Total No. of Questions: 8]

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[5124]-203 M.Sc.

BIOCHEMISTRY

BCH-272: Biostatistics, Computer and Bioinformatics (2013 Pattern) (Credit System) (Semester-II)

Time: 3 Hours [Max. Marks: 50

Instructions to the candidates:

- 1) Answer to both the sections should be written on separate answer sheet.
- 2) Question no. 4 and 8 are compulsory.
- 3) Attempt any two questions from Q.1 to Q.3 and any two from Q.5 to Q.7.
- 4) Figures to the right indicate full marks.
- 5) Supplementary will be provided for checking p-values.
- 6) Graph papers will be provided.

SECTION-I

(Biostatistics and Computers)

Q1) Answer the following:

a) Give importance of biostatistics in life science.

[2]

b) Explain binary and decimal numbers.

- [3]
- c) Find the cumulative and relative frequencies of the following data. [5]

No.of pods	1-9	10-20	21-30	31-40	41-50
No.of plants	4	6	25	15	20

Q2) Attempt the following:

a) Cal<u>culate the mean of the following data.</u>

[2]

- 10 13 14 9 10
- b) Calculate the standard deviation and standard error of data.

[4]

Waxy plants	15	17	7	9	11
No.of plants	18	12	18	15	14

c) Calculate the value of median and also determine it graphically using Ogive. [4]

Variable 1	0-20	20-30	30-40	40-50	50-60	60-70
Frequency	6	8	10	12	14	15

Q3) Answer the following:

a) The following data represents the number of productive tillers per plant of a wheat variety.

Draw a histogram of the following data

[3]

No.of plants	0-4	4-8	8-12	12-16	16-20	20-24
No.of productive	10	11	12	15	20	12
tillers						

b) Data on hair colour and the eye colour are given in the table. Calculate the chi-square value. Determine the association between the hair colour and the eye colour. [5]

		Fair	Brown	Black	Total
	Blue	15	20	5	40
Eye	Grey	20	20	10	50
colour	Brown	25	20	15	60
	Total	60	60	30	150

c) What do you mean by flowchart. Give its uses.

[2]

Q4) Answer any one of the following:

[5]

- a) Explain the programming in BASIC.
- b) Explain input, output and format statements.

SECTION-II

(Bioinformatics)

Q5) Answer the following:

a) Write a note on PAM matrices.

[2]

b) Explain nucleotide sequence database.

[3]

c) Explain and distinguish between global and local alignment.

[5]

Q6) Attempt the following:

a) Explain multiple sequence alignment.

[2]

b) Explain Needleman and Wunsch algorithm.

[5]

c) Explain Pub Med central.

[3]

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Q7) Answer the following:

- What do you mean by Hamming Distance. [2]
- What is Smith-Waterman algorithm. Explain. b) [5]
- State the salient features of any protein 3D structure visualization c) software. [3]

Q8) Answer any one of the following:

[5]

- Explain how sequence data is generated for expressed sequence tags database division of NCBI.
- Explain why there is need of Heuristics approach in database sequence b) search. Explain any one heuristics approach in sequence similarity search.





