University of Mumbai
Examination 2020 under cluster ___ (Lead College Short name)

Program: TE Biotechnology

Curriculum Scheme: Rev 2012

Examination: Third Year Semester V

Course Code: BTC501 and Course Name: Bioinformatics-I

Time: 1 hour   Max. Marks: 50

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

Q1.	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
Q2.	Which one of the following is a command based offline tool for molecular structural visualization?
Option A:	ChemSketch
Option B:	QMol
Option C:	RasMol
Option D:	PyMol
Q3.	Which algorithm is used for solving temporal probabilistic reasoning?
Option A:	Hidden markov model
Option B:	Hill-climbing search
Option C:	Depth-first search
Option D:	Breadth-first search
Q4.	The seeding step in BLAST contains
Option A:	6 residues for protein and 9 residues for DNA sequences
Option B:	3 residues for protein and 9 residues for DNA sequences
Option C:	6 residues for protein and 15 residues for DNA sequences
Option D:	3 residues for protein and 11 residues for DNA sequences
Q5.	Structured Query Language can be used to create
Option A:	Specialized databases
Option B:	Flat file format
Option C:	Object oriented databases
Option D:	Relational databases
Q6.	Which of the following is not a site on internet for alignment of sequence pairs?
Option A:	BLASTX
Option B:	BLASTN
Option C:	SIM
Option D:	BCM Search Launcher
Q7.	Proteins are dynamic entities that undergo _____
Option A:	only fluctuation of flexible loop regions about equilibrium positions when in solution

Option B:	only limited conformational change of amino acid side-chains when in solution
Option C:	both limited conformational change of amino acid side-chains and fluctuation of flexible loop regions about equilibrium positions when in solution
Option D:	illimitable or total conformational change of amino acid side-chains when in solution
Q8.	In HMM, as in a Markov Chain, the probability going from one state to another state is the
Option A:	Emission probability
Option B:	Transition probability
Option C:	Transversion probability
Option D:	None of the above
Q9.	For a given substitution matrix, a negative score means
Option A:	That the frequency of amino acid substitutions found in the data set of homologous sequences is less than would have occurred by random chance
Option B:	That the frequency of amino acid substitutions found in the data set of homologous sequences is greater than would have occurred by random chance
Option C:	That the frequency of amino acid substitutions found in the data set of homologous sequences is equal to that expected by random chance
Option D:	None of the above
Q10.	Phylogenetic analysis of a set of sequences that aligns _____ is straightforward because the positions that correspond in the sequences can be readily identified in a _____ of the sequences.
Option A:	very well, multiple sequence alignment
Option B:	in a distorted way, multiple sequence alignment
Option C:	in a haphazard manner, multiple sequence alignment
Option D:	very well, self-alignment
Q11.	Which of the following act as chain terminator?
Option A:	Exogenous
Option B:	DNA
Option C:	Deoxynucleotides
Option D:	Dideoxynucleotides
Q12.	Which of the following is incorrect regarding Mascot and ProFound?
Option A:	ProFound is a web server with a set of interconnected programs
Option B:	Bayesian algorithm is not involved in ProFound
Option C:	ProFound searches a protein sequence database using MS fingerprinting information
Option D:	Mascot is a web server that identifies proteins based on peptide mass fingerprints, sequence entries, or raw MS/MS data from one or more peptides
Q13.	Correlation of gene expression for pairs of transiently interacting proteins is _____ compared to randomly chosen pairs of proteins.
Option A:	not significant
Option B:	totally significant
Option C:	only marginally significant

Option D:	significant to much extent
Q14.	DDBJ is a _____
Option A:	Nucleotide sequence database
Option B:	Repository
Option C:	Protein bank
Option D:	Secondary database
Q15.	Which of the following is untrue about threading and fold recognition?
Option A:	It assess the compatibility of an amino acid sequence with a known structure in a fold library
Option B:	If the protein fold to be predicted does not exist in the fold library, the method won't necessarily fail
Option C:	If the protein fold to be predicted does not exist in the fold library, the method will fail
Option D:	Threading and fold recognition do not generate fully refined atomic models for the query sequences
Q16.	_____ is a web based program that predicts secondary structure using a combination of evolutionary information and neural networks
Option A:	GOR
Option B:	PHD
Option C:	PSI-BLAST
Option D:	PSIPRED
Q17.	NMR spectroscopy detects spinning patterns of atomic nuclei in a
Option A:	Ionic field
Option B:	Electric field
Option C:	Magnetic field
Option D:	Electric potential region
Q18.	Which of the following is not true about Shotgun Sequencing?
Option A:	When DNA fragments derived from different chromosomal regions have repeats of the same sequence, they will appear to overlap
Option B:	When DNA fragments derived from different chromosomal regions have repeats of the same sequence, they will appear to scrutinize
Option C:	In a new whole shotgun approach, Celera Genomics is sequencing both ends of DNA fragments of short (2 kb), medium (10 kb), and long (BAC or >100 kb) lengths
Option D:	A large number of reads are then assembled by computer
Q19.	Which of the following is untrue about 3D-PSSM?
Option A:	A protein structural superfamily doesn't have sequence-based PSI-BLAST profile
Option B:	It is a web-based program that employs the structural profile method to identify protein folds
Option C:	The profiles for each protein superfamily are constructed by combining multiple smaller profiles
Option D:	In initial steps, protein structures in a superfamily based on the SCOP classification are superimposed

Q20.	_____ is a measure of the strength of shaft in rotation.
Option A:	Polar modulus
Option B:	Torsional modulus
Option C:	Sectional modulus
Option D:	Torsional rigidity
Q21.	The main feature of computer visualization programs is
Option A:	versatality
Option B:	interoperability
Option C:	Searching
Option D:	interactivity
Q22.	Fragment-based lead discovery involves studying how a series of small molecules interact with a target binding site. What term is given to these molecules?
Option A:	Isotopes
Option B:	Isomers
Option C:	Epitopes
Option D:	Aptamers
Q23.	CLUSTALW is a more recent version of CLUSTAL with the W standing for _____
Option A:	Weighting
Option B:	Wiping
Option C:	Winding
Option D:	weakening
Q24.	Database containing chemical information is
Option A:	EMBL
Option B:	PubMed
Option C:	PDB
Option D:	PubChem
Q25.	PHD for secondary structure prediction for protein is a web program based on
Option A:	Ab initio methods
Option B:	Neural Network and Multiple Sequence Alignment
Option C:	Homology based methods
Option D:	only Neural Network method