

University of Mumbai
Examination 2020 under cluster 4 (PCE)

Program: BE Biotechnology

Curriculum Scheme: Rev2012

Examination: Third Year Semester V

Course Code: BTC501 and Course Name: Bioinformatics-I

Time: 1 hour

Max. Marks: 50

Note to the students: - All the Questions are compulsory and carry equal marks.

Q1.	Which of the following is untrue about dot plot method and its applications?
Option A:	This method gives a direct visual statement of the relationship between two sequences
Option B:	One of its advantages is the identification of sequence repeat regions based on the presence of parallel diagonals of the same size vertically or horizontally in the matrix
Option C:	It is not useful in identifying chromosomal repeats
Option D:	The method can be used in identifying nucleic acid secondary structures through detecting self-complementarity of a sequence
Q2.	Which one of the following is actually based on MolView?
Option A:	RasMol
Option B:	Qmol
Option C:	RasWin
Option D:	MolDraw
Q3.	Which of the following is not correct about the Integral Membrane Proteins?
Option A:	Membrane proteins exist in lipid bilayers of cell membranes
Option B:	The exterior of the proteins spanning the membrane must be very hydrophobic to be stable
Option C:	The exterior of the proteins spanning the membrane must be very hydrophilic to be stable
Option D:	Most typical transmembrane segments are α -helices
Q4.	Which of the following is one of the rules in Lipinski's rule of five?
Option A:	A molecular weight equal to 500
Option B:	No more than five hydrogen bond acceptor groups
Option C:	No more than 10 hydrogen bond donor groups

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Option D:	A calculated $\log P$ value less than +5
Q5.	Which of the following is not correct about the X-ray Crystallography?
Option A:	In x-ray protein crystallography, proteins need to be grown into large crystals in which their positions are fixed in a repeated, ordered fashion
Option B:	The protein crystals are illuminated with an intense x-ray beam
Option C:	The x-rays are deflected by the electron clouds surrounding the atoms in the crystal producing a regular pattern of diffraction
Option D:	The protein crystals are illuminated with an intense infrared beam
Q6.	When did Smith–Waterman first describe the algorithm for local alignment?
Option A:	1950
Option B:	1970
Option C:	1981
Option D:	1925
Q7.	Which of the following is wrong about Abstract Syntax Notation Sequence Format?
Option A:	The information is much more difficult to read by eye than a GenBank formatted sequence
Option B:	Abstract Syntax Notation (ASN.1) is a formal data description language that has been developed by the computer industry
Option C:	All the information found in other forms of sequence storage, e.g., the GenBank format, is present. For example, sequences can be retrieved in this format by ENTREZ
Option D:	Taxonomic information and bibliographic information cannot be encoded with this format
Q8.	Which of the following sequencing methods uses PCR for generating sequence templates?
Option A:	Sanger’s method
Option B:	Sanger’s method and LMPCR
Option C:	LMPCR
Option D:	LMPCR and automated DNA sequencing

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Q9.	Automated DNA sequencing is an improvement of Sanger's method where
Option A:	ddNTPS are used for chain termination
Option B:	PCR is used for making sequencing templates
Option C:	Fluorescently labelled dNTPs are used for chain termination
Option D:	Fluorescently labelled ddNTPs are used for chain termination
Q10.	Which of the given statements is incorrect?
Option A:	Computers store sequence information as simple rows of sequence characters called strings, which are similar to the sequences shown on the computer terminal
Option B:	Each character is stored in binary code in the smallest unit of memory, called a byte
Option C:	Each character is stored in binary code in the smallest unit of memory, called a bit
Option D:	By convention, many of these combinations have a specific definition, called their ASCII equivalent
Q11.	Which of the following does not describe local alignment?
Option A:	A local alignment aligns a substring of the query sequence to a substring of the target sequence
Option B:	A local alignment is defined by maximizing the alignment score, so that deleting a column from either end would reduce the score, and adding further columns at either end would also reduce the score
Option C:	Local alignments have terminal gaps
Option D:	The substrings to be examined may be all of one or both sequences; if all of both are included then the local alignment is also global
Q12.	Which of the following is not correct about the NMR?
Option A:	It stands for Nuclear Magnetic Resonance
Option B:	NMR spectroscopy detects spinning patterns of atomic nuclei in a electric field
Option C:	NMR spectroscopy detects spinning patterns of atomic nuclei in a magnetic field
Option D:	Protein samples are labeled with radioisotopes such as ^{13}C and ^{15}N
Q13.	Which of the following statements is false regarding the blood brain barrier?
Option A:	The walls of the capillaries supplying the brain have tight fitting cells making it difficult for polar drugs

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	to leave the capillaries
Option B:	The capillaries in the brain have a fatty coating making it more difficult for drugs to enter the brain
Option C:	The walls of the capillaries supplying the brain are made up of several layers of cells, which act as a barrier to the release of drugs
Option D:	Hydrophobic drugs pass through the blood brain barrier more easily than hydrophilic drugs
Q14.	Which of the following is incorrect about protein structure comparison?
Option A:	The comparative approach is important in finding remote protein homologs
Option B:	Protein structures have a much higher degree of conservation than the sequences
Option C:	Protein structures have a much lesser degree of conservation than the sequences
Option D:	Proteins can share common structures even without sequence similarity
Q15.	Which of the following does not describe local alignment algorithm?
Option A:	Score can be negative
Option B:	Negative score is set to 0
Option C:	First row and first column are set to 0 in initialization step
Option D:	In traceback step, beginning is with the highest score, it ends when 0 is encountered
Q16.	Which of the given statements is untrue?
Option A:	Sequence and other data files that contain non-ASCII characters also may not be transferred correctly from one machine to another and may cause unpredictable behavior of the communications software
Option B:	The ASCII mode is useful for transferring text files, and the binary mode is useful for transferring compressed data files, which also contain non-ASCII characters
Option C:	ASCII and binary modes cannot be set by the user
Option D:	Most sequence analysis programs also require not only that a DNA or protein sequence file be a standard ASCII file, but also that the file be in a particular format such as the FASTA format
Q17.	Which of the following is not a DNA sequencing method?
Option A:	LMPCR

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Option B:	Edmans method
Option C:	Sanger's method
Option D:	Maxam-Gilbert method
Q18.	Sequence of which of the following cannot be determined using the Maxam Gilbert method?
Option A:	Bacteriophage T7
Option B:	Plants
Option C:	Bacteria
Option D:	Plasmid
Q19.	According to standard amino acid code letters which of the given pair is not right?
Option A:	K- lysine
Option B:	Y- tyrosine
Option C:	Q- glutamine
Option D:	R- serine
Q20.	Which of the following does not describe BLOSUM matrices?
Option A:	It stands for BLOcks SUBstitution Matrix
Option B:	It was developed by Henikoff and Henikoff
Option C:	The year it was developed was 1992
Option D:	These matrices are logarithmic identity values
Q21.	Which of the following is incorrect about intermolecular approach?
Option A:	This procedure starts with identifying equivalent residues or atoms
Option B:	After residue-residue correspondence is established, one of the structures is moved laterally and vertically toward the other structure to allow the two structures to be in the same location
Option C:	The structures are rotated relative to each other around the three-dimensional axes
Option D:	The rotation doesn't depend on the intermolecular distance

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Q22.	What term is used to signify a preparation that appears identical to the preparation of an active drug but which has no biological activity?
Option A:	Dummy drug
Option B:	Peptidomimetic
Option C:	Placebo
Option D:	Gazebo
Q23.	Which type of DNA cleavage is done in the Maxam Gilbert method?
Option A:	Edge
Option B:	Interstitial
Option C:	Base-specific
Option D:	Gene-specific
Q24.	Which of the given statements is incorrect about Block multiple sequence alignment format?
Option A:	Identification starts contain a short identifier for the group of sequences from which the block was made and often is the original Prosite group ID
Option B:	The identifier is terminated by a comma, and "BLOCK" indicates the entry type
Option C:	AC contains the block number, a seven-character group number for sequences from which the block was made, followed by a letter (A-Z) indicating the order of the block in the sequences
Option D:	The block number is a 5-digit number preceded by BL (BLOCKS database) or PR (PRINTS database)
Q25.	Which of the following is untrue regarding the gap penalty used in dynamic programming?
Option A:	Gap penalty is subtracted for each gap that has been introduced
Option B:	Gap penalty is added for each gap that has been introduced
Option C:	The gap score defines a penalty given to alignment when we have insertion or deletion
Option D:	Gap open and gap extension has been introduced when there are continuous gaps (five or more)

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Question	Correct Option (Enter either 'A' or 'B' or 'C' or 'D')
Q1.	C
Q2.	B
Q3.	C
Q4	D
Q5	D
Q6	C
Q7	D
Q8.	C
Q9.	D
Q10.	B
Q11.	C
Q12.	B
Q13.	C
Q14.	C
Q15.	A
Q16.	B
Q17.	B
Q18.	A

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Q19.	A
Q20.	D
Q21.	D
Q22.	D
Q23.	C
Q24.	B
Q25.	B