

Enrollment No: _____ Exam Seat No: _____

C.U.SHAH UNIVERSITY

Summer Examination-2017

Subject Name: Bioinformatics and Biostatistics

Subject Code: 4SC04BIB1

Branch: B.Sc.(Microbiology)

Semester: 4

Date : 15/04/2017

Time : 10:30 To 01:30

Marks : 70

Instructions:

- (1) Use of Programmable calculator & any other electronic instrument is prohibited.
- (2) Instructions written on main answer book are strictly to be obeyed.
- (3) Draw neat diagrams and figures (if necessary) at right places.
- (4) Assume suitable data if needed.

Q-1 Attempt the following questions: (14)

- | | |
|--|---|
| a) Define Biostatistics. | 1 |
| b) What is the difference between algorithm and Program? | 1 |
| c) Which is the basic unit of heredity? | 1 |
| d) Enlist the nitrogenous bases present in coding sequences. | 1 |
| e) Give example of any two bioinformatics composite databases. | 1 |
| f) What is the significance of building phylogenetic tree? | 1 |
| g) What is the storage information available in biological database PDB? | 1 |
| h) Enlist major three sources of Data. | 1 |
| i) Define qualitative variables. | 1 |
| j) Give example of any protein structure classification database. | 1 |
| k) Which Institution maintains DDBJ database for DNA sequences? | 1 |
| l) Define SNP database. | 1 |
| m) What is the primary function of NRL-3D database? | 1 |
| n) What is the primary source for PROSITE? | 1 |

Attempt any four questions from Q-2 to Q-8

Q-2 Attempt all questions (14)

- | | |
|---|---|
| a) Write a note on Nucleic acid Primary database GenBank. | 7 |
| b) Discuss PIR (Protein Information Resources) and How it is associated with MIPS (Martinsried Institute for Protein research)? | 7 |

Q-3 Attempt all questions (14)

- | | |
|--|---|
| a) Write a short-note on NRL-3D and Enlist four secondary databases and their primary sources. | 7 |
| b) Explain the expression of protein sequence comparison in form of PRINTS. | 7 |

Q-4 Attempt all questions (14)

- | | |
|--|---|
| a) Write a note on Needleman and Wunch algorithm for sequence alignment. | 7 |
|--|---|



- b) Explain regular expression by multiple sequence alignment of Protein sequences with appropriate example and briefly discuss BLOCKS. 7

Q-5 Attempt all questions (14)

- a) Write a note on Parsimony method for the analysis of multiple sequences to build phylogeny. 7
- b) Write a note on different structural forms of Proteins. 7

Q-6 Attempt all questions (14)

Write a note on Homology modelling and explain different steps followed to perform protein structure prediction.

Q-7 Attempt all questions (14)

- a) Explain different types of sources of data and define all types of variables. 7
- b) Write a note on measurement of central tendency. 7

Q-8 Attempt all questions (14)

- a) Calculate Mean, Mode and Median of the results of randomly selected five students of a same class for given data: 7

Sr. No.	Student	% Scored
1	A	65
2	B	30
3	C	80
4	D	70
5	E	73

- b) Write a note on DDBJ. 7

