Printed Pa	age:-	Subject Code:- A	ABT0304		
	NOIDA INSTITUTE OF ENGINEE				
	(An Autonomous Inst	titute Affiliated to AKTU B.Tech.	, Lucknow)		
	SEM: III - THEORY EX		022) (ONLINE)		
—		ject: Bioinformatics	, , ,		
Time: 0	2:00 Hours		Max. Marks: 100		
General I	nstructions:				
1. <i>All</i>	questions are compulsory. It comprise	es of two Sections A and I	3.		
 Section A - Question No- 1 has 35 objective type questions carrying 2 marks each. Section B - Question No- 2 has 12 subjective type questions carrying 3 marks each. You have to attempt any 10 out of 12 question. No sheet should be left blank. Any written material after a Blank sheet will not be evaluated/checked. 					
	SE	ECTION A	$35 \times 2 = 70$		
1. Attemp	ot ALL parts:-				
1.1.a	The first bioinformatics database wa	as created by	1		
	(a) Richard Durbin				
	(b) Dayhoff				
	(c) Michael J. Dunn				
	(d) Pearson				
1.1.b	Which of the following is patent dat	abase?	1		
	(a) EMBL				
	(b) NCBI				
	(c) EKASWA				
	(d) DDBJ				
1.1.c	Name the sequence submission tool		1		
	(a) SRS				
	(b) BankIt				
	(c) EMBL				
111	(d) PatentScope	~ P	1		
1.1.d	Who coined the term Bioinformatics	S ?	1		
	(a) J.D Watson				
	(b) Pauline Hogeweg(c) Margaret Dayhoff				
	(d) Frederic Sanger				
1.1.e	Which is not a in silico rDNA techn	ology tool	1		
11110	(a) Web cutter	.01087 1001	-		
	(b) WatCut				
	(c) Restriction analyzer				
	(d) Ekaswa				

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Name the biological sequence submission tool of Japan

(a) BankIt(b) Webin(c) Sequin

1.1.f

	(d) Sakura	
1.1.g	Which is the sequence retrieval tool of NCBI?	1
	(a) SRS	
	(b) EMBL	
	(c) ENTREZ	
	(d) Webin	
1.2.a	BLAST was developed and controlled by which organization?	1
	(a) EBI	
	(b) DDBJ	
	(c) NCBI	
	(d) PDB	
1.2.b	Which algorith is used in BLAST?	1
	(a) Needleman	
	(b) Heuristic	
	(c) AI	
	(d) Blast Algo	
1.2.c	Which bioinformatics tool compares protein query sequence against proteins sequence database?	1
	(a) Blastx	
	(b) tblastx	
	(c) blastn	
	(d) blastp	
1.2.d	Which bioinformatics tool compares nucleotide query sequence against translated nucleotide sequence database?	1
	(a) Blastx	
	(b) tblastx	
	(c) blastn	
	(d) blastp	
1.2.e	Which is not the boolean operation in ENTREZ?	1
	(a) NOT	
	(b) AND	
	(c) OR	
	(d) IF	
1.2.f	The matrix used for the best local alignment of protein sequences is	1
	(a) BLOSUM62	
	(b) IUB	
	(c) BLOSUM80	
	(d) PAM20	_
1.2.g	Which algorithm is followed in global alignment? (CO2)	1
	(a) Smith-Waterman algorithm	
	(b) Needleman-Wunch algorithm	
	(c) k-tuple algorithm	
1.2	(d) Heuristic algorithm	1
1.3.a	Which of the following is incorrect regarding the advantages of Molecular data for phylogenetics study?	1
	(a) They are more numerous than fossil records	
	(b) They are easier to obtain as compared to fossil records	

	(c) Clustered Regularly Interspaced Short Palindromic Repeats	
	(b) It is the name of an American candy bar	
	(a) Clustered International Societies of Photosynthesis Research	
1.4.c	What does CRISPR stand for? (CO4)	1
	(d) Cytosine	
	(c) Thymine	
	(b) Guanine	
	(a) Adenine	
1.4.b	In human DNA, which nucleotide base is methylated at the 5' position?	1
	(d) Darwin	
	(c) Needleman-Wunch	
	(b) Smith-Waterman	
1	(a) Conard H. Waddington	1
1.4.a	Who coined the term epigenetics?	1
	(d) ladder method	
	(c) Maximum Likelihood	
	(a) Distance Methods (b) Maximum Parsimony	
1.3.5	(a) Distance Methods	1
1.3.g	Which of the following is not the phylogenetic analysis method	1
	(d) 1876	
	(c) 1870	
	(a) 1867 (b) 1866	
1.3.1	(a) 1867	1
1.3.f	The term "phylogeny" derives from the German Phylogenie, introduced by Haeckel in year?	1
	(d) an example of analogy rather than homology	
	(b) a shared derived character.(c) a character useful for distinguishing birds from mammals	
	(a) a shared ancestral character. (b) a shared derived character	
1.3.e	In a comparison of birds with mammals, having four appendages is	1
120	·	1
	(c) Neighbor joining(d) Maximum Parsimony	
	(b) REBASE (c) Neighbor joining	
	(a) UPGMA	
1.3.d	Which is not a phylogenetic tree construction method? (CO3)	1
101	(d) Primer 3.0	4
	(c) SIGNOR	
	(b) TIGR	
	(a) DNA stride	
1.3.c	Which software is used for constructing phylogenetic tree?	1
	(d) SIGNOR	
	(c) Reactome	
	(b) TIGR	
	(a) REBASE	
1.3.b	Which is Restriction enzyme database?	1
	(d) More clear-cut and robust phylogenetic trees can be constructed with the molecular	data
	(c) Sampling bias is involved	

	(d) Clustered repeat sequences	
1.4.d	In what type of organisms can the CRISPR/Cas system be found naturally?	1
	(a) Eukaryotes	
	(b) Prokaryotes	
	(c) Viruses	
	(d) none of these	
1.4.e	The enzymatic activity of the Cas9 protein can be compared to: (CO4)	1
	(a) An anchor	
	(b) Scissors	
	(c) Glue	
	(d) Stapler	
1.4.f	Where does gene editing occur?	1
	(a) Anywhere in the genome, depending on the sgRNA used	
	(b) Anywhere in the genome, as long as the sgRNA binds upstream of a PAM sequence	
	(c) Anywhere in the genome, as long as the sgRNA binds downstream of a PAM sequence	ce
	(d) Only in exons	
1.4.g	What does sgRNA stand for and why?	1
	(a) Shorter guide RNA, because it is only 100 bp	
	(b) Simple guide RNA, because it makes gene editing simple	
	(c) Short genomic RNA, since it binds genomic DNA	
	(d) Single guide RNA, because it is a fusion of crRNA and tracrRNA	
1.5.a	The study of microbial communities from environmental DNA samples is known as	1
	(a) Microbial genomics	
	(b) Microbial Genetics	
	(c) Metagenomics	
	(d) Megagenomics	
1.5.b	Which of the following methods do we use to find the best fit line for data in Linear Regression?	1
	(a) Least square error	
	(b) Maximum likelihood	
	(c) Logrithimic loss	
	(d) None	
1.5.c	β -pleated sheets are the examples of	1
	(a) Primary structure	
	(b) Secondary Structure	
	(c) Tertiary structure	
	(d) Quaternary structure	
1.5.d	Which of the following are known as helix breakers?	1
	(a) Proline and glycine	
	(b) Isoleucine and leucine	
	(c) Valine	
	(d) Threonine	
1.5.e	What term is used to signify a preparation that appears identical to the preparation of an active drug but which has no biological activity?	1
	(a) Dummy drug	
	(b) Peptidomimetic	

	(c) Placebo	
	(d) Gazebo	
1.5.f	What is meant by ADME in pharmacokinetics?	1
	(a) Affinity, dosage, marketing, efficacy	
	(b) Absorption, distribution, metabolism, excretion	
	(c) Agonism, dependence, mobility, efficiency	
	(d) Antagonism, deficiency, mean, efflux	
1.5.g	What do you meant by molecular docking?	1
	(a) The process by which two different structures are compared by me	olecular modelling
	(b) The process by which a lead compound is simplified by removing groups	ving excess functional
	(c) The process by which drugs are fitted into their target binding modelling.	sites using molecular
	(d) The process by which a pharmacophore is identified	
	SECTION B	$10 \times 3 = 30$
2. Answe	er any <u>TEN</u> of the following:-	
2.1.a	How patent is different from trade secret?	2
2.1.b	What are model organism databases? Name any two. (CO1)	2
2.2.a	What are the various methods of sequence alignment?	2
2.2.b	What are the various types of BLAST programs?	2
2.2.c	Write a short note on Ensembl-Biomart?	2
2.3.a	What do you understand by Dendrograms?	2
2.3.b	Name the different types of geneome sequence technologies?	2
2.3.c	What is importance of Bootstrap algorithm?	2
2.4.a	What are the various types of Biomarkers?	2
2.4.b	What are the various applications of CRISPR? (CO4)	2
2.5.a	Explain classification and regression in terms of machine learning? (CO5)	2
2.5.b	What are Support Vector Machines?	2