

Exam.Code:0043
Sub. Code: 18010

2125
B.Sc. (Hons.) Bio-Informatics
Fifth Semester
BIN-5002: Fundamentals of Genomics

Time allowed: 3 Hours

Max. Marks: 60

NOTE: Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.

x-x-x

I. Give answer in a very short:-

- a) What is blue print of life?
- b) Give names of two sequencing techniques used for genome sequencing.
- c) Write the names of techniques used for genome annotation.
- d) Genome coverage.
- e) Junk DNA.
- f) What is the Solexa?
- g) Write two applications of ENSEMBLE.
- h) What is the reference genome?
- i) Give names of two genome assembly software.
- j) Give name two protein's databases.
- k) What is the 454?
- l) Web based server. (12x1)

UNIT - I

- II. a) Briefly describe the history of first human genome sequencing project.
b) What are the main structural features of human genome? (2x6)
- III. a) Write about the coding regions of eukaryotic genome and its significance.
b) Describe in brief about repetitive sequences in human genome. (2x6)
- IV. a) Briefly describe 454 sequencing methods and its merits.
b) Write a short note on sanger's DNA sequencing method and their roles in genomics. (2x6)

P.T.O.

Sub. Code: 18010

(2)

UNIT - II

- V. a) Write in brief about shotgun sequencing procedure.
b) Write a short note on *Denova* genome assembly. (2x6)
- VI. a) Explained in brief about the genome assembly and its utility.
b) How does the VISTA tool utilize pairwise or multiple genome alignments to identify conserved non-coding elements (CNEs). (2x6)
- VII. a) How can the UCSC Genome Browser be used to visualize gene annotations.
b) What are the advantages of using UCSC tool in large-scale genomic analyses? (2x6)

x-x-x