

**M. SC. BIOINFORMATICS SEM.-III (2013 COURSE)**  
**(CHOICE BASED CREDIT SYSTEMS) : WINTER - 2017**  
**SUBJECT : RECENT TRENDS IN BIOINFORMATICS**

Day : Friday  
Date : 03/11/2017

**W-2017-1019**

Time : 02.00 PM TO 05.00 PM  
Max. Marks : 60

**N.B.:**

- 1) **Q.No.1 and Q.No.5 are COMPULSORY.** Out of the remaining questions attempt **ANY TWO** questions from each section.
- 2) Answers to both the sections should be written in **SEPARATE** answer books.
- 3) Figures to the right indicate **FULL** marks.

**SECTION – I**

- Q.1** Explain any five NGS technologies with their respective principles. [10]
- Q.2** Write short notes on **ANY TWO** of the following: [10]
- a) Relational Databases
  - b) Matlab
  - c) Linux
- Q.3** Answer **ANY TWO** of the following: [10]
- a) What is the output of DNA-seq analysis?
  - b) Differentiate between CHIP-seq and RNA –seq analysis.
  - c) Explain the use of bowtie in brief.
- Q.4** What is Big Data Analysis? What is its scope in today's era? How it is different from NGS analysis? [10]

**OR**

Explain in detail RNA sequencing analysis with TopHat.

**SECTION – II**

- Q.5** Explain the following: [10]
- a) IGV
  - b) EMSEMBL
  - c) Cool BARC
  - d) UCSC Genome Browser
  - e) Circos plots
- Q.6** Write short notes on **ANY TWO** of the following: [10]
- a) R packages in Bioinformatics
  - b) Array Express
  - c) Enrichment Analysis
- Q.7** Answer **ANY TWO** of the following: [10]
- a) How visualization networks works? Explain with example.
  - b) Explain the use of MEGA in phylogenetic analysis.
  - c) Write a note on GeneGo.
- Q.8** Explain why genomics is an easy way to technology as compared to proteomics. Give a comparative account on it. [10]

**OR**

Explain principle, algorithm and applications of BIOBASE and TRANSFAC.

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