

No. of Printed Pages : 8

Question Booklet Code

A

21BOT2S2LP

Question Booklet
Serial Number

M.Sc. II Semester (NEP) Degree Examination, October - 2023
BOTANY

SEC2 : Bioinformatics and Applications in Biology

Time : 1 Hour

Maximum Marks : 30

INSTRUCTIONS TO CANDIDATES

1. The Question Paper will be given in the form of a Question Booklet. There will be four/two versions of Question Booklets with Question Booklet Code viz. **A, B, C & D / A & B / A** only.
2. The Question Booklet Serial Number is printed on the top right margin of the facing sheet. If your Question Booklet is un-numbered, please get it replaced by new Question Booklet with same Code.
3. Immediately after the commencement of the examination, the candidate should check that the Question Booklet supplied to him contains all the 30 questions in serial order. The Question Booklet does not have unprinted or torn or missing pages and if so he/she should bring it to the notice of the Invigilator and get it replaced by a complete booklet with same Code. This is most important.
4. A blank sheet of paper is attached to the Question Booklet. This may be used for Rough Work.
5. **Please read carefully all the instructions on the top of the Answer Sheet before marking your answers.**
6. Each question is provided with four choices **(A), (B), (C)** and **(D)** having one correct answer. Choose the correct answer and darken the bubble corresponding to the question number using **Black Ball-Point Pen** in the OMR Answer Sheet.
7. No candidate will be allowed to leave the examination hall till the end of the session and without handing over his/her Answer Sheet to the Invigilator.
8. Strict compliance of instructions is essential. Any malpractice or attempt to commit any kind of malpractice in the Examination will result in the disqualification of the candidate.
9. First fifteen minutes is provided to fill the general information of the Student. Eg. Student Name, Student ID, etc. in the OMR Answer Sheet
10. Without the instruction of the Invigilator do not open the Question Paper Booklet Seal.

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1

21BOT2S2LP

1. What is the common representation of a phylogenetic tree ?
(A) Circular tree (B) Square tree
(C) Rectangular tree (D) Branching tree

2. What does the root of a phylogenetic tree represent ?
(A) The most common ancestor of all species in the tree
(B) The oldest species in the tree
(C) The most genetically diverse species in the tree
(D) The outgroup species used for comparison

3. Which algorithm is commonly used for inferring phylogenetic trees from molecular data ?
(A) Breadth-First Search (BFS) (B) Depth-First Search (DFS)
(C) Maximum Likelihood (ML) (D) K-Nearest Neighbors (KNN)

4. What is a “phylogeny” in the context of phylogenetic trees ?
(A) To study the geographical distribution of species
(B) The study of the ecological interactions among species
(C) The study of the evolutionary relationships and relatedness of species
(D) The study of the genetic diversity within a population

5. In which year SWISSPROT protein sequence database begin ?
(A) 1988 (B) 1985 (C) 1986 (D) 1987

6. Which of the following tool is used for the identification of motifs ?
(A) BLAST (B) COPIA (C) PROSPECT (D) Pattern hunter

7. Which of the following compounds has desirable properties to become a drug ?
(A) Fit drug (B) Lead (C) Fit compound (D) All of the above
8. The term "*in-vitro*" is the latin word which refers to _____.
(A) Within the lab (B) Within the glass
(C) Outside the lab (D) Outside the glass
9. Application of bioinformatics include :
(A) Data storage and management
(B) Drug Designing
(C) Understand relationships between organisms
(D) All of the above
10. The term bioinformatics was coined by :
(A) J.D. Watson (B) Pauline Hogeweg
(C) Margaret Dayhoff (D) Frederic Sanger
11. The computer simulation refers to _____.
(A) Dry lab (B) *In-vitro* (C) *In-silico* (D) Wet lab
12. Margaret Dayhoff developed the first protein sequence database called :
(A) Swiss-Prot
(B) PDB
(C) Atlas of protein sequence structure
(D) Protein sequence databank



13. Literature databases include :

- (A) MEDLINE and Pubmed (B) Medline and PDB
(C) PubMed and PDB (D) Medline and PDS

14. Which of the following is an *E coli* model organism database ?

- (A) EcoGene (B) EcoBase (C) EcoSeq (D) ColGene

15. Study of structure and functions of genome is :

- (A) Species (B) Genomics (C) Inheritance (D) None of these

16. Enzymes includes _____.

- (A) Carbohydrates (B) Protein
(C) Nucleic acids (D) None of these

17. _____ is the structure of mitochondrial DNA.

- (A) Circular (B) Linear (C) Ladder like (D) None of these

18. Genomics is the study of genomes. Genome refers to the :

- (A) DNA of an organism (B) Total DNA and RNA of an organism
(C) Entire genes of an organism (D) Total DNA, RNA and cDNA of an organism

19. DNA sequencing followed by genome annotation are steps of :

- (A) Comparative genomics (B) Structural genomics
(C) Functional genomics (D) Transcriptomics



20. Small cDNA sequence that represents a unique segment of an active gene is called :

- (A) SNPs (B) SnRNAs (C) ESTs (D) Contigs

21. Variation between individuals due to single base changes is called :

- (A) ESTs (B) Contigs (C) SNPs (D) Transversion

22. Analyzing or comparing genome of species.

- (A) Bioinformatics (B) Genomics
(C) Proteomics (D) Pharmacogenomics

23. Fly Base is a :

- (A) Biodiversity database (B) Model organism database
(C) Literature database (D) Biomolecular database

24. Which of the following is a nucleotide sequence database ?

- (A) EMBL (B) SWISSPROT (C) PROSITE (D) TREMBL

25. Which of the following is a databank exclusively for proteins ?

- (A) EMBL (B) GenBank (C) DDBJ (D) PDB

26. Which of the following is protein structure database ?

- (A) GenBank (B) Swiss-Prot (C) DDBJ (D) PDB

- 27.** Among the following which one is not the approach to the local alignment ?
- (A) Smith-Waterman algorithm (B) K-tuple method
(C) Words method (D) Needleman-Wunsch algorithm
- 28.** Clustal W is :
- (A) Multiple sequence alignment tool
(B) Protein secondary structure predicting tool
(C) Data retrieving tool
(D) Nucleic acid sequence analysis tool
- 29.** GenBank and SWISSPROT are examples of :
- (A) Primary database (B) Secondary database
(C) Composite database (D) None of these
- 30.** A comprehensive database for the study of human genetics and molecular biology is :
- (A) PDB (B) STAG (C) OMIM (D) PSD

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SPACE FOR ROUGH WORK

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7

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