M. SC. BIOINFORMATICS SEM.-III (2013 COURSE)
(CHOICE BASED CREDIT SYSTEMS) : SUMMER - 2018
SUBJECT: BIOLOGICAL DATA MINING

Day: Monday		**Time:** 02.00 PM TO 05.00 PM
Date: 09/04/2018	**S-2018-1132**	**Max. Marks: 60**

N.B:

1) **Q. No. 1and Q. NO. 5 are COMPULSORY.** Out of the remaining questions attempt **ANY TWO** from each sections.
2) Answer to both the sections should be solved in **SEPARATE** answer books.
3) Figures to the right indicate **FULL** marks.

SECTION-I

Q.1 Define: **(10)**

a)	Biological artifacts	b)	Date accuracy parameters
c)	Steepest descent method	d)	Supervised genetic algorithm
e)	*Ab initio* method		

Q.2 Answer the following: (**ANY TWO**) **(10)**

a) What are different errors occurs due to machines? Explain with example.
b) Describe conjugate gradient method in brief.
c) How Newton- Raphson could be utilized in bioinformatics? Give one example.

Q.3 Write short notes on: (**ANY TWO**) **(10)**

a) Foundations of Genetic Algorithms
b) Unsupervised Genetic Algorithms
c) Future prospects of Genetic Algorithms

Q.4 Explain in detail hierarchical and non-hierarchical clustering. How it helps in phylogenetic analysis? Explain with one working example. **(10)**

OR

Give a detailed account on protein array data analysis. Explain the pipe line with the help of Flow-chart. Enlist its applications and drawbacks.

SECTION-II

Q.5 Explain why? **(10)**

a) Similarity and identity are two different parameters.
b) Sensitivity and specificity are deciding features of an algorithm.
c) Local alignment could be global sometimes.
d) Orthologous and paralogous genes gives an ensight to phylogenetic relationship.
e) Twilight zone identify the method of structure prediction.

Q.6 Answer the following: (**ANY TWO**) **(10)**

a) Explain in detail Needleman-Wunch algorithm.
b) How dot plot analyze a sequence alignment? Explain with example.
c) Explain any one structure alignment method.

Q.7 Write short notes on: (**ANY TWO**) **(10)**

a) HMM   b) NN   c) Bayesian modeling

Q.8 Give an account on SVM working principle in bioinformatics. Explain in detail SVM utilization for structure prediction. **(10)**

OR

Explain the fuzzy logic applicability in statistics. How could it be utilized in bioinformatics?

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