JAO-1603220001050100 Seat No. _____

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

November – 2019

BI - 501 : Genomics

(New Course)

Time : $2\frac{1}{2}$ Hours] [Total Marks : **50**

Instructions :

(1) All questions are compulsory.

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

1 Attempt the following : **14**

(a) Answer the following short questions : **4**

(ALL COMPULSORY)

1. What is Genomics ?
2. What is C-Value ?
3. The range of bacterial genome size is _____ to _____ Mb.
4. Full form of HGNC ?

(b) Answer ANY ONE of the following short questions : **2**

1. Explain DNA reassociation kinetics.
2. Explain discovery of intron.

(c) Answer ANY ONE of the following short questions : **3**

1. What is exon ? Explain multigene exon family. Explain various strategies of DNA replication in viruses and prokaryotes.

(d) Explain ANY ONE of the following questions in details : **5**

1. Explain organization of organelle genome.
2. Explain role, mission and three aspects of Gene Ontology Consortium with suitable example.

2 Attempt the following : **14**

(a) Answer the following short questions: **4**

(ALL COMPULSORY)

1. What is pyrosequencing ?
2. What are the applications of NGS ?
3. What is a Contig ?
4. Which sequencing technique has the least error rate ?

(b) Answer ANY ONE of the following short questions : **2**

1. What are the applications of NGS ?
2. What is Optical Mapping ? Explain in brief.

(c) Answer ANY ONE of the following short questions : **3**

1. What is the basic principle difference of first, second and third generation sequencing ?
2. Explain the steps involved in template preparation in SGS ?

(d) Explain ANY ONE of the following questions **5**

in details :

1. Explain Ion Torrent sequencing technique.
2. What is Nanopore sequencing and explain its types ?

3 Attempt the following : **14**

(a) Answer the following short questions: **4**

(ALL COMPULSORY)

1. The complexity of sequence assembly is driven by _____.
2. _____ maps short sequence reads generated by a sequencing machine.
3. _____ format was developed to incorporate the phred-scaled base quality scores to facilitate the assessment of sequence quality.
4. _____ assembly was an early strategy, dating from the mid-1990s to the mid-2000s, to assemble individual genes rather than whole genomes.

(b) Answer ANY ONE of the following short questions : **2**

1. Define Greedy Algorithm
2. What Is Variant Calling

(c) Answer ANY ONE of the following short questions : **3**

1. Explain SNP Detection for DNA Assembly.
2. Explain Identification of New Genetic Markers in Exome Sequencing.

(d) Explain ANY ONE of the following questions in details : **5**

1. Write an essay on Exome Sequencing.
2. Discuss cloud base solution for exome sequencing.

4 Attempt following : **14**

(a) Answer the following short questions : **4**

(ALL COMPULSORY)

1. Name the Methods for measuring the abundance of transcripts.
2. The Ensembl gene annotation process can be divided into which four main phases ?
3. NCBI Prokaryotic Genome Annotation Pipeline.
4. What is Ortholog Conjecture.

(b) Answer ANY ONE of the following short questions : **2**

1. What is Annotation of human chromosome 21 ?
2. Briefly write about the methods implemented in KAAS.

(c) Answer ANY ONE of the following short questions : **3**

1. Write about Genome Browsers.
2. What is an optimized approach for annotation of large eukaryotic genomic sequences using genetic algorithm ?

(d) Explain ANY ONE of the following questions in details : **5**

1. Empirical Methods for genome prediction.
2. Genome annotation: data flow and performance.
3. Explain all possible Gene prediction methods.
4. The Ensembl gene annotation system.

5 Attempt the following : **14**

(a) Answer the following short questions : **4**

(ALL COMPULSORY)

1. What are the two main types of Pseudogenes ?
2. SNP density can be predicted by the presence of _____.
3. How pseudogenes are different from the normal genes ?
4. Give example of early use of personalized medicine.

(b) Answer ANY ONE of the following short questions : **2**

1. What is DreamBase ?
2. What are the types of pseudo genes ? List them.

(c) Answer ANY ONE of the following short questions : **3**

1. How are the pseudogenes predicted ?
2. In all types of SNPs either it would have observable phenotype or it results into disease: Explain the sentence.

(d) Explain ANY ONE of the following questions in details : **5**

1. Explain PharmGKB.
2. What is the importance of SNPs ?
