KATHMANDU UNIVERSITY
End Semester Examination
July/August, 2019

Marks Scored:

Level: B.Tech.
Year : IV

Course : BIOT 414
Semester : II

Exam Roll No.:

Time: 30 mins.

F.M. : 20

Registration No.:

Date :

SECTION "A"

[10Q × 1 = 10 marks]

Mark [✓] in the most appropriate answer.

1. Determination of a full-genome sequence without using a known reference sequence from an individual of the species is called:
   [ ] Resequencing
   [ ] Exome sequencing
   [ ] De novo sequencing
   [ ] Chromatin sequencing

2. Hox gene cluster reveal gene duplications; which of the following organism has seven Hox cluster:
   [ ] Fruit fly
   [ ] Zebra fish
   [ ] Humans
   [ ] Puffer fish

3. If the Phred score (q) is 40; then the error rate during sequencing is? Provided: $q = -10 \log10(p)$
   [ ] 1 in 1000 bases
   [ ] 4 in 1000 bases
   [ ] 1 in 10000 bases
   [ ] 4 in 10000 bases

4. Molecular taxonomy involved hybridization of DNA from different bacterial strains; if the degree of hybridization was 75%; the two DNA samples belonged to:
   [ ] the same genus
   [ ] the same species
   [ ] the same strains
   [ ] the same class

5. Hamming distance between the sequences: ATCGTATA and ACCGATAT is
   [ ] Five
   [ ] Three
   [ ] None
   [ ] Eight

6. In Archea, the membrane phospholipid does not contain:
   [ ] Isoprene unit
   [ ] Phosphate
   [ ] Ether link
   [ ] D-Glycerol

7. The whole genome duplication of T. nigroviridis shows that Human Chromosome X is equivalent to chromosome number _________ of T. nigroviridis genome:
   [ ] 1 & 7
   [ ] 5 & 13
   [ ] 14 & 15
   [ ] 1 & 6

8. A model for evolutionary history of various species indicate that there was______ whole genome duplications and 30 chromosome fusions for Arabidopsis derived from an original eudicot ancestor.
   [ ] 2 whole genome duplications
   [ ] 1 whole genome duplication
   [ ] 0 whole genome duplications
   [ ] 3 whole genome duplications

9. Microarray runs many hybridization experiments in parallel in the model called as:

[ ] One to One [ ] Many to One

[ ] One to Many [ ] Many to Many

10. In yeast 2-hybrid analysis; the protein library fused with activation domain is:

[ ] Bair [ ] Prey

[ ] Reporter [ ] Target

SECTION "B"

[10Q × 1 = 10 marks]

Fill the blanks with the most appropriate answer.

11. ____________________is defined as the number of bases reported from a single experiment on a single fragment.

12. Phenylketouria is a genetic disease caused by deficiency in a metabolic enzyme ____________________________ that converts phenylalanine to tyrosine.

13. Instead of dATP, ____ is used in Sanger Sequencing. (Full name)

14. In viruses; the structural proteins of capsid and matrix is coded by _____________ gene.

15. TBLASTN searches for protein sequence in ____________________________________.

16. Virulence effect of *H. pylori* appears to be associated with ____________ pathogenicity Island.

17. When grouping two or more genes in one species on the same chromosome in the other species; same order was identified, this is called as ________________.

18. The maize version of ______________________ gene represses lateral shoot development compared to Teosinte.

19. A yellow spot on microarray indicates binding of _________________________.

20. For mass spectroscopy analysis; proteins are cleaved into small fragments; those list of fragmented masses are called as ____________________________.

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SECTION "C"

(Long answer questions)
[3Q × 6 = 18 marks]

Attempt *ANY THREE* questions.

1. Explain the process of Sequencing by Oligonucleotide Ligation and Detection with detailed figures. [6]

2. Describe the process behind Microarray. Explain the various types of analysis that can be performed by Microarray. [4+2]

3. Describe the process involved in MALDI-Q/TOF used in mass spectroscopy analysis. Draw mass spectrum for 2-chloropropane. [4+2]

4. Explain the dynamic components of human genome. Write down the biological effects of transposable elements. [3+3]

SECTION "D"

(Short answer questions)
[6Q × 2 = 12 marks]

5. Write short notes on (*ANY SIX*):
    a. Conformation-sensitive gel electrophoresis
    b. STS maps
    c. Yeast whole genome duplications
    d. UPGMA method to create phylogenetic tree
    e. Yeast 2 hybrid method
    f. Whole genome shotgun sequencing
    g. Distribution of cyanobacteria