

1128

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 atleast two questions from each Unit.

x-x-x

I. Attempt the following:-

- a) Name Computational tools for sequencing
- b) Centers involved in sequencing of HOP
- c) Snips
- d) Chromosome walking
- e) Gene Ontology
- f) Base calling
- g) LINES and SINES
- h) NCBI Genome

(8x1½)

UNIT - I

- II. a) When was the Human Genome Project started and what were the objectives of HGP?
b) Explain the organization of Human Mitochondrial genome. (6,6)
- III. a) Discuss the Maxam Gilbert method of DNA sequencing.
b) What is Genome Annotation? Explain briefly how it is done for a newly sequenced genome. (6,6)
- IV. a) What is Pyrosequencing? Discuss briefly.
b) Discuss the principle and applications of Roche 454 sequencing. (6,6)

UNIT - II

- V. a) Describe briefly the Shotgun approach to sequence assembly taking the example of *Haemophilus influenzae* genome.
b) Describe any two tools for Genome sequence assembly software. (6,6)

P.T.O.

(2)

- VI. a) Discuss the salient features of UCSC Genome browser.
b) Write a short note on VISTA Genome browser. (6,6)
- VII. a) Why *Caenorhabditis elegans* is considered as the model organism?
b) Explain the salient features of SGD. (6,6)

x-x-x