# LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034



### M.Sc. DEGREE EXAMINATION - BIOTECHNOLOGY

### THIRD SEMESTER - NOVEMBER 2017

## 16PBT3MC03 - RESEARCH METHODOLOGY AND BIOINFORMATICS

Date: 06-11-2017 Time: 09:00-12:00	Dept. No.	Max. : 100 Marks
Answer ALL the Questions	PART – A	
<ul> <li>a) Stratified sampling</li> <li>c) Systematic sampling</li> <li>2. What type of graph wo</li> <li>a) Bar chart</li> <li>c) Histogram</li> <li>3. The database that house</li> <li>a)UniprotKB</li> <li>c)SCOP</li> <li>4. Choose the heuristic ba</li> <li>a) EMBOSS NEEDLE</li> <li>c) BLAST</li> </ul>	blecting intact groups within def b) Cluster samp d) Random sam uld you use to see the distribution b) Pie chart d) Scatterplot es experimentally determined st b)PDB d)CATH ased approach to study alignment	ion of a scale variable? structures is nt VATER
	alled as variable data.	(5x1=5 Marks) retrieved for subsequent analyses. per is unknown.
<ol> <li>Homoplasy is a result of</li> <li>The Jukes Cantor mode</li> </ol>	of convergent evolution. el assumes that all nucleotides o	occur at equal frequency.
13. Webin is a web based s  14 is a gene p	n the largest and the smallest obsequence submission tool atprediction tool that predicts almost	(5 x 1= 5 Marks)  oservations is called as  nost 80% exons in human genes.  vs the relationship between clades.
<ul><li>IV. Answer the following wit</li><li>16. What is exploratory red</li><li>17. Write a note on t-test.</li><li>18. What is the role of INS</li><li>19. Mention the importance</li><li>20. Define phylogenetics.</li></ul>	learch?	(5 x 1 = 5 Marks)

#### PART B

# Answer the following each within 500 words. Draw diagrams wherever necessary

 $(5 \times 8 = 40 \text{ marks})$ 

21. (a) Enumerate the different objectives of research.

OR

- (b) Give a note on sampling and its types.
- 22. (a) Write about the SPSS software in statistics.

OR

- b) Give a short note on spatial statistics.
- 23. (a)Write an account on sequence retrieval systems and sequence submission tools.

OR

- (b) Give an account on the flat file format of Genbank.
- 24. (a) Compare the dynamic programming algorithm used for sequence analysis.

OR

- (b) Write briefly about scoring matrix and its importance in sequence alignment.
- 25. (a) Illustrate UPGMA method of tree building.

OR

(b)Explain the neutral theory of evolution.

#### PART - C

# Answer any TWO of the following, each within 1500 words. Draw diagrams wherever necessary.

 $(2 \times 20 = 40 \text{ Marks})$ 

- 26. Explain in detail the components of a research proposal.
- 27. Describe the different methods of representation of data.
- 28. Write an essay on the various biological databases.
- 29. Elaborate on the different gene finding methods.

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