

**M.Sc. II Semester Degree Examination, Sept./Oct. - 2024****BOTANY****SEC2 - Bioinformatics and Applications in Biology****(NEP)**

Time : 1 Hour

Maximum Marks : 30

1. Global alignment is based on :
(A) Needleman and Wunsch Algorithm (B) Smith-Waterman algorithm
(C) Dot matrix algorithm (D) Dynamic algorithm
2. Which of the following is a software exclusively for phylogenetic tree construction ?
(A) EMBL (B) GENBANK (C) DDBJ (D) PHYLIP
3. The process of finding the relative location of genes on a chromosome is called _____.
(A) Gene tracking (B) Genome walking
(C) Genome mapping (D) Chromosome walking
4. FASTA format starts with _____ symbol.
(A) / (B) * (C) > (D) #
5. Which of the following is a protein sequence database ?
(A) DDBJ (B) EMBL (C) GenBank (D) PIR
6. Tool used for multiple sequence alignment :
(A) FASTA (B) DOCKING (C) BLAST (D) CLUSTAI-W
7. BLAST programme is used in :
(A) DNA sequencing (B) Amino acid sequencing
(C) DNA barcoding (D) Bioinformatics



- 8.** Phylogenetic relationship can be show by :
- (A) Dendrogram (B) GenBank
(C) Data retrieving tool (D) Data search tool
- 9.** Full form of MEGA software :
- (A) Molecular Evolutionary Genetics Analysis
(B) Molecular Biology of Genetic Analysis
(C) Modern Evolutionary Genetics Analysis
(D) Modern Analysis of Gene Analysis
- 10.** BLAST is an algorithm for comparing :
- (A) Sequences (B) Structures (C) Texts (D) None of these
- 11.** Expand UPGMA :
- (A) Unweighted Pair Group Method with Arithmetic Mean
(B) Unweighted Pair Group Method with All Mean
(C) Upregulated Gene Method with Arithmetic Mean
(D) Unregulated Genome Method with All Mean
- 12.** Identification of drugs through the genomic study is called :
- (A) Genomics (B) Pharmacogenomics
(C) Pharmacogenetics (D) Cheminformatics
- 13.** The procedure of aligning many sequences simultaneously is called :
- (A) Multiple sequence alignment
(B) Pairwise sequence alignment
(C) Global alignment
(D) Local alignment
- 14.** Which of the following is a sequence alignment tool provided by NCBI ?
- (A) Chime (B) BLAST (C) FASTA (D) Clustal W
- 15.** Which programming language is commonly used in Bioinformatics ?
- (A) HTML (B) Jawa (C) Python (D) C++



16. GenBank, the nucleic acid sequence database is maintained by :
- (A) Brookhaven laboratory
 - (B) DNA DataBase Japan (DDBJ)
 - (C) European Molecular Biology Laboratory (EMBL)
 - (D) National Centre for Biotechnology Information (NCBI)
17. It is the transfer of genetic material for the purpose of treating human disease :
- (A) Chemotherapy
 - (B) Gene therapy
 - (C) Gene transfer
 - (D) Gene editing
18. Science of managing and analyzing biological data using advanced computers :
- (A) Bioinformatics
 - (B) Genomics
 - (C) Forensics
 - (D) Human genome project
19. Which of the following is not a variant of BLAST ?
- (A) BLASTX
 - (B) TBLASTNX
 - (C) BLASTP
 - (D) BLASTN
20. All are genome sequencing strategies except :
- (A) Edman degradation method
 - (B) Shot gun method
 - (C) Whole genome shot gun method
 - (D) Directed gene sequencing
21. SWISS PORT is related to :
- (A) Portable data
 - (B) Swiss Bank data
 - (C) Sequence data bank
 - (D) Sequence data
22. Operating System is :
- (A) A collection of hardware components
 - (B) A collection of input-output devices
 - (C) A collection of software routines
 - (D) All of the above



23. MAtDB is a model organism database for :
(A) Mouse (B) Human (C) E. Coli (D) Arabidopsis
24. All are nucleotide sequence databases except :
(A) SwissPort (B) EMBL (C) DDBJ (D) GenBank
25. The human genome contains approximately _____.
(A) 6 billion base pairs (B) 5 billion base pairs
(C) 3 billion base pairs (D) 4 billion base pairs
26. Full form of URL :
(A) Uniform Resource Loader (B) Uniform Resource Line
(C) Uniform Resource Locator (D) Uniform Reading Loader
27. What does proteomics refer to ?
(A) Set of proteins in a specific region
(B) Biomolecules
(C) Set of proteins
(D) The entire set of expressed proteins in the cell
28. The site of gene expression in the cell is _____.
(A) Chromosome (B) Vacuole
(C) Golgi apparatus (D) Centriole
29. Which technique prompted the gene therapy ?
(A) DNA transform (B) Germline manipulation
(C) Retroviral gene therapy (D) Electroporation
30. The first secondary database developed was :
(A) PRINTS (B) PROSITE (C) PDB (D) PIR

