LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY

SECOND SEMESTER – NOVEMBER 2016

BT 2824 - BIOINFORMATICS & RESEARCH METHODS

 Date: 01-11-2016
 Dept. No.

 Time: 01:00-04:00
 Max. : 100 Marks

$\mathbf{PART} - \mathbf{A}$

d) Tukey test

Answer ALL the Questions

I. Choose the correct answer

- 1. Which of the following is not a secondary storage unit?
 - a) Hard disks b) CD c) RAM d) Floppy disks
- 2. The following gives the relative map distances of genes EXCEPT
 - a) Linkage maps b) Cytogenetic maps
 - c) Chromosomal maps d) Sequence based maps
- 3. Which of the following reacts with free cysteines to form S-Nitrothiols?a) NOb) NO₂c) N₂Od) HNO₃
- 4. Darwin's expeditions were examples of which type of research?a) Descriptiveb) Exploratoryc) Empiricald) Analytical
- 5. Choose a non-parametric test equivalent to independent sample t test
 - a) Kruskal-wallis test b)Mann Whitney test
 - c) Rank Sum test

II. State whether the following are true or false

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

III. Complete the following

11. RCSB stands for _____

12. The 3' splice site is also called______.

- 13. The dye used in R banding is _____.
- 14. ______ tool is used to find structurally conserved domains in a protein.
- 15. Incorrect rejection of a true null hypothesis is ______ error.

IV. Answer the following, each within 50 words

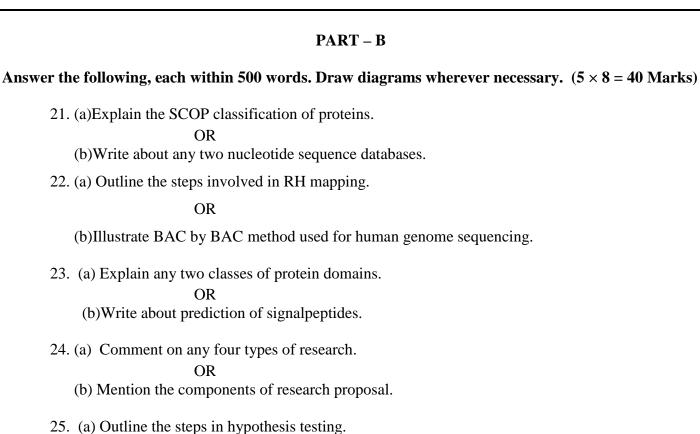
- 16. What is a motif?
- 17. Define a polymorphic marker
- 18. State a difference between mean deviation and standard deviation
- 19. Name a tool to predict N-glycosylation sites
- 20. Give two advantages of a pictograph.

(5 x 1 = 5 Marks)

 $(5 \times 1 = 5 \text{ Marks})$

(5 x 1 = 5 Marks)

 $(5 \times 1 = 5 \text{ Marks})$



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

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.
