C.U.SHAH UNIVERSITY
Summer Examination-2016

Subject Name: Bioinformatics/Biostatistics

Subject Code: 4LS04BOT1/4SC04BIB1   **Branch: B.Sc.(Micro,Biotech)**

Semester: 4   **Date: 05/05/2016**   **Time: 02:30 To 05:30**   **Marks: 70**

Instructions:
(1) Use of Programmable calculator & any other electronic instrument is prohibited.
(2) Instructions written on main answer book are strictly to be obeyed.
(3) Draw neat diagrams and figures (if necessary) at right places.
(4) Assume suitable data if needed.

Q-1	**Attempt the following questions:**	**(14)**

	a)	Define Bioinformatics.	1
	b)	What is MIPS?	1
	c)	What are different forms of secondary structure?	1
	d)	What is use of Pfam in Protein structure prediction?	1
	e)	What is line graph?	1
	f)	What are types of Variables?	1
	g)	Define Biostatistics.	1
	h)	In which year human genome was sequenced?	1
	i)	What is Central dogma of life?	1
	j)	What are stop codons?	1
	k)	What is alignment?	1
	l)	What is dendogram?	1
	m)	In which form of protein structure is superimposed?	1
	n)	Define BLAST.	1

Attempt any four questions from Q-2 to Q-8

Q-2	**Attempt all questions**	**(14)**
a)	What is bioinformatics? Write about Areas, scope and applications of bioinformatics.	
b)	Enlist various databases of proteins and describe.	

Q-3	**Attempt all questions**	**(14)**
	Write a note on Secondary databases.	

Q-4	**Attempt all questions**	**(14)**
a)	Explain in detail about Primary, Secondary and tertiary structure of proteins with diagram.	

Q-5		**Attempt all questions**	**(14)**
	a)	Explain Needleman and Wunch algorithm	
	b)	Explain Smith and waterman algorithm	

Q-6		**Attempt all questions**	**(14)**
	a)	Write a note on GenBank and explain general format followed by genbank.	
	b)	Write a note on Phylogenetic analysis methods.	

Q-7		**Attempt all questions**	**(14)**
	a)	Explain all Primary databases of DNA.	
	b)	Explain comparison of two sequences in detail.	

Q-8		**Attempt all questions**	**(14)**
	a)	What is t-test and chi-test? Explain briefly.	
	b)	Write a note on various secondary databases and their primary sources.	