

LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034



M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY

THIRD SEMESTER – NOVEMBER 2019

16/17/18PBT3MC03 – RESEARCH METHODOLOGY AND BIOINFORMATICS

Date: 02-11-2019

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)

- Findings of Charles Darwin is an example of
 - Descriptive research
 - Formulative research
 - Exploratory research
 - Diagnostic research
- Fat content of two brands of icecreams were recorded. Which test can be used to find whether their mean fat content varies significantly or not?
 - Regression
 - Correlation
 - ANOVA
 - Student T-test
- Which among the following is the regulatory agency of nucleotide sequence database?
 - GenBank
 - EMBL
 - DDBJ
 - INSDC
- The score that indicates the number of alignments in BLAST?
 - Z score
 - P value
 - E value
 - B value
- The following about phylogenetic tree is true EXCEPT
 - Nodes represent taxonomic units
 - A branch can connect more than two nodes
 - Trees can be scaled or unscaled.
 - The branch pattern is called topology.

II. State whether the following are true or false.

(5x1=5 Marks)

- Principle of local control gets rid of bias.
- Interquartile range is based on median.
- Genome data viewer is a Genome database of EMBL.
- The gap extension penalty is more than the gap opening penalty.
- Neutral theory of evolution states that molecular evolution of a gene is constant over time.

III. Complete the following

(5 x 1= 5 Marks)

- _____ is called the power of the test.
- Standard deviation for a population is denoted as _____.
- G query is a search tool at_____.
- PAM matrices was developed by_____.
- _____ refers to evolutionary history of an organism.

IV. Answer the following, each within 50 words

(5 x 1 = 5 Marks)

16. List any two sources of primary literature source.
17. What are parametric tests?
18. Mention any two sequence submission tools.
19. Define gap penalty.
20. Mention a parsimony based program for phylogenetic tree construction.

PART B

Answer the following, each within 500 words.

(5 x 8 = 40 marks)

Draw diagrams wherever necessary

21. (a) Explain experimental design using Latin square method.

OR

- (b) Mention the steps in formulating a research problem.

22. (a) Write about the types of errors in hypothesis testing.

OR

- (a) Explain about any four data representation methods.

23. (a) Give an account on structural databases.

OR

- (b) Summarize the sequence retrieval tools available at various databases.

24. (a) Discuss on Database searching using BLAST.

OR

- (b) Evaluate *ab initio* gene prediction program

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

OR

- (b) Explain neighbourhood joining method.

PART – C

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

(2 x 20 = 40 Marks)

Draw diagrams wherever necessary.

26. Write a detailed essay on the sources, structure and types of literature review.
27. Describe about the various nucleotide databases and add a note on GenBank flatfile format.
28. Elaborate on sequence alignment approaches.
29. Outline the steps involved in phylogenetic tree construction.

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