B. Sc. (Bioinformatics) (Sem. V) (CBCS) Examination

November / December – 2017

BI - 501 : Genomics

(New Course)

Faculty Code : 003

Subject Code : 006501

Time : **2½** Hours]   [Total Marks : **70**

Instructions : (1) All questions are compulsory.

(2) The right side figure indicates total marks of the question.

PART - A (20 Marks)

1 Main task of _____ is to determine the entire sequence of DNA.

2 _____ Genomics focus on genomic, epigenomic and transcript alterations in cancer.

3 The most two characterized epigenetic modifications are _____.

4 Unique molecular patterns in the DNA are referred to as _____

5 Pyrosequencing is a method of DNA sequencing based on _____

6 What is Capillary electrophoresis (CE)?

7 _____ use actual physical distances usually measured in number of base pairs.

8 Single nucleotide difference in the _____ gene that generates the sickle cell anemia allele.

9 To discover segmental gene duplications, the repetitive class of sequences is first removed by a process called _____

10 Pseudogenes do not have introns or _____

11 _____ gene prediction is an intrinsic method based oil gene content and signal detection.

12 Which prokaryote was first completed in comparative genomics?

13 Which prokaryote having smallest genome?

14 Rosetta program is used in ab-initio method in structural genomics. For what purpose it is used for?

15 Gene3D takes _____ domain families.

16 Name any one Agricultural Genomics company in India.

17 How advances in genomics have enhanced Agrigenomics?

18 Name any one 3D structure superposition software.

19 pGenThreader is used for _____.

20 True or False :
Phyre and Phyre2 have 10- 15% better coverage than 3D-PSSM.

PART - B

1 (a) Explain any **three** :   6

      (1) What are the goals of branches of genomics?

      (2) Mention the techniques involved in functional genomics?

      (3) Genome mapping

      (4) Give different tools name used for Pseudogene prediction.

      (5) Write a note on goals of comparative genomics.

      (6) Explain Identification of gene-coding regions.

(b) Explain any **three** : 9

(1) Discuss in detail about Structural Genomics

(2) Why do 3D-PSSM allow a query sequence of only <800 residues?

(3) Write a note on genome organization in eukaryotes.

(4) Sequencing by hybridization.

(5) Explain Gene prediction based on HMM method.

(6) Explain data flow and performance of genome annotation.

(c) Attempt any **two** : 10

(1) Genome structure in viruses and prokaryotes.

(2) Write notes on Genetic mapping.

(3) Write the significance of Gene prediction tools.

(4) Explain in detail about comparative genomics of organelles.

(5) Agricultural genomics.

2 (a) Explain any **three** : 6

(1) Features of GenThreader

(2) PSIpred

(3) What is the need of genome annotation?

(4) Methods of computational tools for gene identification.

(5) List out the DNA sequencing method.

(6) What is sequence assembly?

(b) Explain any **three** :   9

    (1) BLAST *Vs.* PSI-BLAST

    (2) Substantiate SUPERFAMILY is a database for structural assignment

    (3) Explain application of comparative genomics.

    (4) Explain the genome annotation in eukaryotes and prokaryotes.

    (5) Significance of sequence fragment assembly tools.

    (6) How can we identify a functional gene from a pseudo Rene?

(c) Attempt any **two** :   10

    (1) Genomics in combating bacterial pathogenicity.

    (2) Explain DNA sequencing by Capillary array Electrophoresis.

    (3) Explain the types of Pseudogene in detail.

    (4) Write in detail about Structural Genomics.

    (5) Explain : genome annotation with its types.

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