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 + 2sigma, and mu + 3sigma.

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?

<table>
<thead>
<tr>
<th></th>
<th>X</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y1</td>
<td></td>
<td>2</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>10</td>
</tr>
<tr>
<td>Y2</td>
<td></td>
<td>3</td>
<td>6</td>
<td>9</td>
<td>12</td>
<td>15</td>
</tr>
</tbody>
</table>

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.

(This paper contains 2 pages)
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.