



FACULTY OF SCIENCE
M.Sc. IV Semester Examination, April/May 2013
BIOCHEMISTRY

Paper – IV : Computational Methods and Bioinformatics

Time : 3 Hours]

[Max. Marks : 80

Note : Answer all questions of Part – A and Part – B. Each question in Part – A carries 4 marks and in Part – B carries 12 marks.

PART – A

(8×4=32 Marks)

1. What is the difference between a histogram and a bar graph ?
2. What is a Normal distribution ? Draw a labelled diagram of a standard normal distribution showing the area under the curve at $\mu + \sigma$, $\mu + 2\sigma$, and $\mu + 3\sigma$.
3. What is the role of a CPU in a computer ?
4. What is the difference between RAM and ROM ? Which type of memory should you increase to improve the data storage capacity of your computer ?
5. What is array analysis ? Name a database to store array data.
6. What is rational drug design ? How is genomics relevant to drug design ?
7. Which has more elements – human genome or human proteome ? Why (give at least one reason) ?
8. What is pharmacogenomics ? What is the role a biochemist can play in this field ?

PART – B

(4×12=48 Marks)

9. Calculate the correlation of X to Y1 and Y2 in the following sets of data. Which set shows greater correlation ?

X	1	2	3	4	5
Y1	2	4	6	8	10
Y2	3	6	9	12	15

OR

What is a chi-square test of significance ? Explain the meanings of alpha, type – I error and type – II error in tests of significance.



10. Using a labelled diagram, describe the layout of a simple computer. Add a note on how this computer can be a part of a peer-to-peer or a client-server network.

OR

What are the various languages used for computer programs ? Which types of languages are most popular today in bioinformatics programs ?

11. Why do biologists need databases ? Differentiate between public and private databases and between primary and secondary data databases. Give a brief description and 2 examples each for :

- a) DNA sequence database
- b) Protein sequence database and
- c) Protein structure database.

OR

What is alignment of sequences ? What information can be derived from such exercises and name a program that aligns multiple sequences ?

12. How can you predict the 3-dimensional structure of a protein if the sequence is known ?

OR

Short notes on :

- a) Comparing genomes
 - b) ESTs and SNPs
 - c) Repetitive elements.
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