LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

B.Sc. DEGREE EXAMINATION – **MATHS & PHYSICS**

THIRD SEMESTER – NOVEMBER 2011

PB 3208/3204 - BIOINFORMATICS - I

Date : 11-11-2011 Dept. No. Max. : 100 Marks
Time : 9:00 - 12:00

PART- A (20 marks)

Answer all the questions

I Choose the correct answer (5x1=5 marks)

1. What cell organelle is responsible for powering the cell.
   a) endoplasmic reticulum b) golgi apparatus c) mitochondria d) ribosomes
2. The database that classifies protein according to their structure and function is _____.
   a) PIR-PSD b) i Proclass c) ALN d) RESID
3. The cells diagonals that joins in the ascending order of values is _____.
   a) initiation b) scorefill c) traceback d) PEPT
4. Cell were first discovered by _____.
   a) Robert hooke b) George kohler c) Edward jenner d) Pasteur
5. The PDB library is updated
   a) every year b) every month d) every week d) every day

II State whether the following statements are True or False (5x1=5 marks)

6. ProtParam computes various physico-chemical properties of proteins.
7. 3´-5´strand is called a non-coding strand.
8. Carbon bond is found between the bases of DNA.
9. PIR 1 contains fully classified and annotated entries.
10. DE line provides information about the name by which the protein is known.

III Complete the following (5x1=5 marks)

11. Secondary structure of DNA was proposed by _____.
12. The genome that is present inside the nucleus of the cell is called _____.
13. PDB is generated by _____.
14. Low helical stability region is predicted by _____.
15. BLAST program was developed by _____.

IV Answer the following each in about 50 words **(5x1=5 marks)**

16. What are restriction enzymes?
17. Define sequence alignment.
18. Define Motif.
19. Illustrate central dogma of molecular biology.
20. Explain database searching.

PART – B **(5 × 7 = 35 marks)**

V Answer the following, each answer within 350 words, draw diagram wherever necessary

21. a) Briefly explain transcription process.

OR

b) Give an account on the structure of chromosome. Mention its chromosome number.

22. a) Write notes on i) EMBL ii) DDBJ

OR

b) Define genome. Explain any two genomic databases.

23. a) Explain disease database.

OR

b) Explain the steps involved in Needleman and Wunsch algorithm. Give an example.

24. a) Explain the software used in gene prediction method.

OR

b) Give an account on different types of BLAST program.

25. a) Explain the software used for visualizing the 3D structure of proteins.

OR

b) What database is used for predicting the physical properties of DNA sequences?

PART – C **(3 × 15 = 45 marks)**

VI Answer any Three of the following, each within 1500 words; draw diagram wherever necessary

26. Draw a Smith-Watermann algorithm for the following using the values match: 1, mismatch: 0, gap: -1

ADCNGRQCLCRPM

AGCGNRCKCRP

27. Describe the structure and functions of DNA.
28. Explain human genome project. Mention its applications.
29. Explain secondary structure prediction on proteins.
30. Briefly explain the structure of eukaryotic cell.

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