

ADVANCED DIPLOMA IN BIOINFORMATICS SEM.-II
(C.B.C.S.) (2013 COURSE) : WINTER - 2017
SUBJECT: ADVANCED BIOINFORMATICS

Day: Wednesday
Date: 01/11/2017

Time: 02.00 PM TO 05.00 PM
Max. Marks: 60

W-2017-1021

N.B:

- 1) **Q. No. 1 and 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) Data mining b) *Ab-initio* method c) NN simulator
d) Annotation e) BLAST 2
- Q.2** Write short notes on: (ANY TWO) (10)
- a) Dynamic programming
b) Genetic algorithms
c) Probabilistic modeling ad inference
- Q.3** Answer the following: (10)
- a) Explain any two genome alignment methods with their respective applications.
b) Differentiate between protein array and DNA array data analysis.
- Q.4** Explain in detail metabolic pathway engineering. How it is useful in bioinformatics data analysis? (10)

OR

Describe any two protein structure prediction methods in brief. Enlist their respective applications.

SECTION-II

- Q.5** What is? (10)
- a) Sensitivity and specificity
b) True positive and False negative
c) Local and global alignment
d) Similarity and identity
e) Homologous and analogous genes
- Q.6** Write short note on: (10)
- a) Bayesian modeling
b) HMM
- Q.7** Answer the following: (10)
- a) Explain in detail any one gene prediction algorithm.
b) Describe the working principal of any two operon prediction algorithm.
- Q.8** What is gene order comparison tools? Enlist any two gene order comparison tools with their working principles. Explain their applications in brief. (10)

OR

Explain in detail molecular modelling procedure using flow diagram. Enlist its applications.

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