STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI -600 086 (For candidates admitted from the academic year 2019 – 2020 & thereafter)

SUBJECT CODE: 19BI/PC/GP24

M. Sc. DEGREE EXAMINATION, APRIL 2023 **BIOINFORMATICS SECOND SEMESTER**

COURSE PAPER TIME		E OMICS AND PRO INUTES	TEOMICS	MAX. MA	ARKS: 50
ANSWER A	LL THE QUE		ION – A		$(20 \times 1 = 20)$
1. What is the	e consequence sults in loss of b	of a change in the good of a change in the good of the	b) leads to an		ne population
i. tran	scriptomes	atements are not true ii. Contain quences iv. Are sm	RNA sequences		nalysis of
a). i aı	nd ii correct	b) ii and iii correc	t c) i and iii co	orrect d.)) ii and iv correct
i. Is u	used to find exo	atements are not true ons ii. one homologies iv.	Is used to find into	ergenic seque	
a) i co	orrect	b) ii correct	c) iii correct	d) iv	v correct
evolutionary l a) gen		of phylogenetic ar fic genes. Which of		ıld not be the	correct blank?
a) they that b) eac c) they co d) they	y are based on a at code for such the clade is defin y are supported prroborates mol	are strongest when amino acid sequence in proteins contain not need by a single derive by more than one kecular evidence.	o introns. ed character. ind of evidence, s	uch as when	fossil evidence
a) Cor	encing followed mparative genon actional genom		tion are steps of b) Structural g d) transcriptor	_	
		g statements is true	_	on of metabo	lic pathway?

- - a) Most of the metabolic pathways are regulated
 - b) Most of the metabolic pathways are not regulated
 - c) Regulation of metabolic pathways always involves changing the amount of enzymes
 - d) Metabolic regulation always depends on control by hormones

- /2/ 19BI/PC/GP24 8. To apply parsimony to constructing a phylogenetic tree, a) choose the tree that assumes all evolutionary changes are equally probable. b) choose the tree in which the branch points are based on as many shared derived characters as possible. c) base phylogenetic trees only on the fossil record, as this provides the simplest explanation for evolution. d) choose the tree that represents the fewest evolutionary changes, either in DNA sequences or morphology. 9. rsID means a) Reference SNP cluster ID b) Rapid Stain Identification Series c) Resource Sequence International Design d) SNP with random repaeats 10. Which of these might be an advantage to genetic testing of individuals via microarrays? a). Many different potential mutations in a single gene could be tested at once. b). Expression patterns of many different genes can be analyzed simultaneously. c). Microarray analysis can provide relative levels of expression of particular genes. d). All of these. 11. Who created meta-learning? a) Chelsea Finn c) Wolfgang Huber d) Lior Pachter b) Peer Bork 12. In terms of understanding the pathways between genes and behaviour, it is fairly safe to say a) we know more about the environment than the genes b) we know more about the genes than the environment c) the new field of molecular genetics is the best way to gain a full understanding of the gene/environment interactions in the pathways d) QTL analysis has actually hindered the understanding of these pathways by suggesting so many separate gene contributions to basic behaviour processes 13. How many variants are there in dbSNP? a) 15 Millions b) 1 million c) 10 million d) 10 billion 14. How is a microarray constructed? In each spot, there are:
 - a) Copies of all the genes for an organism.
 - b) Multiple copies of one gene; each spot has copies for a different gene.
 - c) Multiple copies of intergenetic sequences, which bind to genes in the samples.
 - d) Copies of intergenetic sequences, which promote the replication of DNA in a sample.
- 15. Which of the four genes has the ability to act as a reliable molecular clock?

a) Histone

b) Helicase

c) DNA polymerase

d) DNA ligase

- 16. Which of the following is incorrect regarding sequence homology?
 - a) It is an important concept in sequence analysis
 - b) When two sequences are descended from a common evolutionary origin, they are said to share homology
 - c) Two sequences can homologous relationship even if have do not have common origin
 - d) When two sequences are descended from a common evolutionary origin, they are said to have a homologous relationship

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- 17. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are:
 - a) RNA editing and alternative splicing.
 - b) Protein folding and posttranslational covalent modifications.
 - c) Alternative splicing and posttranslational covalent modifications.
 - d) Posttranslational covalent modification and transcriptional regulation.
- 18. Which of these is the most important aspect of planning and designing a good proteomics experiment?
 - a) Effective data analysis

- b) Appropriate choice of samples and controls
- c) Robust sample preparation methods
- d) All of the above
- 19. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are:
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- 20. In an analysis of eukaryotic gene, you identify several non-overlapping open reading frames, but they are not all in the same frame. Which explanation makes the most sense?
 - a) By random chance, a second reading frame within the gene also has an open reading frame.
 - b) This gene includes introns which are not multiples of three.
 - c) This is a mutant allele that has had several small insertions.
 - d) All of these.

SECTION - B

ANSWER ANY TWO OF THE FOLLOWING

 $(2 \times 15 = 30)$

- 21. Describe the experimental techniques for gene location and computer analysis of a gene function.
- 22. Explain the following: a. Gene Prediction by ORF analysis; b. Genomes of Chimpanzees.
- 23. Illustrate the working and applications of EST with a detailed note on Clustering and Assembly.
- 24. Describe the importance of Protein Interaction Networks and Mapping Protein modifications.
