LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

M.Sc. DEGREE EXAMINATION –**BIOTECHNOLOGY**

THIRD SEMESTER – **APRIL 2019**

16/17PBT3MC03–RESEARCH METHODOLOGY AND BIOINFORMATICS

Date:09-04-2019   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. _____is a statistical method involving the selection of elements from an ordered sampling frame.
   a) Criterion sampling   b) Homogenous sampling
   c) Systematic sampling   d) Chain Sampling

2. _____the underlying frequency distribution of a set of continuous data.
   a) Pie chart   b)Line plot
   c)Bar graph   d) Histogram

3. The database that houses sequence data of protein is
   a)UniprotKB   b)PDB
   c)SCOP   d)CATH

4. Choose the approach to study global alignment
   a) EMBOSS NEEDLE   b) EMBOSS WATER
   c) BLAST   d) G blocks

5. Which of the following tool is uses Parsimony to build?
   a) Phylogeny.fr   b)PAUP
   c) PHYLIP   d) MEGA

II. State whether the following are true or false. (5x1=5 Marks)
6. Nominal data is data that comprises of categories that can be rank ordered.
7. Questionnaire is a method of data collection.
8. ENTREZ is used to search DDBJ, if accession number is unknown.
9. Homology between species A and B is 50 %.
10. UPGMA is an algorithm for phylogenetic tree building.

III. Complete the following (5 x 1= 5 Marks)
11. Null hypothesis is denoted as _____.
12. Type II error is also called _____.
13. _____ is a web based sequence submission tool at NCBI.
14. GeneID is used to predict_____.
15. _____ is a branching hierarchical tree that shows the relationship between clades.

IV. Answer the following within 50 words (5 x 1 = 5 Marks)
16. Define research
17. What is a two tailed test?
18. Give an example for a structure database.
19. Mention any one tool used for sequence alignment.
20. What is a phylogenetic tree?

1

PART B

Answer the following each within 500 words.   **(5 x 8 = 40 marks)**
Draw diagrams wherever necessary

21. (a) Write briefly about the objectives of research and types of research

OR

    (b) Give a note on any two data presentation methods.

22. (a) Outline the steps involved in Hypothesis testing.

OR

    b) Write a note about the data collection methods.

23. (a)Write an account on sequence submission tools.

OR

    (b) Give an account on the flat file format of Genbank.

24. (a) Compare the tools used for local alignment and global alignment.

OR

    (b) Write briefly about scoring matrix.

25. (a) Illustrate any one method used for tree building.

OR

    (b)Discuss the findings of neutral theory of evolution.

PART – C

Answer any TWO of the following, each within 1500 words.   **(2 x 20 = 40 Marks)**
Draw diagrams wherever necessary.

26. Explain the principles of experimental design with example.

27. Describe the importance of different sampling methods.

28. Elaborate on the methods of eukaryotic gene prediction.

29. Write an essay on the sequence and structure databases.

****