Paper Id: | 154509 | Roll No: | | | | | | | | | | | | | |

B. TECH
(SEM-V) THEORY EXAMINATION 2019-20
BIOINFORMATICS-I

Time: 3 Hours   *Total Marks: 100*

Note: Attempt all Sections. If require any missing data; then choose suitably.

SECTION A

1. **Attempt *all* questions in brief.**   2 x 10 = 20

    a.   What do you understand by BLAST X
    b.   What is CLASTWAL W
    c.   Full Foam of UPGMA
    d.   Explain PHI-BLAST
    e.   What do you understand by N BLAST P
    f.   Full Foam of EMBL
    g.   Full Foam of BLAST
    h.   What is Dot Matrix
    i.   Full Foam of NCBI
    j.   What do you understand by BLAST P

SECTION B

2. **Attempt any *three* of the following:**   10x3=30

    a.   How we can predict the secondary structure of proteins.
    b.   What do u understands biological Databases? Give the classification.
    c.   Give an account of different types of file format used in Bioinformatics?
    d.   How we can apply bioinformatics in drug designing and discovery process.
    e.   Comment on "Bioinformatics is Multidesciplinary field"

SECTION C

3. **Attempt any *one* part of the following:**   10x1=10

    a.   What is the biological significance of multiple sequence alignment?
    b.   Explain PAM & BLOSUM in respect to their biological significance.

4. **Attempt any *one* part of the following:**   10x1=10

    a.   Differentiate between Global alignment and Local alignment.
    b.   Differentiate between Pairwise alignment and Multiple Sequence alignment.

5. **Attempt any *one* part of the following:**   10x1=10

    a.   Give a detail account on Human Genome Project.
    b.   Explain Homology Modeling for Tertiary structure prediction

6. **Attempt any *one* part of the following:**   10x1=10

    a.   Explain the Algorithm of FASTA.
    b.   Explain the Algorithm of BLAST.

7. **Attempt any *one* part of the following:**   10x1=10

    a.   Give a detailed account on Phylogenetic analysis. Also explain their various methods for tree construction. https://www.aktuonline.com
    b.   What are the Dynamic Programming approaches involved in Global and Local Alignment of biological Sequences?