[Total No. of Questions: 12] **[Total No. of Printed Pages: 3]**

UNIVERSITY OF PUNE
[4364]-807
B. E. (I T) Examination - 2013
BIOINFORMATICS (Elective IV) (Sem II) (2008 Course)

[Time: 3 Hours] **[Max. Marks: 100]**

Instructions:

1 *Answer Q1 or Q2, Q3 or Q4, Q5 or Q6 from Section I and Q7 or Q8, Q9 or Q10, Q11 or Q12 from Section II.*
2 *Answer three questions from Section I and three questions from Section II.*
3 *Answers to the two sections should be written in separate answer-books.*
4 *Neat diagrams must be drawn wherever necessary.*
5 *Black figures to the right indicate full marks.*
6 *Assume suitable data, if necessary.*

SECTION -I

Q.1 A What is the scope of bioinformatics? Explain bioinformatics applications related to the following areas: 10
- i) Information search & retrieval.
- ii) Microarrays
- iii) Sequence Assembly
- iv) Pharmacogenomics

B Explain with neat diagram the central dogma of molecular biology. Explain the molecules participating in Information flow and the various Functional sites. 8

OR

Q.2 A Discuss the public bioinformatics databases which are accessible via the internet with appropriate examples. 10

B Explain Data Life Cycle for clinical data management with respect to following steps: 8
- i) Data creation and acquisition
- ii) Use
- iii) Modification
- iv) Archiving and data disposal.

Q. 3 A Define Microarray. Explain the sources of variability in Microarray 8

		preparation and reading. Explain how statistical analysis can be used to reduce variability.	
	B	Explain in brief the data visualization techniques applicable to Bioinformatics. Discuss any two visualization tools with example.	8
		OR	
Q. 4	A	Differentiate between clustering and classification. Discuss in brief the K-means clustering and Decision tree.	8
	B	List the various statistical analysis tools. What is meant by Sensitivity and Specificity of a tool? Explain in brief False Negative, True Negative, True Positive and False positive.	8
Q. 5	A	What are the types of machine processes? Explain any two machine learning processes.	8
	B	Write short notes on: (i)Pairwise Sequence Alignment(PSA) (ii)Multiple Sequence Alignment(MSA)	8
		OR	
Q. 6	A	Explain the text mining with NLP Process.	8
	B	Explain computational methods of Sequence alignment. i) Dynamic programming ii) Word method	8

SECTION II

Q. 7	A	Explain in detail Primary, Secondary, Tertiary and Quaternary structures of Proteins.	10
	B	Explain the process of Drug discovery. What high-throughput screening methods are employed in screening drugs?.	8
		OR	
Q. 8	A	Discuss in brief the components of a modeling and simulation system alongwith the process.	8
	B	Draw and explain Collaboration-Communication model with appropriate examples.	10
Q. 9	A	Explain in detail FASTA algorithm and the recommended steps for a FASTA search.	8
	B	Explain BLAST algorithm. Discuss Gapped BLAST with its major refinements.	8
		OR	

Q. 10	A	Discuss Similarities and Differences of FASTA and BLAST tools for sequence alignment.	8
	B	Discuss the applications of PSI-BLAST program which explores protein family relationships.	8
Q. 11	A	What is biotechnology? What is the scope of bioinformatics in biotechnology?	8
	B	What are the natural causes of degradation of ecosystem?	8
		OR	
Q. 12	A	Define genetic engineering. Discuss current developments in genetic engineering.	8
	B	Write short notes on pollutants in Lithosphere, Hydrosphere and Atmosphere.	8