M.Sc. BIOTECHNOLOGY
THIRD SEMESTER
BIOSTATISTICS, BIOINFORMATICS & IPR
MBT-301

Duration: 3 Hrs. **Marks: 70**

PART : A (OBJECTIVE) = 20
PART : B (DESCRIPTIVE) = 50

[PART-B : Descriptive]

Duration: 2 Hrs. 40 Mins. **Marks: 50**

[Answer question no. One (1) & any four (4) from the rest]

1. What is C-value paradox and how it can be explained? What is EST? What is the principle of ETS mapping? Why ORF scan method of sequence analysis is different in pro- and eukaryotes? How simple ORF scan is modified to study eukaryotic genomic sequences? (2+1+2+2+3=10)

2. What is molecular identification of micro-organisms? What is the logic behind such analysis? Can the same technique be used for identification of plant and why? Describe the technique using a stepwise flow diagram. (2+2+2+4=10)

3. What is differential expression of mRNA? Name four methods by which differential expression of mRNA can be studied. Describe any one method using a stepwise flow diagram. (2+2+6=10)

4. Define the following (within 10-12 words): (2+2+6=10)
   (a) Metabolome; **(b)** Metabolites.
   Describe in brief the separation and detection techniques in metabolomics.

5. Define 'query', 'subject', 'similarity', and 'identity' in context of protein sequence analysis. For predicting protein function by sequence comparison which of the following sequences: 'nucleotide' or 'amino acid', is most important and why? What is hierarchical classification of proteins? What is structural conservation? (4+2+2+2=10)

6. Discuss the basic principle of mass spectrometry. Describe the general components of a mass spectrometer. Discuss the most popular ionization methods in protein mass spectrometry. Write the principles of protein identification by MS/MS analysis. (2+3+2+3=10)

7. Write short notes on any *two* **(2)** of the following topics. (5×2=10)

   a) NGS.

   b) Peptide mass fingerprinting.

   c) NMR.

8. Write a short assay on 'Human Genome project'. (10)

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[PART-A : Objective]

1. Choose the correct answer from the following: **1×10=10**

a) To define a species, "barrier to gene flow" does not apply in prokaryotic world due to:
i) circular nature of the gnome.
ii) compactness of the genome.
iii) vertical gene transfer.
iv) horizontal gene transfer.

b) Which of the following genetic markers present in the highest number in the human genome?
i) RFLP ii) SSLP
iii) SNP iv) Genes which visual phenotypes

c) E. coli genome has:
i) genes distributed all over the genome.
ii) genes organized in operon.
iii) low amount of intergenic DNA.
iv) all of the above.

d) Prokaryotic genome can have:
i) only linear architecture.
ii) only circular architecture.
iii) linear and circular architecture.
iv) only open circular architecture.

e) Which of the following proteases is most commonly used in the proteomics study?
i) Trypsin ii) Chymotrypsin
iii) Pepsin iv) Enterokinase

f) In proteomics analysis, peptide fragmentation is done during:
i) MS/MS analysis ii) 2D SDS-PAGE-MS analysis
iii) Digestion with trypsin iv) None of the above

g) Pyrosequencing is different from dideoxy method as:
i) many more different DNA molecule can be sequenced parallelly by pyrosequencing.
ii) many more nucleotides can be sequenced in short time by pyrosequencing.
iii) pyrosequencing produces high number of short nucleotide sequences.
iv) all of the above.

h) Why transcriptome study can be helpful in diagnosis of human cancers?
i) Each type of cancer has unique transcriptome.
ii) All cancers express same set of cancer causing genes.
iii) Cancer causing genes are not expressed in normal cells.
iv) Transcriptome analysis can detect genes involved in cell proliferation.

i) In which of following computational method structure can be determined of a 10 kDa polypeptide for which no homologous protein can be found?
i) Homology modeling ii) Threading
iii) ClustalW iv) NMR

j) PTM can be determined by:
i) MS/MS analysis ii) 2D SDS-PAGE analysis
iii) Western blotting iv) All of the above

2. Fill in the blanks with appropriate word/words: **1×5=5**

a) The pattern of SNPs in a stretch of DNA is known as.....

b) Permissible phi and psi angles in peptide backbones is visualized by.....

c) The percentage of repetitive DNA in human genome is.....

d) SILAC is a method of protein labeling for .....proteomics.

e) In a protein-protein interactome map the protein with large number of interacting partners are called.....

3. Match the following: **1×5=5**

A	Protein domain	F	PDB
B	Celera Genomics	G	Clone contig method of sequencing
C	International Human Genome Sequencing Consortium	H	System biology
D	Protein crystal structure	I	Pfam
E	KEGG	J	Whole genome shotgun sequencing

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