Exam.Code:0910
Sub. Code: 6316

2054

B.E. (Biotechnology) Sixth Semester

BIO-612: Bio-Informatics

Time allowed: 3 Hours | Max. Marks: 50

NOTE: Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.

x-x-x

I. Answer the following briefly:-

a) Who maintains EMBL?

b) What represent class and architecture in CATH database?

c) Distinguish between cladogram and phylogram.

d) What are three types of scoring functions used in molecular docking?

e) Distinguish between local and global alignment.

f) What is pleismomorphy?

g) Which aminoacids prefer alpha helix?

h) What is structure based drug design?

i) What are two uses of human genome project?

j) What is the Ramachandran plot used for? (10x1)

UNIT - I

II. Give an account on:-

a) Prosite

b) Genbank database

c) Ensembl

d) Uniprot (10)

III. a) Distinguish between pubmed and pubmed central databases? Give a detail account on various options used to explore pubmed database.

b) Compare and contrast BLAST and FASTA algorithms. (2x5)

P.T.O.

IV. Construct the phylogenetic tree among taxas in the matrix given below by NJ method.

	a	b	c	d	e
a	0	5	9	9	8
b	5	0	10	10	9
c	9	10	0	8	7
d	9	10	8	0	3
e	8	9	7	3	0

(10)

UNIT - II

V. a) What is the prokaryotic gene structure?

b) Explain intrinsic and extrinsic method of gene prediction. (3,7)

VI. a) Explain about homology modeling approach to predict 3D structure of protein.

b) What are various secondary structure prediction methods? Explain about Chou Fasman method.

(2x5)

VII. a) What are important features and uses of Rasmol and orf finder?

b) Explain the various steps used in drug discovery. (2x5)

x-x-x