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## Gandhi Institute of Engineering and Technology University, Odisha, Gunupur (GIET UNIVERSITY)

M.Sc. (Second Semester - Regular) Examinations, July - 2025

## 24MBIPC12003- Bioinformatics

(Biotechnology)

Time	e: 3 hrs	Maximum: 60 Marks						
	Answer ALL questions							
(The figures in the right hand margin indicate marks) PART – A (2 x 5 = 10 Marks)								
		$(2 \times 5 =$	CO#	ŕ				
Q.1.	Answer ALL questions		CO#	Blooms Level				
	Write the URL of EMBL database		CO1	K1				
b.	What is the difference between Entrez and SRS		CO1	K1				
c.	How to estimate the secondary structures of protein based on GOR value		CO2	K1				
	What is the Hamming distance between the sequence HLIKLAAIV HLWKLAAIWA	VL and	CO3	K1				
e.	Convert the given molecular marker into MSA							
	TCYGIFVL							
	TCGIFVL		CO4	K1				
	SCYGIFVLSG							
	ACGIFVLSG							
PART – B				arks)				
Ansv	ver ALL the questions	Marks	CO#	Blooms Level				
2. a.	Explain the layer of PIR database	5	CO1	K1				
b.	Write retrieving method and submission tools of PDB database (OR)	5	CO1	K1				
c.	Write short note of CATH and SCOP database	5	CO1	K1				
d.		5	CO1	K1				
3.a.	Find the optimal alignment and alignment score between two sequence							
	GCATGCA and GATTACA by using Needleman-Wunch algorithm (Assume Match= 1, Mismatch = -1 and Gap= -1)	5	CO2	K2				
b.	Define PAM. Find the PAM value of all amino acid of the given MSA							
	ACGCTAFKI							
	GCGCTAFKI							
	ACGCTAFKL	5	CO2	К2				
	GCGCTGFKI							
	GCGCTLFKI							
	ASGCTAFKL							
	ACACTAFKL							
	(OR)							
c.			CO2	V2				
	GGATCGA and GAATTCAGTTA (Assuming match = 5, Mismatch = -3 and ga = -4) By using Smith -Waterman algorithm.	p 5	CO2	K2				
	– -+) Dy using Simui - waterman argorithm.							

Which two sequence are	e very c	losed to	each o	ther just	tify it by	using Hamming			
distance method									
ADIKLAAIKL							5	CO2	K2
ADSKLAAIKA									
KILASDPQWE									
Design a HMM of the gi	iven MS	SA							
VGAH									
V N									
VEA D							_	603	K2
VKG							5	CO3	K2
VYST									
FNA N									
IAGADN									
Suppose there are 20,00	0amino	acid in t	he data	base of	which 2	000 are serin and			
there are 5000 amino a	acids in	helical	confor	mation	of whice	ch 500 are serin.	5	CO3	K2
calculate the type of info	ormation	ı							
		(OR)							
Explain FASTA3 progra	ım. Wri	te its use	e				5	CO3	K1
Design a phylogenetic tr	ree					_			
	A	В	C	D	E				
A		94	111	180	206				
В			115	194	218		5	CO3	К2
С				188	218	-			
D					217				
Е									
Explain different window	ws of Cı	n 3D	I	1		1	5	CO4	K1
Find the fitch and transv	ersion p	arsimor	ıy value	of each	of the p	hylogenetic tree			
•		How ma	ny roote	ed and u	nrooted	phylogenetic			
•	uct.								
							5	CO4	К2
GCACGAC									
		` ′							
•				the prod	cess of s	tudy the dynamic	5	CO4	K1
							_		
* **									K1
							5	CO5	K1
		_		quence-	314159	26535 and patten	5	CO5	К2
sequence 26 using Rabin	ı Krap a	-	n						
W71	) F 1 '	, ,	41 1		1	4 1 4 1 114	_	605	144
						5	CO5	K1	
						5	CO5	K2	
1011101110 and pattern	sequenc		-		_	ing aigorium.			
	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given tree is possible to constructed tree is possible to constructed tree is possible	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MS VGAH VN VEAD VKG VYST FNAN IAGADN Suppose there are 20,000aminor there are 5000 amino acids in calculate the type of information  Explain FASTA3 program. Writh Design a phylogenetic tree    A	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEA D VKG VYST FNA N IAGADN Suppose there are 20,000aminoacid in there are 5000 amino acids in helical calculate the type of information (OR) Explain FASTA3 program. Write its use Design a phylogenetic tree	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEAD VKG VYST FNAN IAGADN Suppose there are 20,000aminoacid in the data there are 5000 amino acids in helical confor calculate the type of information (OR) Explain FASTA3 program. Write its use Design a phylogenetic tree    A   B   C     A   94   111     B   115     C   D     E   D	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEAD VKG VYST FNAN IAGADN Suppose there are 20,000aminoacid in the database of there are 5000 amino acids in helical conformation calculate the type of information (OR) Explain FASTA3 program. Write its use Design a phylogenetic tree    A B C D   A 94 111 180   B 1115 194   C   188   D   Explain different windows of Cn 3D Find the fitch and transversion parsimony value of each constructed of the given MSA. How many rooted and utree is possible to construct. ACAGGAT ACACGCT GTAAGGT GCACGAC (OR) Explain molecular Dynamic Simulation. Write the proceeding the proceeding of t	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEA D VKG VYS - T FNA N IAGADN Suppose there are 20,000aminoacid in the database of which 2there are 5000 amino acids in helical conformation of whice calculate the type of information (OR) Explain FASTA3 program. Write its use Design a phylogenetic tree    A B C D E	ADIKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEAD VKG TFNAN IAGADN Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information (OR) Explain FASTA3 program. Write its use Design a phylogenetic tree    A   B   C   D   E	distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Design a HMM of the given MSA VGAH VN VEAD VKG VYST FNA - N IAGADN Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information (OR)  Explain FASTA3 program. Write its use Design a phylogenetic tree    A   B   C   D   E     A   94   111   180   206     B   115   194   218     C     188   218     D     217     E     2   217     E   2   2   2     Explain different windows of Cn 3D Find the fitch and transversion parsimony value of each of the phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree is possible to construct. ACAGGAT ACACGCT GTAAGGT GCACGAC (OR)  Explain molecular Dynamic Simulation. Write the process of study the dynamic behaviour of protein by AMBER package. Explain type of motif. Draw the flow chart of motif discovery Explain the steps involve in Homology modelling Find the no. of valid shift of the given Test sequence 26 using Rabin Krap algorithm (OR)  What is protein Folding? Explain few methods to estimate the protein stability. What is pattern? Find the no. of valid shift of the given Test sequence 1011101110 and patten sequence 111 using Naïve string-matching algorithm.	distance method ADIKLAAIKL ADISKLAAIKA KILASDPQWE  Design a HMM of the given MSA VGA H V N VEA D VKG VYS -T FNA - N IAGADN Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information (OR)  Explain FASTA3 program. Write its use    A   B   C   D   E     A   94   111   180   206     B   115   194   218     C     188   218     D     217     E                   Explain different windows of Cn 3D       Find the fitch and transversion parsimony value of each of the phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree constructed of the given MSA. 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