

BioTech

Q. P. Code: M981

2 1/2 Hours

Total Marks: 75

52

1. Attempt all questions.
2. All questions carry equal marks.
3. Draw neat labeled diagrams wherever necessary.
4. Use of log tables and non-programmable calculator is allowed.
5. For Q 2, Q 3 and Q 4 attempt A and B OR C and D.

Q 1 Do as directed (Any fifteen)

15

1. _____ is an example of an output device.
a. Plotter b. Stylus c. Keyboard d. Webcam
2. _____ is a protein visualization software.
a. Microsoft Office b. Photoshop c. Pymol d. iOS
3. A _____ is a precise notation used to express algorithms.
a. software b. programming language c. flowchart d. None of the above
4. Optical storage device includes _____
a. CD-ROM b. DVD-ROM c. BD-ROM d. All of the above
5. A set of wires which carries a group of bits in parallel and has an associated control scheme is known as a _____.
a. bus b. controller c. conductor d. driver
6. A _____ is the technical term for the location of a website.
a. address b. webpage c. URL d. bookmark
7. State whether true or false : The internet is a part of the world wide web.
8. Define Gap penalty.
9. Give any one type of BLAST
10. State true or false: BLAST is a heuristic program.
11. Define Homologous sequences.
12. Give any one type of scoring matrices for proteins.
13. What is pairwise sequence alignment?
14. The _____ of the tree is common ancestor of all taxa in phylogenetic tree.
15. The value of coefficient of correlation is _____ if the two variables are not correlated
16. In regression line X on Y, X is _____ variable.
17. For Contingency table in a chi-square test, if there are 2 rows and 3 columns, what will be the degree of freedom?
18. What is a null hypothesis?
19. State true or false: In a Z-test the table value for 5% level of significance is 1.96.
20. Give the formula to compute chi-square test.

Q. 2 A Explain Raw and Processed Databases with suitable examples.

Q. 2 B Elaborate on the different genome information resources available in bioinformatics.

OR

Q. 2 C What is the KEGG database? How is it different from other databases?

Q. 2 D Comment on databases based on structural classification of proteins.

Q. 3 A Explain FASTA algorithm in detail and State the significance of E-value.

Q. 3 B What do you understand by secondary database searching?

OR

Q. 3 C Enlist the goal of Multiple Sequence Alignment.

Q. 3 D Explain in detail Manual methods and Progressive methods for MSA.

Q. 4 A Find regression coefficients b_y and b_{yx} for the following data:

x	1	2	3	4	5
y	10	20	30	40	50

Q. 4 B What is Z test and t-test? How will you calculate standard error for Z and t test? Give the formulae to calculate Z and t-test Single and two means.

OR

Q. 4 C Find Coefficient of correlation for the following data:

X	2	4	6	8	10
Y	3	6	9	12	15

Q. 4 D Explain chi-square with suitable example.

Q. 5 Write Short notes on any three of the following

a. Computer memory.

b. FTP.

c. Analysis packages.

d. Methods of Sequence alignments.

e. Steps in testing statistical hypothesis.

39

08

07

44

08

07

15

47
49
52