B. Sc. BIOTECHNOLOGY
SIXTH SEMESTER
GENOMICS & PROTEOMICS
BBT-602

(Use Separate Answer Scripts for Objective & Descriptive)

Duration : 3 hrs.

Full Marks : 70

[**PART-A: Objective**]

Time : 20 min.

Marks : 20

Choose the correct answer from the following:

1X20=20

1. Which is a genome sequencing method?
   - a. Shotgun
   - b. Maxam Gilbert
   - c. Sanger
   - d. All

2. Which is also known as dideoxy method of DNA sequencing?
   - a. Maxam gilbert
   - b. Sanger sequencing
   - c. Pyrosequencing
   - d. All

3. Which is the size of yeast genome?
   - a. $1.3x10^7$ bp
   - b. 13.5 mb
   - c. Both
   - d. none

4. How much percent of the human genome is not occupied by exon and introns?
   - a. 75%
   - b. 30%
   - c. 25%
   - d. Cant be said

5. Where are tandem repeats found mostly in chromosomes?
   - a. centromere
   - b. telomere
   - c. both
   - d. chromomere

6. Automated sequencing is also known as?
   - a. Next gen sequencing
   - b. High thoroughput sequencing
   - c. Multiplexing
   - d. All

7. Which platform is used by DNA star?
   - a. Illumina
   - b. Sanger
   - c. Both
   - d. None

8. Which software is used for protein level assembly?
   - a. Plass
   - b. Ph rap
   - c. Chromas pro
   - d. All

9. Which is a whole genome assembly software?
   - a. velvet
   - b. Mascura
   - c. Sequencher
   - d. None

[1]

10. How many genes are there in C.elegans genome?
    a. 18424   b. 19000
    c. 20000   d. 17000

11. Which of the peptide will be deflected least?
    a. 720kda   b. 120kda
    c. 500 kda   d. 400 kda

12. A postively charged ion will move towards
    a. cathode   b. anode
    c. both   d. Cant say

13. Polarity is developed by
    a. Electron density   b. charge
    c. Both   d. None

14. Which type of bond is found in acetylene?
    a. Single covalent bond   b. Double covalent bond
    c. Triple covalent bond   d. None

15. What is processed pseudogene?
    a. Which is expressed   b. Which is transcribed
    c. Which is translated   d. None

16. Which enzyme is responsible for converting inorganic phosphate to ATP?
    a. sulfurylase   b. luciferase
    c. luciferin   d. oxyluciferin

17. In Edman degradation, peptide is cleaved from which end?
    a. C terminal   b. N terminal
    c. Alpha carbon   d. None

18. Which software is mostly used for aligning primers?
    a. In silico PCR   b. Blat
    c. Table browser   d. All

19. Which program of VISTA is used for whole genome assemblies?
    a. M VISTA   b. G VISTA
    c. WG VISTA   d. None

20. Ensemble is a service of?
    a. EBI   b. SIB
    c. NIH   d. NLM

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$\boxed{\textbf{PART-B : Descriptive}}$

[Answer question no.1 & any four (4) from the rest]

1. What is the criteria for deflection in mass spectrometry? In which cases you will use mass spectrometry? What is the unique feature of mass spectrometry which is not found in other techniques. Write about the instrumentation with diagram.   2+2+6 =10

2. What are the differences between native and SDS PAGE? Write the advantages of SDS PAGE over native gel.   5+5=10

3. Explain the different types of bonds of protein along with example and diagram.   10

4. Difference between shotgun and clone contig genome sequencing methods. Explain Sanger's sequencing method   3+7=10

5. What are the different stages of pyrosequencing? Explain with diagrams.   10

6. Explain c value paradox with examples. State the contrasting features of yeast and human genome.   5+5=10

7. Explain Ensemble and VISTA browsers highlighting their differences.   5+5=10

8. Explain Edman degradation with reactions.   10

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[3]