## T. Y. B. Sc. (Biotechnology) SEM – VI (CBCS - 2015 COURSE) : SUMMER - 2019

01.00 PM

		Subject: Basics of Bioinformatics		
Day:		·	Time:	10.00 AM TO
Date		S-2019-1391	Max. Marks: 60	
N.B.	:			
1	) Q1 and Q5 are co			
2	2) Answer ANY TV	VO questions from Q 2, 3, 4 in Section I.		
3	•	VO questions from Q 6, 7, 8 in Section II.		
4		the sections to be written in $\S$ SA ME $\S$ answer books.		
5	b) Draw a labeled d	iagram WHEREVER necessary.		
		SECTION - 01		
Q.1) A	Answer the following	g: (ANY FIVE) (2 Marks X 5 = 10)		
a)	UCSC stands for _			
b)	What is INSCD?			
c)	NCBI was founded	in		
d)	Who is father of Bi	oinformatics?		
e)	Prosite database be	gan in		
f)	Which is first preot	ein sequence database?		
O.2) A	Answer the following	g: $(5 \text{ Marks } X 2 = 10)$		
a)	What is Biological			
b)	Explain Scope of B			
O.3) F	Explain the following	g: $(5 \text{ Marks } X \ 2 = 10)$		
a)		nd PMC database features with their respective application	ons.	
b)	Enlist five comands			
0.4) V	Vrite short notes on t	the following: (5 Marks $\times 2 = 10$ )		
	EMBL	the following. (3 Walks A 2 – 10)		
a) b)	GenBank flat file			
U)	Gendank nat me			
		SECTION - 02		
Q.5) A	Answer the following	(ANY FIVE) (2 Marks X 5 = 10)		
a)	Define Family.			
b)	PIR stands for			
c)	BLOSUM metrices	used for		
d)	What is sequence a	lignment?		
e)	Define Homology.			
f)	Define sequence sin	nilarity.		
Q.6) A	answer the following	x : (5  Marks  X 2 = 10)		

- a) What is proteomics? Explain its applications.
- b) Explain Scoring matrices for Nucleic acids.
- Q.7) Explain the following: (5 Marks X = 10)
  - a) Explain Smith-Waterman algorithm.
  - b) Explain in brief Multiple sequence alignment.
- Q.8) Write short notes on the following: (5 Marks X 2 = 10)
  - a) Protein sequencing techniques.
  - b) FASTA

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