B.TECH / BT /7TH SEM/ BIOT 4165/2017
HUMAN GENOMICS
(BIOT 4165)

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 alternative for the following: **10 × 1 = 10**

(i) The largest gene in human is
(a) Dystrophin (b) Titin (c) Insulin (d) Phosphofructokinase.

(ii) Small cDNA sequence that represents a unique sequence of a functional gene is called
(a) EST (b) STS (c) snRNA (d) Contig.

(iii) Variation between individuals due to single base changes is called
(a) SNP (b) Contig (c) EST (d) Transversion.

(iv) Simple sequence repeats are
(a) 1-6 bp log sequences distributed along the chromosome
(b) also called as Microsatelittes
(c) individual specific number and position
(d) all of these.

(v) Expression of genes can be analyzed by
(a) microarray (b) southern analysis
(c) comparative genomics (d) RNA interference.

(vi) A genetic distance 1cM is approximately equal to a physical distance of
(a) 1million bp (1Mb) (b) 1Megabase (1MB)
(c) 1milimeter (1mm) (d) 1centimeter (1cm).

(vii) What is the advantage of using DNA microarray over filter hybridization to screen for single nucleotide mutations?
(a) Whole cells can be used for DNA template
(b) No probes are necessary
(c) PCR is not necessary
(d) Hundreds of thousands of experiments can be done at the same time.

(viii) Gene Expression Omnibus is a /an
(a) molecular biology repository
(b) protein expression databank
(c) genomics database
(d) inherited disorder expression database.

(ix) Macrorestriction maps allows DNA pieces to be located in regions measuring about
(a) 100,000 bp to 1Mb (b) 1bp to 10 million bp
(c) Above 100bp (d) 1mm.

(x) Contig construction can be verified by
(a) RAPD (b) FISH (c) PCR (d) Western Blot.

Group - B

2. (a) What do you mean by clone contigs?
(b) Describe the process of AFLP with a flow diagram.
(c) Briefly describe the process of Hybrid sequencing.

4+ 4 + 4 = 12

3. (a) "There is no single pathway towards reaching a plausible candidate gene"- mention the different ways for arriving at the final identification.
(b) Justify the statement in order to discuss the possible strategies of identifying disease genes with help of a suitable diagram.

4+ 5 + 3 = 12

Group - C

4. (a) Define EST.
(b) Mention the advantages and drawbacks of EST.
(c) Describe briefly the EST index construction.
(d) Name two EST cluster databases and their unique properties.

2 + (2 + 2) + 2 +(2 + 2)=12

5. (a) Mention the three aims of functional genomics and comparative genomics.
(b) In which system the lateral gene transfer occurs? Mention how this event has a relationship with its recent occurrences.
(c) Mention how gene order plays an impact in comparative genomics.

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

Group - D

6. (a) What is Chromosome walking?

   (b) Comment on the impact of 'Junk DNA' on human genome organization.

   (c) Discuss the implications of HGP on medical and forensic science.

4 + 4 + 4 = 12

7. (a) What are snoRNA genes?

   (b) What do you mean by genes within genes? Give an example.

   (c) Discuss the concept of partially overlapping genes with an example.

4 + 4 + 4 = 12

Group - E

8. (a) What is a Haplotype?

   (b) What are the potential benefits of the HapMap Project?

   (c) Discuss how association studies help in disease diagnostics.

   (d) How do QTL studies help in genomics research?

2 + 2 + 4 + 4 = 12

9. (a) Mention how gene transfer technologies can be used to modify the function of endogenous genes.

   (b) Mention any three genes with their chromosomal location and their functions associated with diabetes.

6 + (2 ×3) = 12