



**LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034**

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

SECOND SEMESTER – NOVEMBER 2016

**BT 2824 - BIOINFORMATICS & RESEARCH METHODS**

Date: 01-11-2016  
Time: 01:00-04:00

Dept. No.

Max. : 100 Marks

**PART – A**

**Answer ALL the Questions**

**I. Choose the correct answer**

**(5 x 1 = 5 Marks)**

- Which of the following is not a secondary storage unit?  
a) Hard disks      b) CD      c) RAM      d) Floppy disks
- The following gives the relative map distances of genes EXCEPT  
a) Linkage maps      b) Cytogenetic maps  
c) Chromosomal maps      d) Sequence based maps
- Which of the following reacts with free cysteines to form S-Nitrothiols?  
a) NO      b) NO<sub>2</sub>      c) N<sub>2</sub>O      d) HNO<sub>3</sub>
- Darwin's expeditions were examples of which type of research?  
a) Descriptive      b) Exploratory      c) Empirical      d) Analytical
- Choose a non-parametric test equivalent to independent sample t test  
a) Kruskal-wallis test      b) Mann Whitney test  
c) Rank Sum test      d) Tukey test

**II. State whether the following are true or false**

**(5 x 1 = 5 Marks)**

- Smith waterman algorithm is used for local alignment.
- Eucaryotic genes are polycistronic.
- The recombinant offsprings are always higher in number in a testcross.
- Motifs are super secondary structures.
- Histograms are used for continuous data perm has mitochondria.

**III. Complete the following**

**(5 x 1 = 5 Marks)**

- RCSB stands for \_\_\_\_\_.
- The 3' splice site is also called \_\_\_\_\_.
- The dye used in R banding is \_\_\_\_\_.
- \_\_\_\_\_ tool is used to find structurally conserved domains in a protein.
- Incorrect rejection of a true null hypothesis is \_\_\_\_\_ error.

**IV. Answer the following, each within 50 words**

**(5 x 1 = 5 Marks)**

- What is a motif?
- Define a polymorphic marker
- State a difference between mean deviation and standard deviation
- Name a tool to predict N-glycosylation sites
- Give two advantages of a pictograph.

**PART – B**

**Answer the following, each within 500 words. Draw diagrams wherever necessary. (5 × 8 = 40 Marks)**

21. (a) Explain the SCOP classification of proteins.

OR

(b) Write about any two nucleotide sequence databases.

22. (a) Outline the steps involved in RH mapping.

OR

(b) Illustrate BAC by BAC method used for human genome sequencing.

23. (a) Explain any two classes of protein domains.

OR

(b) Write about prediction of signalpeptides.

24. (a) Comment on any four types of research.

OR

(b) Mention the components of research proposal.

25. (a) Outline the steps in hypothesis testing.

OR

(b) Evaluate the advantages of any four data representation methods in research.

**PART – C**

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

**(2 × 20 = 40 Marks)**

26. Elaborate on the biological sequence and structure databases.

27. Write in detail about cDNA library construction, EST sequence quality and EST clustering

28. Elaborate on *ab initio* and comparative gene prediction methods.

29. Review the various methods for protein structure prediction and analysis.

\*\*\*\*\*