**SUBJECT CODE: 15BI/PC/BI24**

**M. Sc. DEGREE EXAMINATION, APRIL 2018**
**BIOINFORMATICS**
**SECOND SEMESTER**

**COURSE** : **MAJOR – CORE**
**PAPER** : **BIOINFORMATICS**
**TIME** : **3 HOURS**                                    MAX. MARKS:  100
**SECTION – A**
**ANSWER ALL THE QUESTIONS**                                    **(20 X 1 =20)**

1. SGD

2. PMC

3. EMBL

4. Write examples of Secondary database

5. Orthologs

6. E-value

7. PSSM

8. Global Alignment.

9. tblastx

10. HSP

11. IgBLAST

12. Low-complexity regions

13. Sequence motif

14. HMM

15. MUSCLE

16. Protein domain

17. Cladistics

18. Greedy algorithm

19. Bootstrapping

20. Maximum likelihood estimation

## SECTION – B

**ANSWER ANY FOUR OF THE FOLLOWING; EACH ANSWERS NOT EXCEEDING 500 WORDS.   DRAW DIAGRAM WHEREVER NECESSARY.          (4 X 10 =40)**

21. How to submit sequence data to GenBank?

22. Write in detail about Scoring Matrix?

23. Explain in detail about pairwise  sequence alignment methods.

24. Brief about specialized BLAST tools?

25. Write about motif databases?

26. Write about Multiple Sequence Alignment and its steps?

27. Brief about different types of phylogenetic trees?

## SECTION – C

**ANSWER ANY TWO OF THE FOLLOWING, EACH ANSWER NOT EXCEEDING 1200 WORDS.   DRAW DIAGRAM WHEREVER NECESSARY.          (2 X 20 = 40)**

28. Write in detail about nucleotide database?

29. Explain steps involved in Needleman-Wunsch algorithm with an example?

30. Brief BLAST algorithm in detail and its application?

31. Write in details about phylogenetic tree construction methods?

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