.

(d) What is a drug? Write an essay on the role of Bioinformatics in rational drug design.

2+8=10