(iv) Clinical utility of genomewide SNP testing refers to the
(a) likelihood that the alleles detected are actually present in the test subject
(b) degree to which a genotype predicts odds of disease
(c) confidence internal for an estimate of odds of disease
(d) degree to which test results guide clinical decision making.

(v) Small solid supports which are spotted with numerous tiny drops of DNA used to screen gene expression form a
(a) DNA microarray (b) cloning library
(c) Southern blot (d) PCR.

(vi) Homologous genes would be expected to
(a) have very similar sequences in related organisms
(b) be more similar in distantly related organisms than in organisms that are closely related
(c) become similar to each other by random mutation
(d) all of these.

(vii) In the analysis of biomacromolecular structure, neutron diffraction is useful for determining
(a) the 3D-structure of the macromolecule
(b) hydrogen exchange dynamics
(c) transitions between different electronic states
(d) the decay of electronically excited molecules.

(viii) Protein-nucleic acid complexes include
(a) Ribosomes
(b) Splicing and repair particles
(c) Transcription regulation complexes
(d) All of the above.

(ix) Which of the following methods is NOT a basis for prediction of protein-protein interactions
(a) domain fusion (b) gene linkage pattern
(c) sequence homology (d) phylogenetic information.

(x) The intermolecular approach to protein structure comparison is normally applied to
(a) relatively dissimilar structures
(b) relatively similar structures

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Group - E

8. (a) Define phophoproteomics. What are the layers of information provided by phosphoproteomics? Using examples, explain how signal transduction dynamics are analyzed through phosphoproteomics.

(b) Define glycoproteomics. Name 2 methodological approaches and 2 bioanalytical techniques used in glycoproteomics. Draw a flowchart of glycoproteomics analysis. Name 2 clinical applications of glycoproteomics.

(1+2+3) + (1+2+2+1) =12

9. (a) What is purpose of x-ray backscattering as far as biophysical applications are concerned in proteomics?

(b) How can torsion angle and distance restraints in NMR be used for quantitative estimation of protein? Define T1 and T2 relaxation times in NMR.

(c) What are the three techniques in cryo-electron microscopy? How are biological specimens prepared in cryo-electron microscopy and why is this important technique-wise? What are some of the important macromolecular structures determined by cryoelectron microscopy?

2 + (2+2) + (2+3+1) = 12

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2016

GENOMICS & PROTEOMICS
(BIOT 5241)

Time Allotted : 3 hrs **Full Marks : 70**

Figures out of the right margin indicate full marks.

Candidates are required to answer Group A and any 5 (five) from Group B to E, taking at least one from each group.

Candidates are required to give answer in their own words as far as practicable.

Group – A
(Multiple Choice Type Questions)

1. Choose the correct alternatives for the following: **10 x 1=10**

   (i) Which area of genomics studies similarities and differences among the genomes of multiple organisms?
   (a) comparative genomics (b) structural genomics
   (c) functional genomics (d)evolutionary genomics.

   (ii) cDNA library contains
   (a) mRNA (b) genomics DNA
   (c) introns (d) miRNA.

   (iii) Co-immunoprecipitation is used
   (a) to determine if a protein-of-interest binds to a specific DNA sequence.
   (b) to examine protein-protein interaction in the nucleus instead of in the cytoplasm.
   (c) to examine protein-protein interactions in the cytoplasm instead of the nucleus.
   (d) to allow protein to be expressed in mammalian cell culture.

(c) structures with a RMSD > 5 Angstroms
(d) structures that cannot be aligned.

Group - B

2. (a) Describe the top-down approach to create a minimal cell genome.

   (b) Give a comparative analysis between satellite, minisatellite and microsatellite DNA.

   (c) What do you mean by genes within genes?

   (d) What are snRNA genes?

4+4+2+2 = 12

3. (a) Discuss the applications of genomics in agriculture and bioremediation.

   (b) Illustrate the process of Chromosome walking.

   (c) What is a Haplotype? What are the potential benefits of a HapMap?

4 + 4 + 4 = 12

Group - C

4. (a) Name one of the high throughput approaches to genome-wide profiling of gene expression based on sequence based approach whose tag lengths are more than 200 nucleotides. Mention characteristics, advantages and disadvantages of this approach.
   Mention one NCBI based cluster database which is used for this approach.

   (b) Elucidate the following terminologies with respect to functional genomics: Orthologs and Paralogs.

   (c) Briefly describe the process of horizontal gene transfer.

(2+4+1) + 2 + 3 = 12

5. (a) The similarities and differences among the genome sequences appear in four levels –state the levels.

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(b) Mention the importance of duplication event in the mechanism of evolution.

(c) Mention briefly the phenomenon of duplication and dispersal through the genome of globin genes during animal evolution with suitable figure.

4 + 2 + (4+2) = 12

Group - D

6. (a) Define protein and proteome?

(b) Describe the life cycle of protein with a diagram.

(c) Describe the basic principles of the 2D-PAGE with labeled diagram.

(d) Write the basic principles, steps with labeled diagram and application of about any <u>one</u> of the following:
(i) Affinity pull down assay**,**
(ii) Phage display**,**
(iii) Yeast two hybrid**.**

2 + 2 + 4 + 4 =12

7. (a) Describe the basic principles of MALDI-TOF.

(b) Write the advantages of MALDI-MS over ESI-MS.

(c) What is peptide mass finger printing? Describe with diagram.

(d) An unknown peptide was analyzed by mass spectrometric and chromatographic methods as follows:
(i) MALDI-TOF mass spectrometry of the peptide gave two signal at m/z = 3569 and 1785;
(ii) The data obtained from analysis of the peptide using coupled HPLC-MS operating through an ESI source were m/z =510.7, 595.7, 714.6, 893.0 and 1190.3.
Determine a molecular mass of the peptide.

2 + 2 + 4 + 4 = 12

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