HUMAN GENOMICS (BIOT 4122)

Time Allotted : 3 hrs

Full Marks: 70

 $10 \times 1 = 10$

Figures out of the right margin indicate full marks.

Candidates are required to answer Group A and <u>any 5 (five)</u> from Group B to E, taking <u>at least one</u> 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:
 - (i) The first completed genome sequencing project was of
 (a) E. Coli
 (b) Haemophilus influenzae
 (c) Mus musculus
 (d) Drosophila melanogaster
 - (ii) The phenomenon which shows the lack of correlation in genome size and genetic complexity is called

 (a) Histogram
 (b) Karyogram
 (c) Dendogram
 (d) C-value paradox
 - (iii) In hierarchical genome sequencing approach, based on the results of ______ mapping, ______of the BAC clones on a chromosome can be determined.
 (a) physical, the locations and orders (b) physical, only the locations
 (c) cytological, only the locations (d) physical, only the orders
 - (iv) A cDNA library contains clones representing which of the following?
 (a) mRNA
 (b) Genomic DNA
 (c) Intron
 (d) microRNA
 - (v) Which of the following repeated sequences includes an open reading frame for reverse transcriptase?
 (a) LINE
 (b) SINE
 - (a) LINE(b) SINE(c) Segmental duplication(d) DNA transposon
 - (vi) Which of the following is not a gene expression database?
 (a) Flyview
 (b) Genbank
 (c) Bodymap
 (d) None of these
 - (vii) Short sub-sequence of a cDNA sequence is
 (a) Expressed sequence tag
 (b) Sequence tagged site
 (c) Contig
 (d) YAC
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- (viii) Which of the following is untrue about comparative genomics?
 - (a) It is comparison of whole genomes from different organisms.
 - (b) It includes comparison of gene number, gene location, and gene content from these genomes.
 - (c) It provides insights into the mechanism of genome evolution and gene transfer among genomes.
 - (d) It doesn't help to reveal the extent of conservation among genomes.
- (ix) In which of the following models might a compensatory mechanism mask the effect of a genetic manipulation?
 - (a) Knockouts only

- (b) Knockins only
- (c) Knockouts and Knockins (d) All model
- (x) Which of these projects would be best suited for Next Generation Sequencing?
 (a) To determine if a tumour sample contains a common missense mutation
 (b) To find the transcriptome of a tumour sample
 (c) To genetime ten genemic DNA samples for a lineum SND
 - (c) To genotype ten genomic DNA samples for a known SNP
 - (d) All of the above.

Group-B

2. (a) Comment about the challenges in human genome sequencing.

[(CO1) (Understand/LOCQ)]

- (b) Analyze the process of whole genome shotgun sequencing. [(CO1) (Analyze/IOCQ)]
- (c) The 454 sequencing has revolutionized DNA sequencing Justify the statement with reasons. [(CO1)(Justify/HOCQ)]

4 + 4 + 4 = 12

- 3. (a) The high resolution physical mapping involves two approaches describe them with suitable diagrams. [(CO1) (Explain/IOCQ)]
 - (b) Write the characteristics of chromosomal map and cDNA map along with their importance. [(CO1) (Remember/LOCQ)]

(3+3) + (3+3) = 12

Group - C

4. (a) Design one high throughput sequence based approach used in functional genomics where the sample size is 200-400bp and cite its characteristics.

[(CO2) (Design/HOCQ)]

- (b) This approach plays an immense role in organising redundant informative sequence information. Analyse how it is done. [(CO2) (Analyse/HOCQ)]
- (c) Analyze how the NCBI informative cluster database is constructed following this approach. [(CO2) (Analyse/IOCQ)]

(1+3)+4+4=12

- 5. (a) Describe the steps of the different levels of genome sequence assembly along with its constraints. [(CO2) (Explain/IOCQ)]
 - (b) "The field of genomics comprises not a single area rather encompasses analysis of gene information and analysis by virtue of tools". Mention the areas that fall under this category. Cite two characteristics and correlation for those areas.

[(CO2) (Correlate/IOCQ)] 4 + (4 + 4) = 12

Group - D

- 6. (a) The HGP showed that less than 2% of the human genome codes for functional proteins Criticize the statement with reasons. [(CO3) (Criticize/HOCQ)]
 - (b) Analyze the significance of microbial genomics in human welfare and research. [(CO3) (Analyze/IOCQ)]
 - (c) Discuss how mtDNA and Y-chromosomal DNA markers help in tracing human evolution. [(CO3)(Understand/LOCQ)]

4 + 4 + 4 = 12

7. (a) What do you mean by genes within genes? Give example.

[(CO4) (Remember/LOCQ)]

- (b) Explain with examples what do you mean by a gene family and gene superfamily. [(CO4) (Analyze/IOCQ)]
- (c) The snRNA and snoRNA genes provide important information about DNA repeats. Criticize the statement with reasons. [(CO4)(Criticize/HOCQ)]

4 + 4 + 4 = 12

Group - E

- 8. (a) What were the main objectives of HapMap project? [(CO4) (Remember/LOCQ)]
 - (b) Analyze one dye-based method for detection of SNP. [(CO4) (Analyze/IOCQ)]
 - (c) Discuss the concept of QTL in quantitative genomics approach.

[(CO4)(Analyze/IOCQ)] 4 + 4 + 4 = 12

- 9. (a) "It is been observed that genes affect our reaction to drugs". Criticize the statement with suitable example. [(CO5)(Evaluate/HOCQ)]
 - (b) Elucidate the clinical implications of Pharmacogenomics with suitable example. [(CO5)(Analyze/IOCQ)]
 - (c) Cite two FDA-approved diagnostic tests commercially available for commonly prescribed pharmacologic therapies. [(CO5) Remember/LOCQ)]

4 + 4 + 4 = 12

Cognition Level	LOCQ	IOCQ	HOCQ
Percentage distribution	27%	52%	21%

Course Outcome (CO):

At the end of this course students will be able to:

- 1. Develop a concept of the different genome mapping techniques and the genome assembly methods.
- 2. Understand the usage of functional genomics tools, different methods of gene transfer and applications of comparative genomics.
- 3. Understand the background of the Human Genome Project along with its findings on genome anatomy, gene family, gene diversity and gene markers.
- 4. Analyze the haplotypes and SNPs by various quantitative techniques.
- 5. Interpret the findings of Human Genome Project in the domain of pharmacogenomics and polygenic disorders.

*LOCQ: Lower Order Cognitive Question; IOCQ: Intermediate Order Cognitive Question; HOCQ: Higher Order Cognitive Question

Department & Section	Submission Link	
ВТ	https://classroom.google.com/c/NDIwMzczMTYxNjIy/a/NDY0MTU5MzIyNjUx/details	