



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)

नीचे दर्शायेव निशानीवाणी विगतो उत्तरवही पर अवश्य लपनी. Fillup strictly the details of signs on your answer book.	Seat No. :
Name of the Examination :	<input type="text"/>
<input type="text" value="M. SC. (SEM. IV) (MICROBIOLOGY)"/>	<input type="text"/>
Name of the Subject :	<input type="text"/>
<input (new)"="" omics"="" type="text" value="MB - 402 : BIOINFORMATICS & "/>	<input type="text"/>
Subject Code No. : <input type="text" value="1"/> <input type="text" value="6"/> <input type="text" value="3"/> <input type="text" value="9"/>	<input type="text"/>
Section No. (1, 2,.....) : <input type="text" value="Nil"/>	<input type="text"/>
	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) **18**
- (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) **16**
- (a) BLOCK and eMOTIF
 - (b) Softwares for phylogenetic analysis
 - (c) Simulation techniques.
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