TO A THE REPORT OF
--

National Institute of Technology Meghalaya

An Institute of National Importance

CURRICULUM

	COP TECHNIN																		
Programme		me	Bachelor of Technology in Computer Science and Engineering										Academic Year of Regulation				2018-19		
Departmer		ent Computer Science and Engineering									Semester			ster	VIII				
Co	urse	Course Name									Credit	Structure	tructure			Marks Distribution			
Code										L	Т	Р	C	INT	MID	END)	Total	
CS 426		Bioinformatics								3	0	0	3	50	50	100		200	
		This course introduces the importance of bioinformatics and analysis of biological databases									CO1	Able to discover different problems prevailing in bioinformatic domain						ormatics	
Course Objectives		This course explains the different types of bioinformatics techniques This course introduces the different bioinformatics and machine learning techniques to different application domains									CO2	Able to assess different bioinformatics techniques Able to design computational framework for solving problem related to biological data analysis							
											CO3						oblems		
		Iteration domains Outcomes Iterated to biological data and											<u>y 313</u>						
	COs	Mapping with Program Outcomes (POs)														pping v	with PSOs		
No.		PO	1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PS	02	PSO3	
1	CO1	1		1	-	-	-	-	-	-	-	-	-	-	1	1		-	
2	CO2	1		2	-	-	-	-	-	-	-	-	-	-	1	1		-	
3	CO3	1		2	2	-	2	-	-	-	-	-	-	-	2	2	2	-	
									SYLLA	BUS									
No.								Content							Hours		C	Cos	
	Introduction, Disinformatical goals, soons, applications and limitations. Designall exclusions. The structure																		
	content and scale of deoxyribonucleic acid (DNA), Genes and proteins, Central dogma, Importance of proteins.										06		CO1						
	Gene and cell regulation, Biological Databases, Information Retrieval from Biological Databases												00						
	Seque	Sequence Alignment: Pair-wise sequence alignment, Sequence homology versus sequence similarity,																	
	seque	ence sin ence alic	nilari Inme	ity versu ent	s sequen	ice identii	iy, Metho	ds for se	quence	alignment	Statistic	al signific	cance of				CO 1	I, CO2	
					_		_					_	_		08				
	Multiple Sequence Alignment : Scoring function, Exhaustive algorithms, Heuristic algorithms, practical Issues													les					
Database similarity searching : Basic Local Alignment Search Tool (BLAST), FASTA, Comparison of FASTA and																			
	BLAST																C	;02	
	Protei	Protein motifs and domain prediction :Identification of motifs and domains in multiple sequence alignment, Mot																	
Ш	and domain databases using regular expressions, Motif and Domain Databases Using statistical models														14				
	Gene	Gene Prediction : Gene prediction in prokaryotes and in eukaryotes																	
	Phylo	genetic	s : T	erminol	ogy, Gen	e phyloge	eny versu	is species	s phylog	geny, Phyl	ogenetic	tree cons	truction,						
	Distance – based methods, Character- based methods, Phylogenetic tree evaluation																		
11/	F																		
	DNA r	nonal Ge microarr	enon ays	nics : 50	quence-b	asea app	noacnes,	wiicroarr	ay-pase	eu approac	nes, con	iparison	UT SAGE	and	~~~		CO2	& CO3	
IV															08			-	
	Case	studies	tor n	nachine	learning	technique	es based	analysis	ot biolo	gical data	sets								
	Total Hours													36	36				
Esse	ential R	eadings																	
1	. J. Xio	ong. "Es	senti	al bioinfo	rmatics".	Cambrida	e Univers	ity Press.	1st edition	on, 2006.									

 E. Keedwell, and A. Narayanan. "Intelligent bioinformatics: The application of artificial intelligence techniques to bioinformatics problems". John Wiley & Sons, 1st edition, 2005

3. J.M. Claverie, and C. Notredame. "Bioinformatics for dummies". John Wiley & Sons, 2nd edition, 2007

Supplementary Readings

- 1. S. Mitra, S. Datta, T. Perkins, and G. Michailidis. "Introduction to machine learning and bioinformatics". CRC Press, 1st edition, 2008.
- 2. Z.R. Yang. "Machine learning approaches to bioinformatics". World scientific, 1st edition, 2010

3. Y.Q. Zhang, and J.C. Rajapakse. "Machine learning in bioinformatics", Wiley, 1st edition, 2009