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(27) Sardar Patel University

M. Sc. Genetics, Second Semester Theory examination, April, 2016 Saturday, 02nd April, 2016; Time:10:30 a.m. to 1:30 p.m. Subject: PS02CGEN01: Biostatistics and Bioinformatics

Total Marks: 70

Notes: - 1) Figures to the right indicate marks.

		2) Draw neat and labeled diagram, wherever necessary.	
Q.1		Choose the Correct Answers of the Following.	[0
	1.	Taking the relevant root of the product of all non-zero and positive values are called:	•
		a) Geometric mean b) Arithmetic mean	
		c) Harmonic mean d) Combined mean	
	2.	In a moderately skewed distribution, Mean = 45 and Median = 30, then the value of mode is:	
		a) 30 b) 0 c) 45 d) 180	
	3.	A bag contains 10 red balls and 7 blue balls. A ball is drawn at random. The probability that ball drawn is not red is	
		a) 7 b) 7/17 c) 10/17 d) 3/17	
	4.	If Ho is true and we reject it is called:	
		a) Type-I error b) Type-II error c) Standard error d) Sampling error	
	5.	Functional structure of protein is available from database.	
		a) PDB b) NCBI c) EMBL d) BOLD	
	6.	File format ".ab1" is for	
		a) DNA sequence b) NGS data c) protein sequence d) protein structure	
	7.	Primary structure of protein is	
		a) functional state of protein b) 3D configuration of protein	
		c) sequence of amino acids d) sequence of m-RNA	
	8.	Docking of compound with protein is a part of	
		a) computer aided drug designing b) phylogenetic analysis	
		c) RNA structure prediction d) comparison of protein structures	
Q.2		Answer the following in short. (Attempt Any Seven)	[1
	1.	Enlist the types of graphs and Narrate the significance of graphic representation of data.	•
	2.	Write merits and demerits of Geometric Mean.	
	3.	Define the terms: 1. Unit 2. Variable	
	4.	Write about types of errors in testing of hypothesis.	
	5.	Represent types of correlation with scatter diagram.	
	6.	Enlist types and application of BLAST.	

7. Explain application of Algorithms - Needleman and Wunsch, Smith and Watermann for

sequence analysis.

- Give difference between the primary, secondary, tertiary and quaternary structure of protein.
- 9. What is the application of phylogenetic tree construction?
- Q.3 (A) Find the standard deviation and standard error of intelligence quotient (I.Q) of 68 [0 students of the following data:

I.Q.	10-20	20-30	30-40	40-50	50-60	60-70	70-80
No. of	05	12	15	20	10	04	02
Students				************			

Q.3 (B) The numbers of pods per plant of a pulse are given below. Calculate the Mean, Mode and Standard deviation.

No. of pods	0-10	10-20	20-30	30-40	40-50	50-60	60-70	70-80
No. of	06	12	22	48	56	32	18	06
plants								

OR

Q.3 (B) Suppose that the following represent the number of children for 10 physicians on a particular hospital staff: 3, 2, 0, 1, 4, 7, 3, 2, 4, 2. Find the following descriptive measures: a) The arithmetic mean; b) The geometric mean; c) The harmonic mean

[06]

[06]

Q.4 (A) In an ecological study, data recorded on fresh and dry weights for a sample of an experimental material. Calculate the correlation coefficient (r) between the two categories and find out its level of significance. [Tabulated 't' value for p=0.05 is 2.31 at 8 degrees of freedom]

[06]

Fresh weight (gm.)	6	10	12	4	15	12	14	8	7	5
Dry weight (gm.)	3	3	4	1	5	3	3	2	2	2

Q.4 (B) Ten individuals are chosen at random from a population and their heights in inches are found to be: 63, 63, 66, 67, 68, 69, 70, 70, 71, 71. In the light of these data, mentioning the null hypothesis, discuss the suggestion that the mean height in the population is 66 inches. [Tabulated $t_{0.05}$ (9 d.f) = 2.262]

[06]

OR

Q.4 (B) In Mirabillis jalapa when plants with red flowers (RR) are crossed with plants having white flowers (rr), the F1 hybrid plants (Rr) bear pink flowers. When these F1 plants with pink flowers are self-pollinated, they develop 41 red, 84 pink, and 43 white flowered plants. Determine the pattern of segregation. Do these results support the theory that the ratio of the flower colours should be 1 red: 2 Pink: 1 White?

[06]

[Tabulated ' χ^2 ' value 5.99 at 5% level of probability for Two degree of freedom]

Q.5 (A) Enlist different types of databases and their significant contribution.

[06]

Q.5 (B) Explain structure of FASTA, GCG, EMBL and NEXUS file formats.

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Q.5 (B)	Explain the types and applications of DNA sequence alignment.	[06]
Q.6 (A)	Explain the structural configurations α -helix, β -sheet and β -turn in protein structure.	[06]
Q.6 (B)	Give a note on RNA structure prediction through bioinformatics tools.	[06]
	OR	
Q.6 (B)	Explain the procedure and application for molecular docking with target protein.	[06]
