AAI-003-001623   Seat No. _____

B. Sc. (Sem. VI) (CBCS) Examination

March / April - 2016

BT-603 : Advance Molecular Techniques & Bioinformatics

Faculty Code : 003
Subject Code : 001623

Time : $2\frac{1}{2}$ Hours]   [Total Marks : **70**

Instructions : (1) All questions are compulsory.
              (2) Figures at right side indicates marks of the question.

SECTION - I

1   Multiple Choice Questions : (Each Question carries 1 Mark)

(1) Reverse transcriptase PCR uses

(A) mRNA as a template to form DNA

(B) RNA as a template to form DNA

(C) DNA as a template to form ssDNA

(D) all of these

(2) Which of the following is NOT required for a PCR reaction?

(A) A thermostable DNA polymerase

(B) Dideoxy-dNTPs (ddNTPs)

(C) Primers

(D) Template DNA

(3) Which of the following is chemical nucleotide sequencing method?

(A) Sanger Method

(B) Maxum – Gillbert Method

(C) Edmans Method

(D) Automated Sequencing Method

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(4) The technique used to locate specific genes in chromosomes is

(A) Colony hybridization

(B) insitu hybridization

(C) dot blot technique

(D) western blotting

(5) Western blotting is the technique for detection of

(A) Specific DNA in the Sample

(B) Specific RNA in the Sample

(C) Specific protein in the Sample

(D) Specific glycolipid in the Sample

(6) All of the following are thermostable polymerase except

(A) Taq polymerase

(B) Vent polymerase

(C) DNA polymerase III

(D) Pfu polymerase

(7) Arrange the following in correct order

(1) Southern Blotting   (a)   Alwine

(2) Western Blotting   (b)   E.M. Southern

(3) Northern Blotting   (c)   A. Jeffry

(4) DNA Fingerprinting (d)   Towbin

(A) (1)-(a), (2)-(c), (3)-(d), (4)-(b)

(B) (1)-(b), (2)-(d), (3)-(a), (4)-(c)

(C) (1)-(b), (2)-(a), (3)-(d), (4)-(c)

(D) (1)-(b), (2)-(c), (3)-(a), (4)-(d)

(8) Aminobenzyloxymethyl filter paper is commonly for the transfer in

    (A) Southern Blotting   (B) Northern Blotting

    (C) Western Blotting   (D) Dot Blotting

(9) Molecular markers include

    (A) RFLP   (B) RAPD

    (C) AFLP   (D) all of these

(10) RAPD molecular markers are

    (A) recessive   (B) co dominant

    (C) dominant   (D) neutral

(11) Which of the following is correct regarding genomics?

    (A) It include mapping of genome

    (B) it include genome analysis

    (C) It include genome sequencing

    (D) All of the above

(12) The alignment method suitable for finding out conserved pattern in DNA or protein sequence is

    (A) Multiple sequence alignment

    (B) Global alignment

    (C) Pairwise alignments

    (D) Local alignment

(13) Small cDNA sequence that represents a unique segment of an active gene is called

    (A) SNP   (B) EST

    (C) SnRNAs   (D) Contig

(14) The tertiary structure of protein can be determined by

    (A) X-ray crystallography

    (B) NMR

    (C) Electron microscopy

    (D) all of these

(15) An example of Homology & similarity tool -

(A) PROSPECT   (B) RASMOL

(C) EMBOSS   (D) BLAST

(16) Which of the following is phylogenetic tree evaluation method?

(A) UPGMA method

(B) Bootstrapping

(C) Maximum Parsimony method

(D) All

(17) Databases such as CATH and SCOP are used to identify:

(A) the structural family to which a protein belongs

(B) the genic family to which a protein belongs

(C) homologous proteins

(D) analogous proteins

(18) If you want literature information, what is the best database to refer?

(A) OMIM   (B) Entrez

(C) PubMed   (D) PROSITE

(19) If you want to BLAST the non-redundant database using a new protein sequence as query, which is the BEST search program to use?

(A) BLASTP   (B) TBLASTXL

(C) BLASTN   (D) BLASTX

(20) Example of biological data file formats is

(A) FASTA format   (B) ASN. 1

(C) Genbank format   (D) All

SECTION - II

2 **(a)** Attempt any 3 of 6 : (2 Marks each)   6

   (1) What is the difference between Chromosome walking and Chromosome Jumping ?

   (2) Write short notes on: Autoradiography.

   (3) Pyrosequencing method.

   (4) You are providing 3 sequences calculate the no. of unrooted possible trees.

   (5) Mention the name of any one software used for microarray database analysis.

   (6) What Boolean operations can be used in NCBI/Entrez searches?

(b) Attempt any 3 of 6 : (3 Marks each)   9

   (1) Discuss the DNA foot printing technique.

   (2) Write down short note on Real Time PCR.

   (3) Explain the principle of Sangers Dideoxy Method.

   (4) What do you mean by database? Draw graphical representation of the biological databases.

   (5) Write short note on nature of biological data.

   (6) Write down the future prospective of human genome project.

(c) Attempt any 2 of 5 : (5 Marks each)   10

   (1) What are the basic steps of conventional PCR? Briefly mention the types of PCR.

   (2) Why is primer designing and important parameter for successful PCR? Describe various criteria required for successful primer designing.

   (3) Discuss about Bioinformatics and its applications in different areas.

   (4) Describe microarray and its application.

   (5) Write down the Genbank file format in detail.

3 (a) Attempt any 3 of 6 : (2 Marks each) **6**

    (1) Give the names of any three primer designing software.

    (2) Difference between Dominant & Co dominant Marker.

    (3) Draw the following tree (((A, B) , (C, E)), D).

    (4) Schematically write down the submission and retrieval tool for major biological databases.

    (5) What is E value? Describe the range of e value for the significant result of BLAST.

    (6) In context of sensitivity and specificity compare BLAST and FASTA.

(b) Attempt any 3 of 6 : (3 Marks each) **9**

    (1) What is Restriction Mapping? Gives its application?

    (2) Describe Western Blotting technique.

    (3) What are probes? Discuss its role in Southern Hybridization.

    (4) Short note on Multiple Sequence Alignment.

    (5) Briefly discuss comparative genomics.

    (6) Describe structural classification of proteins.

(c) Attempt any 2 of 5 : (5 Marks each) **10**

    (1) What is Gene Machine? Describe phosphoramidite approach of DNA Synthesis.

    (2) Describe various DNA sequencing techniques.

    (3) What are the sequence similarity search tools? Discuss BLAST in detail.

    (4) Discuss about major protein databases in detail.

(5) What do you mean by phylogenetic analysis? Use maximum parsimony method to reconstruct the phylogenetic tree of the given sequences

Species	A	A	T	G	T	C
	B	A	G	G	T	A
	C	A	G	C	A	T
	D	A	T	C	A	G

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