

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

**Day:** Wednesday  
**Date:** 01/11/2017

**W-2017-1021**

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

**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 and 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 principle 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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