**DB-003-001623**    Seat No. _____

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

April / May – 2015

# BT - 603 : Advance Molecular Techniques & Bioinformatics

**Faculty Code : 003**

**Subject Code : 001623**

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

Instructions : (1)   Question 1 covers 20 MCQ questions of 20 marks.

(2)   Figures in the right indicates marks.

(3)   Give answers of MCQ in main answer sheet.

**1**    Multiple choice questions :                                **20**

(1)   Which of the following is a multiple sequence tools :

(A)   PDB                (B)   Clustal

(C)   Dismol             (D)   TIGR

(2)   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

(3)   Phylogenetic relationship can be shown by :

(A)   Dendrogram

(B)   Gene Bank

(C)   Data retrieving tool

(D)   Data search tool

(4)   BLAST X program is used for :

(A)   translate protein sequence

(B)   translate DNA database

(C)   translate input sequence

(D)   none of these

(5)   Which is the data retrieving tool ?

(A)   ENTREZ          (B)   EMBL

(C)   PDB             (D)   All of these

(6)   The BLAST program was designed by :

(A)   Stephen Altschul

(B)   David J. Lipman

(C)   William R. Pearson

(D)   Alexei G. Murzin

(7)   Microarray analysis is NOT appropriate for which of the following ?

(A)   Monitoring individual gene expression

(B)   Tentatively assigning gene functions

(C)   Observing patterns of gene expression

(D)   Determining phylogenetic relationships

(8)   Which type of genomic analysis provides information about microbial evolution ?

(A)   structural genomics

(B)   functional genomics

(C)   comparative genomics

(D)   none of the above

(9) What percentage of environmental microbes grow in the laboratory ?

(A) 1%  (B) 20%

(C) 60%  (D) Nearly 100%

(10) A comprehensive database for the study of human genetics is :
(A) PDB  (B) STAG

(C) OMIM  (D) PSD

(11) RAPD is a :

(A) DNA sequencing based method

(B) PCR based method

(C) Restriction digestion based method

(D) All of these

(12) Which of the following is the chemical sequencing method ?

(A) Edman's method

(B) Sanger's method

(C) Maxam-Gilbert method

(D) None of the above

(13) Sanger sequenced the first complete genome of :

(A) T4 pahge  (B) C. elegans

(C) TMV  (D) $\phi \times 174$

(14) The 5'DMT group of phosphoramidite molecule is removed by the treatment with :

(A) Trichloroacetic acid

(B) Tricarboxylic acid

(C) Triacetic acid

(D) All of the above

(15) Which of the following steps are catalysed by Taq polymerase in a PCR reaction ?

(A) Denaturation of template DNA

(B) Annealing of primers to template DNA

(C) Extension of primer end on the template DNA

(D) All of the above

(16) Which of the following methods is used for the detection sequence specific DNA binding proteins ?

(A) PCR

(B) DNA sequencing

(C) DNA foot printing

(D) All of the above

(17) Northern blotting is used for the separation of :

(A) DNA

(B) mRNA

(C) Protein

(D) Protein DNA interactions

(18) Comparative genomics is a powerful tool for :

(A) studying evolutionary changes

(B) helping to identify genes that are conserved

(C) organism its unique characteristics

(D) all of the above

(19) A primer is a short synthetic

(A) Protein (B) Oligonucleotide

(C) Nucleoside (D) None of the above

(20) PCR is a :

(A) DNA modification technique

(B) DNA degradation technique

(C) DNA amplification

(D) DNA sequencing

2 (a) Write any **three** out of **six** : 6

(1) Define molecular markers.

(2) What are the uses autoradiography.

(3) What is CATH ?

(4) What is comparative genomics ?

(5) What is EST ?

(b) Write any **three** out of **six** : 9

(1) How microarray technology works ?

(2) What are different levels of SCOP ?

(3) Which are the core databases of UnitProt ?

(4) Explain the mechanism of chain termination method of sequencing.

(5) Explain the principle of RFLP.

(6) How does Q-PCR work ?

(c) Write any **two** out of **five** : 10

    (1) Write a note on comparative genomics.

    (2) Enlist and explain different types of PCR.

    (3) Explain the role of bioinformatics in biotechnology.

    (4) Explain different divisions of biological databases.

    (5) Sanger's method of DNA sequencing.

3 (a) Write any **three** out of **six** : 6

    (1) What is annotation ?

    (2) Uses of restriction mapping.

    (3) What is molecular Beacons ?

    (4) What are the types of BLAST ?

    (5) What is database ?

    (6) What is Human Genome Project ?

(b) Write any **three** out of **six** : 9

    (1) How primer can be designed ?

    (2) What is global and local alignment ?

    (3) What are the goals of human genome project ?

    (4) Explain the principle of microarray.

    (5) Applications of Autoradiography.

    (6) Mechanism of pyrosequencing.

(c) Write any **two** out of **five** :                     **10**

   (1) Explain phosphoramidite method of DNA synthetizing.

   (2) Explain different blotting techniques.

   (3) Write a note on Multiple sequence alignment.

   (4) Explain the principle and application of DNA foot-printing.

   (5) Explain the similarity search tools used in bioinformatics.

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