B.TECH/BT/7 TH SEM/BIOT 4165/2018 HUMAN GENOMICS (BIOT 4165)			3	(vii)	The first completed genome sequencing project is of (a) E. Coli (b) Haemophilus influenza (c) X174	
Time Allotted : 3 hrsFull Marks : 70			Full Marks : 70		(d) Drosophila melanogaster .	
Figures out of the right margin indicate full marks.			narks.	(viii)	Human Genome Project was initiated by	
Candidates are required to answer Group A and <u>anv 5 (five)</u> from Group B to E, takin <u>g at least one</u> from each group.			and m each group.	(ix)	(a) NIH (b) DOE (c) NIH and OS DOE (d) Celera Genomics. Which of the following is not a gene expression database?	
Candidates are required to give answer in their own words as far as practicable. Group – A (Multiple Choice Type Questions)					 (a) GenBank (b) Fly view (c) SeedGenes (d) BodyMap. 	
				(x)	The process of introduction of foreign DNA into an animal cell is called	
1. Choos (i)	e the correct alternative for the Which of the genetic markers ar	e following: re present in highest r	$10 \times 1 = 10$ numbers in the human		(a) transversion(b) conversion(c) inversion(d) transfection	(d) transfection
	genome? (a) RELP (b) Minisatellite (c) Microsatellite (d)VNTR			Group – B		
(ii)	SNPs are formed as a result of	(c) merosatenne		2. (a)	What do you mean by high throughput sequencing? Explain with example:	s.
	(a) point mutation	(b) transition		(b)	Describe the technique of 454 sequencing.	
(iii)	(c) deletion Which of the following is obtained	ed via cDNA clones?		(c)	Illustrate the process of pyrosequencing.	
	(a)EST (b) STS	(c) VNTR	(d) STR.		4+4+4=1	2
(iv)	 Short DNA sequence having single occurrence in genome is (a) expressed sequence tag (b) sequence tagged site (c) Contig (d) YAC. Which of the following is untrue about Whole Genome Alignment? 		3. (a)	Mention the approach followed for identification of a specific disease gen where nothing is known except its approximate chromosomal location.	ıe	
(v)			(b)	Describe briefly the steps in above approach. Name the disease which we identified first following this approach.	as	
 (a) This helps to reveal the presence of conserved functional elements. (b) It doesn't help to understand sequence conservation between genomes. (c) It be accomplished through direct genome comparison or genome alignment. (d) The alignment at the genome level is fundamentally no different from the basic sequence alignment. 			on between genomes.	(c)	State the logic of this approach in a step wise manner.	
			ally no different from		2 +(6 + 1)+ 3= 12 Group - C	!
(vi)	Which of the following is untrue about Gene Order Comparison?			4. (a)	Mention in detail the experimental procedure of SAGE along with a suitab diagram.	le
 (a) when the order of a humber of mixed genes is conserved between genomes, it is called synteny. (b) Generally, gene order is much more conserved compared with gene sequences. (c) Generally, gene order is much less conserved compared with gene sequences. 			s conserved between	(b)	Mention the drawbacks of this technique.	
			compared with gene	(c)	Give examples of two SAGE databases.	
			compared with gene		(5 + 3) + 2 + 2= 12	
	(d) It is in fact rarely observed a	mong divergent spec	es.			
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- 5. (a) "Standardization of protein functional description has been spurred due to usage of different terminologies for same type of protein or gene in different organisms" name the project which has been developed. Describe it on the basis of a specific protein.
- (b) Describe the steps of the different levels of genome sequence assembly along with its constraints.

$$(1 + 5) + (4 + 2) = 12$$

Group – D

- 6. (a) Mention the implications of Human Genome Project on medical diagnostics.
- (b) Give a brief description of the mitochondrial genome.
- (c) Discuss how one can trace human migration with the help of genetic markers.

7. (a) What do you mean by gene family and superfamily?

- (b) Discuss about partially overlapping genes.
- (c) Give a comparative account of satellite, minisatellite and microsatellite genes.

4+4+4=12

4+4+4=12

Group – E

- 8. (a) Discuss the importance of SNPs in genomics research.
- (b) What are the applications of molecular beacons in genomics research?
- (c) What do you mean by linkage disequilibrium?

4 + 4 + 4 = 12

- 9. (a) Define selectable marker gene. Briefly describe each category of selectable markers for animal cells with suitable examples for those categories.
- (b) Mention three genes along with the chromosomal location linked to obesity. $(1 + 5)+(3 \times 2) = 12$