This question paper contains **3** printed pages]

Roll No. | | | | | | | | | | | |

S. No. of Question Paper : **5762**

Unique Paper Code : **3182014701**

Name of the Paper : **Bioinformatics and Omics**

Name of the Course : **B.Sc. (Hons.) Biomedical Science (NEP)**

Semester : **VII**

Duration : **2 Hours** Maximum Marks : **60**

(Write your Roll No. on the top immediately on receipt of this question paper.)

Attempt *four* questions in all.

Question No. **1** is compulsory.

(Subparts of the questions should be attempted together)

Give illustrations and examples wherever required.

Use of non-programmable scientific calculators is allowed.

1. (*a*) Briefly explain the following (any *four*) : 4×1.5=6

(*i*) Metabolomics

(*ii*) Heatmaps

(*iii*) Paralog

(*iv*) Data normalization

(*v*) Phylogram.

P.T.O.

(*b*) Differentiate between the following (any *two*) : 2×3=6

(*i*) Genomics and Epigenomics

(*ii*) Oligonucleotide arrays and cDNA arrays

(*iii*) Monophyletic and polyphyletic groups

(*c*) Expand the following (any *three*) : 3×1=3

(*i*) INSDC

(*ii*) OMIM

(*iii*) CNV

(*iv*) UPGMA.

2. (*a*) Differentiate between primary and secondary biological databases with suitable examples.

(*b*) What is an accession number ? Discuss their importance in bioinformatics with suitable examples.

(*c*) What is BLAST ? Compare different types of BLAST programs. Explain e-value and bit-score in BLAST search results. 5,4,6

3. (*a*) Find the global alignment for the following sequences, X and Y using a suitable dynamic programming (DP) algorithm. Consider a match score of 1, mismatch score of –1, and Gap penalty of –2. Name the algorithm used for this purpose. Show and explain all the steps involved.

Sequence X : ATGTACG

Sequence Y : AAGTAG

(*b*) What is phylogenetic analysis ? Diagrammatically show different components of a phylogenetic tree. 9,6

4. (*a*) What is NGS ? Compare Illumina and Oxford Nanopore sequencing in terms of principle, read length, accuracy, throughput and applications.

(*b*) What is Gene Ontology (GO) ? How is GO analysis used to understand the functions of differentially expressed genes ? 9,6

5. (*a*) As a researcher, design a microarray experiment to identify differentially expressed genes involved in cancer resistance in response to a treatment. Clearly describe the experimental controls, replicates, sample processing and data preprocessing steps you would perform.

(*b*) Name any *two* gene expression databases and explain their significance. 10,5

6. Write short notes on the following (any *three*) : 3×5=15

(*a*) RNA-seq

(*b*) Proteomics

(*c*) Character-based methods of phylogenetic analysis

(*d*) Amino acid substitution scoring matrices.