

**M. SC. BIOINFORMATICS SEM.-I (C.B.C.S.) (2013
COURSE) / ADVANCED DIPLOMA IN BIOINFORMATICS
SEM.-I (C.B.C.S.) (2013 COURSE) : SUMMER - 2018
SUBJECT : BIOLOGICAL INFORMATICS**

Day : **Thursday**
Date : **05/04/2018**

Time : **10.00 AM TO 01.00 PM**
Max. Marks : 60

S-2018-1122

N.B.:

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

SECTION – I

- Q.1** Explain the following with two applications: [10]
a) PMC
b) Biosystems
c) Patent database
d) PMD
e) CSW
- Q.2** Write short notes on **ANY TWO** of the following: [10]
a) Uniprot KB
b) BankIt
c) Database filters
- Q.3** Give a comparative statement on NCBI, EMBL and DDBJ. [10]
OR
Explain with example the hierarchy of biological database.
- Q.4** Differentiate between **ANY TWO** of the following: [10]
a) Dynamic programming and heuristic methods
b) PAM and BLOSUM
c) Paralogous genes and orthologous genes

SECTION – II

- Q.5** Answer in brief why? [10]
a) Local alignment could be a global alignment?
b) MSA is an extension of PSA.
c) Protein structure validation is necessary.
d) Proteomics is harder to deal with than Genomics.
e) ORF ID and ORF finder are different.
- Q.6** Explain the BLAST algorithm in detail. Mention all its available versions with their applications. [10]
OR
Explain MSA algorithm in detail. Mention all its available versions with their applications.
- Q.7** Give a comparative accounts of **ANY TWO** of the following: [10]
a) PDB and SCOP
b) PROSITE and PRODOM
c) OMIM and Pubmed Health
- Q.8** Enlist five molecular visualization tools with their applications. [10]
OR
Enlist all available DNA/RNA sequence analysis tools with their applications.

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