SRI VENKATESWARA COLLEGE OF ENGINEERING

COURSE DELIVERY PLAN - THEORY   Page 1 of 6

Department of Biotechnology	LP: BT18703
	Rev. No: 00
B.E/B.Tech/M.E/M.Tech : B.Tech (Biotechnology) Regulation: 2018	Date: 04.07.23
PG Specialisation : -	
Sub. Code / Sub. Name : BT18703 – Bioinformatics and Computational Biology	
Unit : I	

Unit Syllabus: 12 hrs

Introduction to Operating systems, Linux commands, File transfer protocols ftp and telnet, Introduction to Bioinformatics and Computational Biology, Biological sequences, Biological databases, Genome specific databases, Data file formats, Data life cycle, Database management system models, Basics of Structured Query Language (SQL).

Objective: The course aims to gain detailed knowledge in operating systems and biological databases

Session No *	Topics to be covered	Ref	Teaching Aids
1	Introduction to Operating Systems, Features of UNIX, Linux commands	TB – 5 (87-113)	BB/LCD
2	File transfer protocols ftp and telnet	TB – 5 (114-117)	BB/LCD
3	Introduction to Bioinformatics and Computational Biology, Biological sequences	RB – 4 (148-151)	BB/LCD
4	Biological databases	RB – 4 (109-113)	BB/LCD
5	Biological databases	TB -3 (45-46)	BB/LCD
6	Genome specific databases - I	TB -1(80-100)	BB/LCD
7	Genome specific databases - II	TB – 1 (80-100) TB – 1 (124)	BB/LCD
8	Data file formats, Data life cycle	TB -3 (49-75)	BB/LCD
9	Database management system models-I	TB – 5 (350-360)	BB/LCD
10	Database management system models - II	TB – 5 (350-360)	BB/LCD
11	Basics of Structured Query Language - I	TB – 5 (361-370)	BB/LCD
12	Basics of Structured Query Language - II	RB – 4 (114-123)	BB/LCD

Content beyond syllabus covered (if any): -Features of UNIX

* Session duration: 50 minutes

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Sub. Code / Sub. Name: BT18703 – Bioinformatics and Computational Biology	
Unit : II	

Unit Syllabus :   12 hrs

Sequence Analysis, Pairwise alignment, Dynamic programming algorithms for computing edit distance, string similarity, shotgun DNA sequencing, end space free alignment. Multiple sequence alignment, Algorithms for Multiple sequence alignment, Generating motifs and profiles, Local and Global alignment, Needleman and Wunsch algorithm, Smith Waterman algorithm, BLAST, PSIBLAST and PHIBLAST algorithms.

Objective: This course aims to explore knowledge in sequence analysis and its algorithms

Session No *	Topics to be covered	Ref	Teaching Aids
1	Sequence analysis, Pairwise alignment, FASTA algorithm	TB - 1(157-185) RB – 2 (80-81)	BB/LCD
2	FASTA algorithm	TB – 2 (121-162) TB -3 (51-91)	BB/LCD
3	Dynamic programming algorithms for computing edit distance, string similarity	TB - 1(176-181)	BB/LCD
4	Shotgun DNA sequencing, end space free alignment	RB – 4 (293-298)	BB/LCD
5	Multiple sequence alignment	TB -3 (327 – 329) TB – 1(186-197)	BB/LCD
6	Algorithms for multiple sequence alignment - I	TB -3 (327 – 329) TB- 1 (186-197)	BB/LCD
7	Algorithms for multiple sequence alignment - II	TB – 2 (163-226) RB – 3 (134-159)	BB/LCD
8	Generating motifs and profiles, Local and Global alignment	TB – 5 (205-214) TB -3 (308)	BB/LCD
9	Needleman and Wunsch algorithm	TB – 2 (9-13)	BB/LCD
10	Smith Waterman algorithm	TB - 2 (9-13)	BB/LCD
11	BLAST, PSI-BLAST and PHI-BLAST algorithms - I	RB – 1 (59-82)	BB/LCD
12	BLAST, PSI-BLAST and PHI-BLAST algorithms- II	RB – 4 (179- 189)	BB/LCD
Content beyond syllabus covered (if any): FASTA algorithm			

* Session duration: 50 mins

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COURSE DELIVERY PLAN - THEORY

Sub. Code / Sub. Name: BT18703 – Bioinformatics and Computational Biology

Unit : III

Unit Syllabus :   11 hrs

Introduction to phylogenetics, Distance based trees UPGMA trees, Molecular clock theory, Ultrametric trees, Parsimonious trees, Neighbour joining trees, trees based on morphological traits, Bootstrapping. Protein Secondary structure and tertiary structure prediction methods, Homology modeling, *abinitio* approaches, Threading, Critical Assessment of Structure Prediction, Structural genomics.

Objective: This course provides information on phylogenetics and protein structure prediction

Session No *	Topics to be covered	Ref	Teaching Aids
1	Introduction to phylogenetics, Distance based trees	TB - 2 (286 – 294)	BB/LCD
2	Introduction to phylogenetics, Distance based trees	TB – 1 (198-208)	BB/LCD
3	UPGMA trees	TB - 2 (306 – 309)	BB/LCD
4	Molecular clock theory, Ultrametric trees	TB - 2 (256 – 263)	BB/LCD
5	Parsimonious trees, Neighbour joining trees, trees based on morphological traits, Bootstrapping	TB - 2 (296 – 301)	BB/LCD
6	Parsimonious trees, Neighbour joining trees, trees based on morphological traits, Bootstrapping	RB – 3 (173-180)	BB/LCD
7	Protein secondary structure and tertiary structure prediction methods	TB - 2 (427 – 484)	BB/LCD
8	Homology modeling, *abinitio* approaches, Threading	TB- 1 (250-255)	BB/LCD
9	Homology modeling, *abinitio* approaches, Threading	TB – 3 (317 – 354)	BB/LCD
10	Critical Assessment of Structure Prediction, Structural genomics	TB – 1 (240-249) TB - 2 (511 – 519)	BB/LCD
11	Critical Assessment of Structure Prediction, Structural genomics	RB – 1 (123-164)	BB/LCD
Content beyond syllabus covered (if any): -NIL-			

* Session duration: 50 mins

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COURSE DELIVERY PLAN - THEORY

Sub. Code / Sub. Name: BT18703 – Bioinformatics and Computational Biology

Unit : IV

Unit Syllabus :   14 hrs

Machine learning techniques: Artificial Neural Networks in protein secondary structure prediction, Hidden Markov Models for gene finding, Decision trees, Support Vector Machines. Introduction to Systems Biology and Synthetic Biology, Microarray analysis, DNA computing, Bioinformatics approaches for drug discovery, Applications of informatics techniques in genomics and proteomics: Assembling the genome, STS content mapping for clone contigs, Functional annotation, Peptide mass fingerprinting.

Objective: This course helps to gain knowledge in machine learning techniques, systems biology, genomics and proteomics

Session No *	Topics to be covered	Ref	Teaching Aids
1	Machine learning techniques: Neural Networks in protein secondary structure prediction	TB – 3 (283 – 284)	BB/LCD
2	Machine learning techniques: Neural Networks in protein secondary structure prediction	RB – 3 (99-164)	BB/LCD
3	Hidden Markov Models for gene finding	RB – 4 (289 – 290) RB – 2 (46-79)	BB/LCD
4	Hidden Markov Models for gene finding	RB – 3 (165-224) TB - 3 (209-224) RB – 4 (229- 232)	BB/LCD
5	Decision trees, Support Vector Machines	TB – 3 (285-288)	BB/LCD
6	Introduction to Systems Biology and Synthetic Biology	RB – 4 (332 – 340)	BB/LCD
7	Microarray analysis-I	TB – 3 (222 – 231), RB – 4 (301 – 308)	BB/LCD
8	Microarray analysis-II	TB – 3 (254 – 258) RB – 3 (299-322)	BB/LCD
9	DNA computing	RB – 4 (340 – 343)	BB/LCD
10	Bioinformatics approaches for drug discovery	RB – 4 (340 – 343)	BB/LCD
11	Applications of informatics techniques in genomics and proteomics	TB - 2 (511 – 519)	BB/LCD
12	Assembling the genome, STS content mapping for clone contigs	RB – 4 (293-301)	BB/LCD
13	Functional annotation	RB – 4 (320-331)	BB/LCD
14	Peptide mass fingerprinting	RB – 4 (312-319)	BB/LCD
Content beyond syllabus covered (if any): -NIL-			

* Session duration: 50 mins

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Sub. Code / Sub. Name: BT18703 – Bioinformatics and Computational Biology

Unit : V

Unit Syllabus :   11 hrs

Basics of PERL programming for Bioinformatics: Datatypes: scalars and collections, operators, Program control flow constructs, Library Functions: String specific functions, User defined functions, File handling.

Objective: This course provides knowledge in development of programming skills in PERL

Session No *	Topics to be covered	Ref	Teaching Aids
1	Basics of PERL programming for Bioinformatics - I	TB -4 (20-41)	BB/LCD
2	Basics of PERL programming for Bioinformatics - II	RB – 4 (74-85)	BB/LCD
3	Datatypes: scalars and collections - I	TB – 4 (49-54)	BB/LCD
4	Datatypes: scalars and collections - II	RB - 4 (86-90)	BB/LCD
5	Operators	TB – 4 (361 – 372)	BB/LCD
6	Program control flow constructs	TB – 4 (72 – 98)	BB/LCD
7	Library Functions: String specific functions	TB – 4 (42 – 71)	BB/LCD
8	User defined functions	TB – 4 (104-123)	BB/LCD
9	File handling - I	TB – 4 (99 – 103)	BB/LCD
10	File handling - II	RB – 4 (86-90)	BB/LCD
11	Comparison of C programming with PERL programming	RB – 4 (86-90)	BB/LCD
Content beyond syllabus covered (if any): Comparison of C programming with PERL programming.			

* Session duration: 50 mins
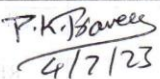
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REFERENCES:

TEXT BOOK (TB):

1. Lesk, A. K., "Introduction to Bioinformatics" 2nd Edition, Oxford University Press, 2005
2. Mount, D.W., "Bioinformatics Sequence and Genome Analysis" 2nd Edition, Cold Spring Harbor Laboratory Press, 2004
3. B.Bergeron, Bioinformatics Computing, PHI, 2002
4. Tisdall, J., "Beginning Perl for Bioinformatics: An introduction to Perl for Biologists" 1st Edition, O'Reilly Media, 2001
5. Cynthia Gibas, Per Jambeck, Developing Bioinformatics Skills, O'Reilly, 2005.

REFERENCE BOOK (RB):

1. Westhead D.R, Parish J.H, Twyman R.M, Instant notes in Bioinformatics, 1st Edition, BIOS Scientific Publishers, 2000.
2. Durbin, R., Eddy, S., Krogh, A., and Mitchison, G., "Biological Sequence Analysis Probabilistic Models of proteins and nucleic acids" Cambridge, UK: Cambridge University Press, 1998.
3. Baldi, P. and Brunak, S., "Bioinformatics: The Machine Learning Approach" 2nd Edition, MIT Press, 2001.
4. S.C. Rastogi, Namita Mendirtatta, Parag Rastogi, Bioinformatics Concepts, Skills & Applications, CBS, 2011.

	Prepared by	Approved by
Signature	*P.K.Bavees 4/7/23*	*(signature) 4/7/23*
Name	Dr. P.K.PRAVEEN KUMAR	Dr. E. NAKKEERAN
Designation	PROFESSOR	PROFESSOR & HOD
Date	04.07.2023	04.07.2023
Remarks *: The same lesson plan will be followed in subsequent semester.		
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