

(6 pages)

Reg. No. :

Code No. : 70160

Sub. Code : RCCB 2

CERTIFICATE COURSE IN COMPUTATIONAL
BIOLOGY EXAMINATION, APRIL 2022.

Non-Semester

COMPUTATIONAL METHODS FOR SEQUENCE
ANALYSIS

(For those who joined in July 2012 onwards)

Time : Three hours

Maximum : 100 marks

PART A — (10 × 1 = 10 marks)

Answer ALL questions.

Choose the correct answer :

1. Example for primary nucleotide sequence database
- (a) OMIM (b) PDB
- (c) Unigene (d) DDBJ

2. CATH is
- (a) Nucleotide sequence database
- (b) Protein sequence database
- (c) Protein structure database
- (d) Micro array database
3. Scoring of alignments between divergent protein sequences is done by
- (a) BLOSUM (b) CLUSTAL W
- (c) SRS (d) Entrez
4. BLASTn refers to
- (a) Protein - Nucleotide Blast
- (b) Nucleotide - Nucleotide Blast
- (c) Nucleotide - Protein Blast
- (d) Protein - Protein Blast
5. Single letter code for Aspartic acid
- (a) D (b) A
- (c) S (d) C



6. SNP is
- (a) Single Nucleotide Polymorphism
 - (b) Simple Nucleotide Polymorphism
 - (c) Small Network Polymorphism
 - (d) Species Nucleotide Polymorphism
7. Ramachandran plot is useful for
- (a) Homology modelling
 - (b) Validation
 - (c) Transmembrane
 - (d) Visualization
8. Protein secondary structure can be predicted by
- (a) Chou and Fasman method
 - (b) GOR method
 - (c) Neural Network model
 - (d) All of these
9. FASTA format symbol
- (a) =
 - (b) //
 - (c) >
 - (d) <

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10. Monophyletic taxon is called as
- (a) Taxon
 - (b) Branch
 - (c) Clade
 - (d) Node

PART B — (5 × 6 = 30 marks)

Answer ALL questions, choosing either (a) or (b).

11. (a) Write short note on EMBL.

Or

- (b) Write an account on DDBJ.

12. (a) Explain Local and Global Alignment.

Or

- (b) Write short notes on SRS.

13. (a) Write short notes on ORF.

Or

- (b) Explain dbSNP.

14. (a) Write short notes on Chou and Fasman method.

Or

- (b) Briefly explain Ramachandran Plot.

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[P.T.O.]



15. (a) Write an short notes on MEGA.

Or

- (b) Differentiate Rooted and unrooted tree.

PART C — (5 × 12 = 60 marks)

Answer ALL questions, choosing either (a) or (b)

16. (a) Give an account on Secondary nucleotide sequence databases.

Or

- (b) Discuss about Protein structure databases.

17. (a) Write down the scoring matrices in bioinformatics.

Or

- (b) Explain Similarity search tools in bioinformatics.

18. (a) Write an account on data formats in bioinformatics.

Or

- (b) Explain Fragment assembly.

19. (a) Explain Homology modelling.

Or

- (b) Give in detail about protein visualizing tools.

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20. (a) Explain in detail about the distance matrix methods in phylogenetic analysis.

Or

- (b) Write an account on role of Maximum likelihood in phylogenetic analysis.
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