[Time: 2½ Hours]   **[Marks:60]**

Please check whether you have got the right question paper.

N.B: 1. **All** questions are **compulsory**.
2. **Use** of **simple calculator** is **allowed**.
3. **Figures** to the **right** indicate **full marks**.

Q.1   1. If there is an extremely high confidence that the database match is the result of homologous   **12**
relationship; then what would be the E-value.
2. Define E value.
3. Full form of FASTA.
4. If the match is extremely significant, what would be the Z-score?
5. Give the URL for CLUSTALW.
6. Full form of BLAST & its URL.
7. Under which condition a profile is constructed in Multiple Sequence Alignment?
8. Define Pseudo counts.
9.   Define Molecular Clock Assumption.
10. How a tree is designed w,r.t to the below given Newick format?
(((B,C),A),(D,E))
11. Define Homoplasy.
12. List the major task of Data Mining.

Q.2   A)   In order to find matches for a short stretch of identical residues with a length of K. explain how   **06**
FASTA algorithm is helpful.
B)   Elaborate on PSI-BLAST in details   **06**
OR
C)   Explain BLAST algorithm in detail.   **06**
D) In order to search a defined pattern in a query sequence against a database; explain how PHI BLAST **06**
is performed.

Q.3   A) How the construction of PSSM takes place. Explain in detail.   **06**
B) Write Short Note on:-   **06**
1. HMM & its applications
2. Dendogram & its applications
OR
C) Write short note on :-   **06**
1. Markov Model
2. PRRN Programme.
D) Write a note on various algorithms of MSA. Give its various applications.   **06**

Q.4   A) Write a note on :-   **06**
1. Maximum Likelihood Method.
2. PAUP & PHYLIP
B) Explain Character Based Method in detail. Give its advantages over other method.   **06**
OR

1

C) Elaborate on the procedure used for designing phylogenetic tree. **60**
D) Construct phylogenetic tree w.r.t to UPGMA method. **60**

	A	B	C
B	0.40		
C	0.18	0.80	
D	0.90	0.60	0.70

Q.5 A) What is Data mining? Give its various applications in detail. **06**
B) How data mining method is useful in microarray analysis. Explain. **06**
<div align="center">OR</div>
C) Explain in detail Data warehousing & its relationship with Data Mining. **06**
D) How data mining studies are useful to analyze the global database. Explain. **06**

_____