LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

**B.Sc.** DEGREE EXAMINATION – **COMPUTER SCI. APPL., PHYSICS**

FOURTH SEMESTER – APRIL 2011

# PB 4208 / 4213 - BIOINFORMATICS - II (GENOMICS & PROTEOMICS)

Date : 05-04-2011 Dept. No. Max. : 100 Marks

Time : 1:00 - 4:00

**Answer all questions (20marks)**

**I Choose the correct answer (5 x 1 = 5)**

1. A codon is a series of \_\_\_\_\_\_\_\_\_\_ nucleotide.
2. 1 b) 3 c) 5 d) 4
3. Electrophoresis is carried out at \_\_\_\_\_\_\_\_\_ temperature.
4. 80ºC b) 70ºC c) 50ºC d) 20 ºC
5. The genome size of *Arabidopsis thaliana is*
6. 125Mb b) 3300Mb c) 0.58Mb d) 466Mb
7. \_\_\_\_\_\_\_\_\_\_\_\_\_\_ pathway turns the gene on or off.
8. Metabolic b) Gene regulation c) Biological d) Cell signaling
9. Sequencing of \_\_\_\_\_\_\_\_\_\_\_\_ was done in the year 1997.
10. *E.coli*  b) *S.cerevisiae*  c) *M.musculus*  d) *Fugurubripes*

**II Say whether the following statements are True or False (5 x 1 = 5)**

1. ATG is stop codon.
2. InterPro is a cross reference of several protein family databases.
3. BLAST is Basic Local Algorithm Search Tool.
4. Topology refers to both the orientation and connectivity of secondary structures.
5. OrthoMCL is a database for mammals.

**III Complete the following (5 x 1 = 5)**

1. The biological information contained in a genome is programmed in its \_\_\_\_\_\_\_.
2. RNA is synthesized from DNA through a process known as \_\_\_\_\_\_\_\_\_\_.
3. \_\_\_\_\_\_\_\_\_ model is used to find & classify genes of different types.
4. Protein Data Bank was generated by \_\_\_\_\_\_\_\_\_\_\_\_\_\_.
5. \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ database consists of 30programs and is a command line program.

**IV Answer in one or two sentences, each in about 50 words**  **(5 x 1 = 5)**

1. Define spliceosome.
2. Write any two applications of DNA sequencing.
3. Differentiate between sensitivity and specificity.
4. Define hydrogen bonding.
5. Differentiate between orthologous and paralogous.

**Section B**

**V Answer any FIVE of the following, each in about 350 words (5 x 8 = 40)**

21. Write notes on:

i) ORF

ii) Alternative splicing

22. Briefly explain Dideoxynucleotide method.

23. Write short note on Promoter elements.

24. Briefly explain microbial genome database and Karyn’s genome database.

25. Write notes on inter-molecular interactions.

26. What is a biological pathway? Explain the different types.

27. Briefly explain DNA microarray with suitable diagram.

28. Draw a dynamic programming using Needlemann algorithm for the following

sequence.

Sequence1: GATCTA

Sequence2: GATCA

**Section C**

**VI Answer the following, each in about 1500 words (2 x 20 = 40)**

29. (a) Explain any five protein family databases

OR

(b) Explain how to find genes in large genomes

30. (a) Define post-translational modification and explain the various modifications

OR

(b) What is Human Genome Project? Explain its types, goals and applications

\*\*\*\*\*\*\*\*\*\*