LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

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

SECOND SEMESTER – APRIL 2017

BT 2824- BIOINFORMATICS & RESEARCH METHODS

Date: 06-05-2017   Dept. No.   Max. : 100 Marks
09:00-12:00

PART – A

Answer ALL the Questions

I. Choose the correct answer   (5 x 1 = 5 Marks)

1. Which of the following is the first genome database?
   a) Flybase   b) Wormbase   c) Acedb   d) Aeedb
2. Choose the high resolution map from the following.
   a) Cytogenetic map   b) Linkage map   c) RH map   d) Sequence map
3. Tryptophan synthase belongs to which class of protein?
   a) Class α   b) Class β   c) Class α/β   d) Class α+β
4. The following are probability sampling techniques EXCEPT
   a) Stratified sampling   b) Deliberate sampling
c) Simple random sampling   d) Cluster sampling
5. Which of the following is required to calculate σ?
   a) Mean   b) Median   c) Skewness   d) Kurtosis

II. State whether the following are true or false, if false, give reason   (5x1=5 Marks).

6. PIR is the first structural database.
7. R banding stains GC rich regions.
8. In the complete absence of similar structures, fold recognition can be done for proteins.
9. Systematic sampling is purely judgemental in nature.
10. In a normal data distribution mean, median and mode are unequal.

III. Complete the following   (5 x 1= 5 Marks)
11. The sequence retrieval system of NCBI is _____.
12. _____ is the official repository of mapping data from human genome project.
13. ROSETTA is a tool for _____ modeling of proteins.
14. Orthologs are gene in _____ species having a common ancestor.
15. Gender is classified as _____ variable.

IV. Answer the following, each within 50 words   (5 x 1 = 5 Marks)

16. Give an example for secondary storage device.

17. Mention one advantage of EST clustering.

18. When fold recognition used in protein structure prediction

19. List any two types of variables.

20. What is the non-parametric equivalent to independent sample t test?

PART B   **(5x 8 = 40 marks)**

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

21. (a) Write an account on any two structure databases.

OR

   (b) Explain the Genbank flat file format.

22. (a) The results of a testcross study between two traits Red, Shrunken (CCss) and White, Plump(ccSS) Red is as follows,
       Red, plump -12   Red, shrunken-3420
   White, plump-3334 White, shrunken-126
   Calculate the map units between C, c and S, s.
                OR
   (b) Evaluate the different banding methods in karyotyping.

23. (a) Classify proteins based on their secondary structures.
                OR

   (b) Explain phosphorylation and lipidation of proteins.

24. (a) Compare any two formal experimental designs.
                OR
   (b) What are the different types of data and how are they collected?

25. (a) Given an account on:
           i. External validity ii. Internal validity   iii. Blinding iv. Confounding
                OR
   (b) Discuss the essential components of a research thesis.

PART – C   **(2 x 20 = 40 Marks)**

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

26. Write in detail about shot gun cloning and hierarchial shot gun cloning used for human genome mapping.

27. Elaborate on homology modeling and *ab initio* modeling of proteins.

28. Describe in detail objectives of research, types of research, research problem and components of a research proposal.

29. Explain hypothesis testing using inferential statistics and discuss about any four data representation methods.

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