DMM-1639
M. Sc. (Sem. IV) (Microbiology) Examination
April / May - 2016
MB - 402 : Bioinformatics & "OMICS"
(New Course)

Time : 3 Hours] [Total Marks : 70

Instructions :
(1) Fill up strictly the details of ⬤ signs on your answer book.
Name of the Examination : M. SC. (SEM. IV) (MICROBIOLOGY)
Name of the Subject : MB - 402 : BIOINFORMATICS & "OMICS" (NEW)

Seat No.:

Student’s Signature:

(2) Figures to the right indicate full marks of the question.
(3) Draw neat and labelled diagrams whenever necessary.

1 Answer the following : (any two) 18
(a) Explain in detail the Hidden Markov model 1 for gene prediction.
(b) What are the benefits of next generation sequencing. Explain in detail real time sequencing.
(c) Justify : Annotation bridges the gap from the sequence to the biology of organisms.

2 Answer the following : (any two) 18
(a) Define genome, transcriptome, proteome and metabolome. Justify : Interplay of genome, transcriptome and proteome is metabolome.
(b) Describe in detail the techniques and technologies for the analysis of transcriptome.
(c) Justify : Genomics and proteomics are synergistic. Proteome analysis is attempt to describe molecular basis of physiological processes.
3. Answer the following: (any two)
   
   (a) What are the main functions of biological databases. Justify: Biological databases can be broadly classified into sequence and structure databases.
   
   (b) Discuss in detail EMBL and DDBJ.
   
   (c) Give a detailed account of CATH and SCOPE.

4. Write short notes: (any two)
   
   (a) BLOCK and eMOTIF
   
   (b) Softwares for phylogenetic analysis
   
   (c) Simulation techniques.