

PREVIEW QUESTION BANK

Module Name : Bioinformatics - 69-ENG
Exam Date : 29-Jun-2024 Batch : 14:30-16:30

Sr. No.	Client Question ID	Question Body and Alternatives	Marks	Negative Marks
Objective Question				
1	201	Movement of DNA from one bacterium to another through a tubular bridge or pilus: 1. Conjugation 2. Transposition 3. Transfection 4. Transduction A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
2	202	Which of the following is responsible for eliminating toxic oxygen by-products from cells? 1. Mitochondria 2. Golgi complex 3. Peroxisomes 4. Chloroplasts A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
3	203	A form of multiple parasitism in which a parasite preferentially attacks a host that is already parasitized by another species is known as 1. Cleptoparasitism 2. Ectoparasitoid 3. Obligate parasitism 4. Superparasitism A1 : 1	4.0	1.00

		A2 : 2		
		A3 : 3		
		A4 : 4		
Objective Question				
4	204	For mass multiplication of DD-136 nematode, the common host used is 1. Silk moth 2. Fruit sucking moth 3. Codling moth 4. Lesser wax moth A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
5	205	Chlorpyrifos methyl is effective against stored product insects except 1. <i>Rhizopertha dominica</i> 2. <i>Tribolium castaneum</i> 3. <i>Caryedon serratus</i> 4. <i>Oryzaephilus surinamensis</i> A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
6	206	Which of the following insects often cause inhalational allergies in human following large emergence of adult insects 1. Stick insects 2. May flies 3. Ear wigs 4. Preying mantis A1 : 1 A2 : 2	4.0	1.00

A3 : 3

A4 : 4

Objective Question

7 207

4.0 1.00

Given below are two statements:

Statement (I): Climate is a weather condition related to smaller areas at a given place and at a given time,

Statement (II): Weather is a condition of atmosphere at a given place and at a given time

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

8 208

4.0 1.00

The local name of cyclone in Phillippines is

1. Hurricane
2. Cyclone
3. Baquio
4. Typhoon

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

9 209

4.0 1.00

Which one of the following are secondary tillage implements?

- (A). Subsoiler
- (B). Cultivator
- (C). Disc harrow
- (D). Wetland plough

Choose the **correct** answer from the options given below:

- 1. (A), (B) and (D) only.
- 2. (B) and (C) only.
- 3. (B), (C) and (D).
- 4. (B) and (D) only.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

10 210

_____ is the most suitable, drought resistant and persistent grass?

- 1. *Alyosia sp.*
- 2. *Cenchrus ciliaris*
- 3. *Stylosanthes hamata*
- 4. *Sorghum bicolor*

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0

1.00

Objective Question

11 211

The rainfed area in India is approximately

- 1. 30 mha
- 2. 40 mha
- 3. 57 mha
- 4. 70 mha

A1 : 1

A2 : 2

4.0

1.00

A3 : 3

A4 : 4

Objective Question

12	212	Which nutrient is often a limiting factor in agricultural production? 1. Nitrogen 2. Carbon 3. Oxygen 4. Hydrogen A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	-----	---	-----	------

Objective Question

13	213	What is a potential disadvantage of agroforestry systems? 1. Increased soil erosion 2. Decreased carbon sequestration 3. Reduced biodiversity 4. Enhanced susceptibility to pests A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	-----	---	-----	------

Objective Question

14	214	Pungency in mustard oil is due to 1. Amino acid 2. Allyl isothiocyanate 3. Erusic acid 4. Oxalic acid A1 : 1 A2 : 2	4.0	1.00
----	-----	---	-----	------

		A3 : 3		
		A4 : 4		
Objective Question				
15	215	Sesamum belongs to the family 1. Chenopodiaceae 2. Papilionaceae 3. Leguminosae 4. Pedaliaceae A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
16	216	Dark period is critical in which type of plant? 1. Short day plant 2. Long day plant 3. Day neutral plant 4. All the options A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
17	217	Which of the following is NOT a significant contributor to greenhouse gas emissions from livestock farming? 1. Carbon dioxide 2. Methane 3. Nitrous oxide 4. Ammonia A1 : 1 A2 : 2 A3 : 3	4.0	1.00

A4 : 4

Objective Question

18	218	Fe deficiency is mostly seen in crops growing on 1. Calcareous or alkaline soils 2. Salt affected soils 3. Acidic soils 4. Neutral soils A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	-----	--	-----	------

Objective Question

19	219	EDV (Essentially Derived Varieties) are those which are derived from: 1. crossing two commercially known varieties 2. hybrid introduced from other countries 3. existing variety through genetic engineering or mutation 4. crossing commercially known variety with its wild relative A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	-----	--	-----	------

Objective Question

20	220	What is the role of "companion planting" in agriculture? 1. Enhancing soil fertility through crop rotation 2. Growing different crop species together to deter pests 3. Cultivating plants in hydroponic system 4. Increasing soil compaction through cover cropping A1 : 1 A2 : 2 A3 : 3	4.0	1.00
----	-----	--	-----	------

		A4 : 4		
Objective Question				
21	2901	If the correlation coefficient between body weight of full sibs is 0.25, then the heritability of this trait in this population is 1. less than 0.25 2. 0.35 3. 0.50 4. 0.75 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
22	2902	At what allelic frequency is the heterozygous genotype (Aa) twice as frequent as the homozygous genotype (aa) in a Hardy-Weinberg population? 1. $p = 0.2$; $q = 0.8$ 2. $p = 0.3$; $q = 0.7$ 3. $p = 0.4$; $q = 0.6$ 4. $p = 0.5$; $q = 0.5$ A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
23	2903	If $X \sim N(0,1)$ and $Y = X^2$, then the correlation between X and Y is 1. -1 2. 0 3. 0.5 4. 1 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00

Objective Question

24	2904	If an individual of genotype AaBbCcDd is testcrossed, how many different phenotypes can appear in the progeny? 1. 16 2. 32 3. 64 4. 256 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	------	---	-----	------

Objective Question

25	2905	If in the analysis of variance of a completely randomized design, the d.f. for the treatment sum of squares is 4 and the mean sum of squares due to error is 2, while the observed F-value for testing significance of treatment differences is 12.5, then which one of the following represents correctly the treatment sum of squares? 1. 25 2. 50 3. 75 4. 100 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	------	---	-----	------

Objective Question

26	2906	If two Latin squares each of the same order are such that when one is superimposed over the other, each symbol of one falls on each symbol of the other once and only once, then the two Latin squares are said to be 1. Conjugate 2. Self-conjugate 3. Orthogonal 4. Reduced A1 : 1 A2 : 2 A3 : 3	4.0	1.00
----	------	---	-----	------

		A4 : 4																		
Objective Question																				
27	2907	The following is a BIBD with parameters $v = 4, b = 4, k = 3, r = 3, \lambda = 2$ <table><tr><td>Block 1</td><td>1</td><td>3</td><td>4</td></tr><tr><td>Block 2</td><td>2</td><td>3</td><td>4</td></tr><tr><td>Block 3</td><td>1</td><td>2</td><td>4</td></tr><tr><td>Block 4</td><td></td><td></td><td></td></tr></table> Block 4 contains 1. 1 4 2 2. 2 4 3 3. 2 3 1 4. 4 1 3 A1 : 1 A2 : 2 A3 : 3 A4 : 4	Block 1	1	3	4	Block 2	2	3	4	Block 3	1	2	4	Block 4				4.0	1.00
Block 1	1	3	4																	
Block 2	2	3	4																	
Block 3	1	2	4																	
Block 4																				
Objective Question																				
28	2908	A coin is tossed until a head appears. What is the expectation of the number of tosses required? 1. 0.5 2. 1 3. 2 4. 4 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00																
Objective Question																				
29	2909		4.0	1.00																

Of the 36 accounts drawn randomly from a very large number of accounts in a certain bank, 12 had a deposit of less than Rs. 1500. The estimated standard error for the estimate of the proportion of accounts having a deposit of less than Rs. 1500 is

1. $\frac{2}{105}$
2. $\frac{2}{315}$
3. $\frac{1}{3} \sqrt{\frac{2}{35}}$
4. $\frac{1}{9\sqrt{2}}$

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

30 2910

Two samples of size n are selected, one according to SRSWR and the other according to SRSWOR. Under SRSWR, V_1 stands for variance of sample mean based on all units while V_2 stands for the variance of sample mean based on distinct units. V_3 stands for the variance of sample mean based on SRSWOR. Which one of the following holds ?

1. $V_1 \geq V_2 \geq V_3$
2. $V_2 \geq V_1 \geq V_3$
3. $V_3 \geq V_2 \geq V_1$
4. $V_3 \geq V_1 \geq V_2$

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question

31 2911

A simple random sample of 4 households was drawn from a village containing 120 households. The number of persons per household in the sample were 6, 4, 7 and 3. The estimate of the total number of people in the village is

1. 20
2. 80
3. 600
4. 2400

A1 : 1

A2 : 2

A3 : 3

4.0 1.00

		A4 : 4		
Objective Question				
32	2912	If the events $A_1, A_2, \dots, A_n$ are independent and $P(A_i) = \frac{1}{1+i}$ for $1 \leq i \leq n$, then the probability that none of these n events occurs is 1. $1/(n+1)$ 2. $\frac{1}{(n+1)!}$ 3. $n/(n+1)$ 4. $1 - \frac{1}{(n+1)!}$ A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
33	2913	A committee of 4 people is to be appointed from 3 officers of the production department, 4 officers of the purchase department, 2 officers of the sales department and 1 chartered accountant. The probability that the chartered accountant must be in the committee is: 1. 8/70 2. 1/14 3. 13/14 4. 2/5 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
34	2914	In an experiment, the experimenter observes proportion of individuals affected by a disease in each of the plots by examining a random sample of individuals within each plot. If p is the observed proportion, then the appropriate variance stabilizing transformation in this case will be 1. Square root transformation 2. Sine inverse transformation 3. Logarithmic transformation 4. Fisher's z-transformation A1 : 1	4.0	1.00

		A2 : 2		
		A3 : 3		
		A4 : 4		
Objective Question				
35	2915	The Neyman-Pearson fundamental lemma gives the method of construction of 1. Uniformly most powerful test 2. Most powerful test 3. Randomized test 4. Unbiased test A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
36	2916	Which one of the following non-parametric tests is analogous to Chi-square test of goodness of fit? 1. Median test 2. Kolmogorov-Smirnov test 3. Mann-Whitney Test 4. Wilcoxon Test A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
37	2917		4.0	1.00

Which of the following statement(s) are correct?

- (A). Mean and variance are equal for Poisson distribution.
- (B). Mean is greater than variance for binomial distribution.
- (C). Mean is less than variance for Chi-square distribution.

Choose the **correct** answer from the options given below:

1. (A) and (B) only.
2. (B) and (C) only.
3. (A) and (C) only.
4. (A), (B) and (C) .

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

38	2918	In a Chi-square test, the contingency table has 5 rows and 5 columns. What is the number of degrees of freedom? 1. 10 2. 12 3. 16 4. 25 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	------	---	-----	------

Objective Question

39	2919		4.0	1.00
----	------	--	-----	------

Match **List-I** with **List-II**

List-I	List-II
(A). Internal level	(I). Represents the overall logical structure of the entire database.
(B). Conceptual level	(II). Defines individual user views or schemas
(C). External level	(III). Hides the physical details of the database from users
(D). Data abstraction	(IV). Describes how data is physically stored in the database.

Choose the **correct** answer from the options given below:

1. (A) - (I), (B) - (II), (C) - (III), (D) - (IV)
2. (A) - (IV), (B) - (I), (C) - (II), (D) - (III)
3. (A) - (I), (B) - (II), (C) - (IV), (D) - (III)
4. (A) - (III), (B) - (IV), (C) - (I), (D) - (II)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

40 2920

4.0 1.00

Which of the following is NOT a bioinformatics database?

1. GenBank
2. UniProt
3. Sequin
4. PDB (Protein Data Bank)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

41 2921

4.0 1.00

The term "phylogenetic tree" is used in:

1. Genome assembly
2. Evolutionary biology
3. Protein structure prediction
4. Statistical genomics

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

42 2922

What is a common application of bioinformatics in personalized medicine?

1. Genome-wide association studies
2. Protein crystallization
3. Virus isolation
4. mRNA isolation

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question

43 2923

The central dogma of molecular biology states that:

1. DNA is transcribed into RNA, which is translated into proteins
2. Proteins are transcribed into RNA, which is reverse-translated into DNA
3. DNA directly produces proteins in a cell
4. Only RNA is involved in gene expression

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question

44 2924

4.0 1.00

In bioinformatics, the term "homology" refers to:

1. Two proteins with different functions
2. Similarity in DNA sequences due to convergent evolution
3. Evolutionarily related genes or proteins
4. Unrelated genetic sequences

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

45 2925

Which of the following is an example of a bioinformatics algorithm used for sequence alignment?

1. Smith-Waterman algorithm
2. PCR amplification
3. Southern blotting
4. Protein purification

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0

1.00

Objective Question

46 2926

Computational biology involves the use of:

1. Microscopes for protein visualization
2. Computer algorithms to analyze biological data
3. Molecular cloning techniques
4. Gel electrophoresis for DNA separation

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0

1.00

Objective Question

47 2927

4.0

1.00

Which one of the following is an example of primary database?

1. KEGG
2. EMBL
3. RefSeq
4. CATH

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

48 2928

4.0 1.00

Given below are two statements regarding substitution matrices:

Statement (I): The PAM substitution matrices were derived using local multiple alignments.

Statement (II): The BLOSUM matrices were derived using substitution frequencies derived from sets of closely related protein sequences.

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

49 2929

4.0 1.00

Consider the following terminologies used in phylogenetic analysis:

(A). The lines in a tree are called branches or edges.

(B). Internal branch is located between two nodes.

(C). Root is the common ancestor of all taxa.

Choose the **correct** answer from the options given below:

1. Only (A) and (B) are true.
2. Only (A) and (C) are true.
3. Only (B) and (C) are true.
4. All (A), (B) and (C) are true.

		A1 : 1		
		A2 : 2		
		A3 : 3		
		A4 : 4		
Objective Question				
50	2930	The number of possible unrooted trees for 5 operational taxonomic units is 3 15 105 954 A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
51	2931	Given below are two statements regarding protein structure prediction methods: Statement (I): <i>Ab initio</i> method predicts protein structures based on sequence homology with known structures. Statement (II): Homology modeling, also known as comparative modeling attempts to produce all-atom protein models based on sequence information alone without the aid of known protein structures. In light of the above statements, choose the <i>most appropriate</i> answer from the options given below. - Both Statement (I) and Statement (II) are true. - Both Statement (I) and Statement (II) are false. - Statement (I) is true but Statement (II) is false. - Statement (I) is false but Statement (II) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
52	2932		4.0	1.00

Match **List-I** with **List-II**

List-I	List-II
(A). Procheck	(I). Multiple sequence alignment program
(B). ClustalW	(II). Software to check the stereochemical quality of a protein structure
(C). Swiss-Model	(III). Molecular visualization software
(D). Cn3D	(IV). Automated, flexible docking program
(E). Affinity	(V). An automated comparative protein modeling server

Choose the **correct** answer from the options given below:

- (A) - (II), (B) - (I), (C) - (V), (D) - (III), (E) - (IV)
- (A) - (III), (B) - (I), (C) - (V), (D) - (II), (E) - (IV)
- (A) - (III), (B) - (IV), (C) - (V), (D) - (II), (E) - (I)
- (A) - (II), (B) - (I), (C) - (IV), (D) - (III), (E) - (V)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

53 2933

Consider the following statements regarding various functions used in Perl:

- (A). The splice() function is a general purpose function to add or remove array elements.
- (B). The push() function may be used to append a list of items to the beginning of an array.
- (C). The unshift() function prepends a list of items to the end of an array.

Choose the **correct** answer from the options given below:

- Only (A) is true.
- Only (A) and (B) are true.
- Only (A) and (C) are true.
- Only (B) and (C) are true.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question				
54	2934	Which of the following is not a supervised learning method? 1. Support vector machine 2. K-means clustering 3. Decision tree 4. Linear regression A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
55	2935	In Artificial Intelligence, an environment is uncertain if it is 1. Not fully observable and not deterministic 2. Not fully observable or not deterministic 3. Fully observable but not deterministic 4. Not fully observable but deterministic A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
56	2936	Choose the one which is not an Ensemble Modeling Technique: 1. Bagging 2. Boosting 3. Blending 4. Stacking A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00

Objective Question				
57	2937	Software does not wear-out in the traditional sense of the term, but software does tend to deteriorate as it evolves, because: 1. Software suffers from exposure to hostile environments. 2. Defects are more likely to arise after software has been used often. 3. Multiple change requests introduce errors in component interactions. 4. Software spare parts become harder to order A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
58	2938	Which statement is correct about the Multiplexer? 1. Produces multiple output signals 2. Produces single output signal 3. Encodes the input signals 4. Decodes the input signals A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
59	2939	Which one of the following is a FIFO data structure 1. Stacks 2. Linked List 3. Queues 4. Graphs A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				

60	2940	Thomson Reuters was created by the Thomson Corporation's purchase of the -----company, Reuters Group. 1. German 2. Canadian 3. French 4. British A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
61	2941	Following is used for storing a single Bit in Computer : 1. Multiplexer 2. Encoder 3. Flip Flop 4. Decoder A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
62	2942	Which of the following is not an application software? 1. Windows 10 2. WordPad 3. Photoshop 4. MS-excel A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
63	2943		4.0	1.00

The maximum number of processes that can be in ready state for a computer system with n CPUs is :

1. n
2. n^2
3. 2^n
4. Independent of n

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

64 2944

4.0 1.00

Consider the process given below:

Process	Arrival time	Service Time
P1	0.000	3
P2	1.001	6
P3	4.001	4
P4	6.001	2

What is the waiting time of process P3 using shortest job first (pre-emptive)?

1. 1
2. 3
3. 2
4. 0

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

65 2945

4.0 1.00

Which of the communication modes support two way traffic but only one direction at a time?

1. Simplex
2. Half Duplex
3. Three-quarter's duplex
4. Full duplex

A1 : 1

		A2 : 2		
		A3 : 3		
		A4 : 4		
Objective Question				
66	2946	The loss in signal power as light travels down the fibre is called: 1. Attenuation 2. Propagation 3. Scattering 4. Interruption A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
67	2947	_____ of a set of n elements is an arrangement of the elements in a given order: 1. Combination 2. Permutation 3. Exponent 4. Logarithm A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
68	2948		4.0	1.00

Which of the following are non linear type of data structure?

- (A).Tree
- (B).Graphs
- (C).Hash tables
- (D).List

Choose the **correct** answer from the options given below:

1. (A), (B) and (C) only.
2. (B), (C) and (D) only.
3. (A), (C) and (D).
4. All (A), (B), (C) and (D).

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

69 2949

Which of the following is a type of polymorphism in JAVA Programming?

1. Multiple Polymorphism
2. Compile Polymorphism
3. Multilevel Polymorphism
4. Execution time polymorphism

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question

70 2950

Using which of the following keywords can an exception be generated?

1. Threw
2. Throws
3. Throw
4. Catch

A1 : 1

A2 : 2

4.0 1.00

A3 : 3

A4 : 4

Objective Question

71	1003601	Gene silencing can be achieved through which of the following mechanisms? (A). RNA interference (RNAi) (B). Antisense RNA (C). DNA methylation (D). DNA duplication Choose the correct answer from the options given below: 1. (A), (B) and (C) only. 2. (A), (B) and (D) only. 3. (A), (B), (C) and (D). 4. (B), (C) and (D) only. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	--	-----	------

Objective Question

72	1003602	Chromosome walking is a technique used to: 1. Locate and isolate specific genes within a chromosome 2. Determine the order of genes on a chromosome 3. Identify gene interactions and networks 4. Compare genetic sequences between species A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	--	-----	------

Objective Question

73	1003603		4.0	1.00
----	---------	--	-----	------

Given below are two statements:

Statement (I): A genomic library contains all DNA sequences in an organism's genome

Statement (II): A cDNA library contains only sequences that are transcribed into mRNA

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

74	1003604	Which of the following gene silencing techniques involves the use of small RNA molecules? (A). RNA interference (RNAi) (B). MicroRNAs (miRNAs) (C). Antisense RNA (D). Small interfering RNAs (siRNAs) Choose the correct answer from the options given below: 1. (A), (B) and (C) only. 2. (A), (B) and (D) only. 3. (A), (B), (C) and (D). 4. (B), (C) and (D) only. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	--	-----	------

Objective Question

75	1003605	Which of the following best describes the role of non-coding RNA in gene regulation? 1. Non-coding RNA can modulate transcription and translation through various mechanisms 2. Non-coding RNA is primarily involved in the structural organization of the genome 3. Non-coding RNA is synthesized from repetitive sequences in the genome 4. Non-coding RNA does not play a significant role in gene regulation	4.0	1.00
----	---------	--	-----	------

		A1 : 1		
		A2 : 2		
		A3 : 3		
		A4 : 4		
Objective Question				
76	1003606	Bio-chips are commonly used in which of the following applications? (A). Genomic and proteomic analysis (B). Gene expression profiling (C). Detection of genetic variations (D). Metabolomic analysis Choose the correct answer from the options given below: 1. (A), (B) and (D) only. 2. (A), (B) and (C) only. 3. (A), (B), (C) and (D). 4. (B), (C) and (D) only. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
77	1003607	Which of the following is a commonly used method for retrieving data from biological databases? 1. BLAST 2. PCR 3. Southern blotting 4. DNA sequencing A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
78	1003608		4.0	1.00

Given below are two statements, one is labelled as Assertion (A) and other one labelled as Reason (R).

Assertion (A) : High-throughput sequencing technologies are prone to sequencing errors.

Reason (R) : Errors in sequencing can results from imperfect base calling and sequencing artifacts.

In light of the above statements, choose the *correct* answer from the options given below.

1. Both (A) and (R) are true and (R) is the correct explanation of (A).
2. Both (A) and (R) are true but (R) is NOT the correct explanation of (A).
3. (A) is true but (R) is false.
4. (A) is false but (R) is true.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

79	1003609	4.0	1.00
Given below are two statements, one is labelled as Assertion (A) and other one labelled as Reason (R). Assertion (A) : Comparative assembly is an approach where a genome is assembled using a reference genome Reason (R) : Assembly relies on algorithms that piece together overlapping sequencing reads In light of the above statements, choose the <i>correct</i> answer from the options given below. 1. Both (A) and (R) are true and (R) is the correct explanation of (A). 2. Both (A) and (R) are true but (R) is NOT the correct explanation of (A). 3. (A) is true but (R) is false. 4. (A) is false but (R) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4			

Objective Question

80	1003610	4.0	1.00

Which of the following types of sequencing errors is most likely to occur during high-throughput sequencing?

- (A). Base calling errors
- (B). Adapter contamination
- (C). Misassembly due to repetitive sequences
- (D). Ambiguous bases

Choose the **correct** answer from the options given below:

1. (A), (B) and (C) only.
2. (A), (B) and (D) only.
3. (A), (B), (C) and (D).
4. (B), (C) and (D) only.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

81 1003611

4.0 1.00

Match **List-I** with **List-II**

List-I	List-II
(A). De novo Assembly	(I). Genome assembly using a reference genome from a related species
(B). Comparative Assembly	(II). Genome assembly without using a reference genome
(C). Reference-based Assembly	(III). Genome assembly that combines data from different sequencing platforms
(D). Hybrid Assembly	(IV). Genome assembly using a reference genome from the same species

Choose the **correct** answer from the options given below:

1. (A) - (I), (B) - (II), (C) - (III), (D) - (IV)
2. (A) - (II), (B) - (I), (C) - (IV), (D) - (III)
3. (A) - (I), (B) - (II), (C) - (IV), (D) - (III)
4. (A) - (III), (B) - (IV), (C) - (I), (D) - (II)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

82 1003612

4.0 1.00

Read coverage in genome sequencing refers to:

1. The average number of times a base in the genome is sequenced
2. The proportion of the genome that has been sequenced
3. The number of sequencing reads obtained from a genome
4. The number of overlaps between sequencing read

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

83 1003613

4.0 1.00

Given below are two statements, one is labelled as Assertion (A) and other one labelled as Reason (R).

Assertion (A) : Assembly evaluation involves assessing the accuracy and completeness of the assembled genome.

Reason (R) : Evaluation metrics such as sensitivity, specificity, precision are commonly used to measure genome assembly quality.

In light of the above statements, choose the *correct* answer from the options given below.

1. Both (A) and (R) are true and (R) is the correct explanation of (A).
2. Both (A) and (R) are true but (R) is NOT the correct explanation of (A).
3. (A) is true but (R) is false.
4. (A) is false but (R) is true.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

84 1003614

4.0 1.00

Which genome assembly tool is designed specifically for large-scale assembly of mammalian genomes?

1. ALLPATHS-LG
2. SOAPdenovo
3. Bambus2
4. SGA

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

85	1003615	Which of the following graphical representations is most suitable for displaying a frequency distribution? 1. Pie chart 2. Scatter plot 3. Histogram 4. Line plot A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	---	-----	------

Objective Question

86	1003616	A husband and wife appear in an interview for two vacancies in the same post. The probability of husband's selection is $\frac{1}{7}$ and that of wife's selection is $\frac{1}{5}$. Then the probability that only one of them will be selected is 1. $\frac{2}{7}$ 2. $\frac{4}{35}$ 3. $\frac{6}{35}$ 4. $\frac{24}{35}$ A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	---	-----	------

Objective Question

871003617

4.01.00

Match **List-I** with **List-II**

List-I	List-II
(A). Binomial Distribution	(I). Often used for hypothesis testing in categorical data analysis
(B). Poisson Distribution	(II). Has a symmetrical bell-shaped curve with a mean and standard deviation
(C). Normal Distribution	(III). Models the number of rare events in a fixed interval of time or space
(D). Chi-Square Distribution	(IV). Models the number of successes in a fixed number of trials with a constant probability of success

Choose the **correct** answer from the options given below:

1. (A) - (I), (B) - (II), (C) - (IV), (D) - (III)

2. (A) - (I), (B) - (II), (C) - (III), (D) - (IV)

3. (A) - (I), (B) - (III), (C) - (IV), (D) - (II)

4. (A) - (IV), (B) - (III), (C) - (II), (D) - (I)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

88	1003618		4.0	1.00
----	---------	--	-----	------

Which of the following are true about sampling distributions?

- (A). Sampling distributions represent the distribution of a statistic from repeated samples
- (B). The Central Limit Theorem states that the sampling distribution of the mean approaches a normal distribution with larger samples
- (C). Sampling distribution of the sample mean will have the same standard deviation as the original population
- (D). Sampling distributions are used to estimate population parameters

Choose the **correct** answer from the options given below:

- 1. (A), (B) and (C) only.
- 2. (A), (B) and (D) only.
- 3. (A), (B), (C) and (D).
- 4. (B), (C) and (D) only.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

89	1003619	Given below are two statements, one is labelled as Assertion (A) and other one labelled as Reason (R). Assertion (A) : The correlation between relatives helps estimate heritability in quantitative genetics Reason (R) : Heritability is the proportion of phenotypic variance due to genetic and environmental variance. In light of the above statements, choose the correct answer from the options given below. 1. Both (A) and (R) are true and (R) is the correct explanation of (A). 2. Both (A) and (R) are true but (R) is NOT the correct explanation of (A). 3. (A) is true but (R) is false. 4. (A) is false but (R) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	---	-----	------

Objective Question

90	1003620		4.0	1.00
----	---------	--	-----	------

The breeding value of an individual in quantitative genetics refers to:

1. The ability of an individual to reproduce successfully
2. The expected contribution of that individual's genotype to the phenotype of its offspring
3. The dominance of alleles in the individual's genotype
4. The measure of the effect of a single gene on a quantitative trait

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

91	1003621	Which of the following correctly describes the three-level architecture of a DBMS? 1. External, Conceptual and Internal levels 2. External, Conceptual and Physical levels 3. External, Logical and Physical Levels 4. External, Conceptual and Virtual Levels A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
----	---------	---	-----	------

Objective Question

92	1003622		4.0	1.00
----	---------	--	-----	------

Match **List-I** with **List-II**

List-I	List-II
(A). Primary Key	(I). A unique identifier for a record in a table
(B). Foreign Key	(II). A key that is derived from more than one column
(C). Composite Key	(III). A key that refers to the primary key in another table
(D). Candidate Key	(IV). A key that could potentially be chosen as the primary key

Choose the **correct** answer from the options given below:

- (A) - (I), (B) - (II), (C) - (III), (D) - (IV)
- (A) - (I), (B) - (III), (C) - (II), (D) - (IV)
- (A) - (I), (B) - (II), (C) - (IV), (D) - (III)
- (A) - (III), (B) - (IV), (C) - (I), (D) - (II)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

93	1003623	Which SQL command is used to modify an existing record in a table?	4.0	1.00
- UPDATE - INSERT - SELECT - DELETE				
A1 : 1				
A2 : 2				
A3 : 3				
A4 : 4				

Objective Question

94	1003624		4.0	1.00
----	---------	--	-----	------

Given below are two statements regarding biological database:

Statement (I): Primary databases accept or include original data from researchers, with relatively little checking or validation.

Statement (II): Uniprot, SCOP and TrEMBL are examples of primary protein sequence database.

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

95	1003625	Which of the following is not a Data Definition Language (DDL) command?	4.0	1.00
1. CREATE TABLE 2. ALTER TABLE 3. DROP TABLE 4. SELECT				
A1 : 1				
A2 : 2				
A3 : 3				
A4 : 4				

Objective Question

96	1003626	BankIt is a sequence submission tool at	4.0	1.00
1. DDBJ 2. EMBL 3. GenBank 4. PIR				
A1 : 1				
A2 : 2				
A3 : 3				

		A4 : 4		
Objective Question				
97	1003627	Which of the following is a literature database? 1. ChEBI 2. MIAME 3. DALI 4. MEDLINE A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
98	1003628	Which of the following is not true regarding PAM and BLOSUM scoring matrices? 1. BLOSUM is derived from the local alignments of proteins. 2. PAM is derived from the global alignments of proteins. 3. BLOSUM matrices with low numbers or high PAM numbers are best suited to detect distantly related proteins. 4. PAM was discovered by S. Henikoff and J. Henikoff in 1992 and BLOSUM by Margaret Dayhoff in 1970s. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
Objective Question				
99	1003629	Consider the following statements: (A). Pairwise sequence alignment can be performed using dot matrix analysis, dynamic programming algorithm and word or k-tuple methods. (B). Dot matrix can be used to identify intrasequence repeats in DNA and protein sequences. (C). Needleman-Wunsch algorithm can be used for local alignments. Choose the correct answer from the options given below: 1. Only (A) is true. 2. Only (A) and (B) are true. 3. Only (A) and (C) are true. 4. All (A), (B) and (C) are true. A1 : 1	4.0	1.00

A2 : 2

A3 : 3

A4 : 4

Objective Question

100	1003630	Given below are two statements: Statement (I): The accession number of GenBank/EMBL/DDBJ nucleotide sequence records is usually one letter followed by five digits or two letters followed by six digits. Statement (II): The accession number of RefSeq nucleotide sequence records is three letters followed by five digits. In light of the above statements, choose the <i>most appropriate</i> answer from the options given below. 1. Both Statement (I) and Statement (II) are true. 2. Both Statement (I) and Statement (II) are false. 3. Statement (I) is true but Statement (II) is false. 4. Statement (I) is false but Statement (II) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	---	-----	------

Objective Question

101	1003631		4.0	1.00
-----	---------	--	-----	------

Match the following BLAST programs (**List-I**) with their correct description (**List-II**)

List-I	List-II
(A). blastn	(I). Amino acid query sequence against a protein sequence database
(B). blastp	(II). Translated nucleotide query against a translated nucleotide sequence database
(C). blastx	(III). Protein query against a translated nucleotide sequence database
(D). tblastx	(IV). Nucleotide query sequence against a nucleotide sequence database
(E). tblastn	(V). Translated nucleotide query against a protein database

Choose the **correct** answer from the options given below:

1. (A) - (V), (B) - (III), (C) - (I), (D) - (IV), (E) - (II)
2. (A) - (IV), (B) - (II), (C) - (V), (D) - (I), (E) - (III)
3. (A) - (IV), (B) - (I), (C) - (V), (D) - (II), (E) - (III)
4. (A) - (IV), (B) - (I), (C) - (III), (D) - (II), (E) - (V)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

102 1003632

Which of the following is **not** correct regarding the terminologies used in phylogenetic analysis?

1. The branching pattern in a tree is called topology.
2. Internal branch is located between two nodes.
3. Root is the common ancestor of all taxa.
4. The lines in a tree are called nodes.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0 1.00

Objective Question

103	1003633	Which of following is not a distance-based phylogenetic algorithm? 1. Minimum Evolution 2. Neighbor Joining 3. Fitch and Margoliash Method 4. Maximum Likelihood A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	---	-----	------

Objective Question

104	1003634	Given below are two statements regarding the number of possible rooted or unrooted trees for a given number of operational taxonomic units (OTUs): Statement (I): For two OTUs, only two trees are possible. Statement (II): For three or more than three OTUs, the number of possible rooted trees is always less than the number of possible unrooted trees. In light of the above statements, choose the <i>most appropriate</i> answer from the options given below. 1. Both Statement (I) and Statement (II) are true. 2. Both Statement (I) and Statement (II) are false. 3. Statement (I) is true but Statement (II) is false. 4. Statement (I) is false but Statement (II) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	--	-----	------

Objective Question

105	1003635		4.0	1.00
-----	---------	--	-----	------

Given below are two statements:

Statement (I): Proteins are homologous if and only if they are descended from a common ancestor.

Statement (II): Homologues in different species, descended from a single ancestral protein, are orthologues.

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

106	1003636	The five stages of molecular phylogenetic analyses are given below in random order: (A). Selection of sequences for analysis (B). Specification of a statistical model of amino acid or nucleotide evolution (C). Tree evaluation (D). Multiple sequence alignment of homologous protein or nucleic acid sequences (E). Tree building Choose the correct answer (correct order) from the options given below: 1. (A), (D), (B), (C), (E) 2. (B), (A), (D), (C), (E) 3. (B), (A), (D), (E), (C) 4. (A), (D), (B), (E), (C) A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	--	-----	------

Objective Question

107	1003637		4.0	1.00
-----	---------	--	-----	------

Given below are two statements regarding the neighbor joining method of tree construction, one is labelled as Assertion (A) and other one labelled as Reason (R).

Assertion (A) : The neighbor joining method produces a unrooted tree topology, unless an outgroup is specified or midpoint rooting is applied.

Reason (R) : The neighbor joining method assumes a constant rate of evolution.

In light of the above statements, choose the *most appropriate* answer from the options given below .

1. Both (A) and (R) are correct and (R) is the correct explanation of (A).
2. Both (A) and (R) are correct but (R) is NOT the correct explanation of (A).
3. (A) is correct but (R) is not correct.
4. (A) is not correct but (R) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

108	1003638	Which of the following is used to predict RNA secondary structure?	4.0	1.00
		1. RasMol 2. MFold 3. GenTHREADER 4. RESTML		
		A1 : 1		
		A2 : 2		
		A3 : 3		
		A4 : 4		

Objective Question

109	1003639	Which of the following is not true about <i>ab initio</i> protein structure prediction?	4.0	1.00
		1. It is based on the assumption that the structure of a protein is contained in its amino acid sequence. 2. It assumes that a globular protein folds into the structure with the lowest free energy. 3. The <i>ab initio</i> prediction method attempts to produce protein structure based on sequence information along with the aid of known structure of its homologous proteins as template. 4. Th <i>ab initio</i> prediction method can be used in the absence of detectable homologs.		
		A1 : 1		
		A2 : 2		

A3 : 3

A4 : 4

Objective Question

110	1003640	Given below are two statements regarding the Structural Classification of Proteins (SCOP) database: Statement (I): In the SCOP database, the class α/β comprises mainly segregated α helices and antiparallel β sheets. Statement (II): In the SCOP database, the class $\alpha + \beta$ comprises mainly parallel β sheets with intervening α helices, but may also have mixed β sheets. In light of the above statements, choose the <i>most appropriate</i> answer from the options given below. - Both Statement (I) and Statement (II) are true. - Both Statement (I) and Statement (II) are false. - Statement (I) is true but Statement (II) is false. - Statement (I) is false but Statement (II) is true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	---	-----	------

Objective Question

111	1003641	Consider the following statements regarding the Chou-Fasman (1978) method of predicting secondary structure of proteins: (A). The method calculates the propensity of each residue to form part of a helix, strand, or coil in the context of a sliding window of amino acids. (B). The method is based on analyzing the frequencies of each of the 20 amino acids found in α helices, β sheets, and turns. (C). The method was initially trained on only 15 amino acid sequences with experimentally determined structures. Choose the correct answer from the options given below: - Only (A) and B are true. - Only (B) and (C) are true. - Only (A) and (C) are true. - All (A), (B) and (C) are true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	--	-----	------

Objective Question

112	1003642		4.0	1.00
-----	---------	--	-----	------

Given below are two statements:

Statement (I): Molecular docking is a computational method through which it is possible to predict interactions between two structures, which may be between a protein and a ligand or between two proteins.

Statement (II): AutoDock is a computational docking program based on an empirical free energy force field and rapid Lamarckian genetic algorithm search method.

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are true.
2. Both Statement (I) and Statement (II) are false.
3. Statement (I) is true but Statement (II) is false.
4. Statement (I) is false but Statement (II) is true.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

113 1003643

4.0

1.00

Match List-I with List-II

List-I	List-II
(A). PROCHECK	(I). Protein secondary structure prediction program
(B). FRED	(II). Molecular visualization software
(C). Swiss-Model	(III). An automated comparative protein modelling webserver
(D). Predator	(IV). Quality assessment of protein structures
(E). Cn3D	(V). Molecular docking program

Choose the **correct** answer from the options given below:

1. (A) - (II), (B) - (III), (C) - (V), (D) - (I), (E) - (IV)
2. (A) - (IV), (B) - (V), (C) - (II), (D) - (I), (E) - (III)
3. (A) - (V), (B) - (IV), (C) - (III), (D) - (I), (E) - (II)
4. (A) - (IV), (B) - (V), (C) - (III), (D) - (I), (E) - (II)

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

114	1003644	In object-oriented programming language C++, insulation of data from direct access by the program is called 1. Dynamic binding 2. Message passing 3. Inheritance 4. Data hiding A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	---	-----	------

Objective Question

115	1003645	Consider the following statements regarding C++ object-oriented programming language: (A). Public members (both functions and data) can be accessed from outside the class. (B). Only the member functions can have access to the private data members and private functions. (C). By default, members of a class are public. Choose the correct answer from the options given below: 1. Only (A) and (B) are true. 2. Only (A) and (C) are true. 3. Only (B) and (C) are true. 4. All (A), (B) and (C) true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	--	-----	------

Objective Question

116	1003646		4.0	1.00
-----	---------	--	-----	------

Consider the Perl program given below:

```
@bases = ('A', 'G', 'C', 'T');
```

```
$base1 = shift @bases;
```

```
print "@bases";
```

What will be printed on the screen after running the above code?

1. A G C
2. G C T
3. A
4. G C T A

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

117	1003647	Consider the following statements related to perl programming language: (A). The length function is used by perl to return the length of any string. (B). The chop function is used for removing the last character from the line. (C). Hashes are preceded by (\$) sign and accessed using keys. Choose the correct answer from the options given below: 1. Only (A) and (B) are true. 2. Only (A) and (C) are true. 3. Only (B) and (C) are true. 4. All (A), (B) and (C) are true. A1 : 1 A2 : 2 A3 : 3 A4 : 4	4.0	1.00
-----	---------	---	-----	------

Objective Question

118	1003648		4.0	1.00
-----	---------	--	-----	------

Given below are two statements regarding normalization of microarray data:

Statement (I): One of the reasons to normalize microarray data is that the efficiency of dye incorporation (or radioactivity incorporation) may vary for different samples.

Statement (II): Quantile normalization is a parametric method of data normalization that produces the same overall distribution for all the arrays within an experiment.

In light of the above statements, choose the *most appropriate* answer from the options given below.

1. Both Statement (I) and Statement (II) are correct.
2. Both Statement (I) and Statement (II) are incorrect.
3. Statement (I) is correct but Statement (II) is incorrect.
4. Statement (I) is incorrect but Statement (II) is correct.

A1 : 1

A2 : 2

A3 : 3

A4 : 4

Objective Question

119 1003649

Consider a two-input neuron with the following weight factors, $W = [3, 2]$, input vector $X = [-5, 7]^T$ and bias, $b = 1$. Which of the following transfer or activation function can be used to produce an output of 0.5?

1. Hard limit
2. Symmetrical hard limit
3. Linear
4. Log-sigmoid

A1 : 1

A2 : 2

A3 : 3

A4 : 4

4.0

1.00

Objective Question

120 1003650

4.0

1.00

Match **List-I** with **List-II**

List-I	List-II
(A). FastQC	(I). Supervised machine learning algorithm
(B). Support vector machine	(II). Online tool for gene set enrichment and pathway analysis
(C). K-means clustering	(III). A quality control tool for high throughput sequence data
(D). DAVID	(IV). Unsupervised machine learning algorithm

Choose the **correct** answer from the options given below:

1. (A) - (II), (B) - (IV), (C) - (III), (D) - (I)
2. (A) - (III), (B) - (I), (C) - (II), (D) - (IV)
3. (A) - (III), (B) - (I), (C) - (IV), (D) - (II)
4. (A) - (IV), (B) - (II), (C) - (I), (D) - (III)

A1 : 1

A2 : 2

A3 : 3

A4 : 4