



Date: 29-10-2018

Dept. No.

Max. : 100 Marks

Time: 09:00-12:00

PART – A

Answer ALL the Questions

I. Choose the correct answer

(5 x 1 = 5 Marks)

1. Which section of the journal article is provided in most electronic database?
a) Introduction b) Results c) Conclusion d) Abstract
2. In a study fat content of 3 brands of icecreams are compared. Brand is a _____ variable
a) Ordinal b) Nominal c) Continuous d) Discrete
3. Specific sequence information from DDBJ can be retrieved using _____.
a) ARSA b) BankIt c) getentry d) EB-eye
4. Which of the following is used to find highly similar sequences?
a) ClustalW b) Blastn c) Megablast d) FASTA
5. Choose a tool used for phylogenetic tree construction?
a) BLAST b) Genscan c) MEGA d) Clustal Omega

II. State whether the following are true or false.

(5x1=5 Marks)

6. Randomization protects against extraneous variables.
7. Leptokurtic curves possess heavy tails.
8. INSDC provides free and unrestricted access to the nucleotide databases worldwide.
9. Homology between sequences is indicated in percentage.
10. Phylogenetic trees can be rooted or unrooted.

III. Complete the following

(5 x 1= 5 Marks)

11. A two tailed test is characterized by _____ rejection area.
12. _____ is a definite design to obtain samples from a population.
13. ROD in Genbank flatfile corresponds to _____.
14. _____ value is subtracted from the gross alignment score to get final alignment score.
15. _____ is a branching hierarchical tree that shows relationship between clades.

IV. Answer the following within 50 words

(5 x 1 = 5 Marks)

16. Differentiate fundamental research from applied research.
17. Mention the statistical test is used to find the goodness of fit?
18. Name any two sequence submission tools
19. What is a scoring matrix?
20. Define phylogenetics.

PART B

Answer the following each within 500 words.

(5 x 8 = 40 marks)

Draw diagrams wherever necessary

21. (a) Explain the structure of literature review

OR

(b) Analyze the need for formulation of research problem.

22. (a) Mention the measures of dispersion and discuss the need for it.

OR

(b) Evaluate any four data representation methods.

23. (a) Comment on ENTREZ and SRS

OR

(b) Write notes on structure databases.

24. (a) Give an account on gaps and gap penalty.

OR

(b) Compare and contrast PAM and BLOSUM

25. (a) Mention the factors affecting gene frequencies.

OR

(b) Explain the neutral theory of evolution.

PART – C

Answer any TWO of the following, each within 1500 words.

(2 x 20 = 20 Marks)

Draw diagrams wherever necessary.

26. Write an essay on biological databases.

27. Describe gene prediction and add a note on any two tools used for prediction.

28. Elaborate on the principles and any two experimental designs.

29. Describe any two methods for phylogenetic tree construction methods.

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