Course No : **ICT- 231** Course Title : **Information & Communication Technology**
Credits : **3(2+1)** Semester : **III**

Theory

UNIT I

IT and its importance; IT tools; IT-enabled services and their impact on society; Computer fundamentals; Hardware and software; Input and output devices; Word and character representation.

UNIT II

Features of machine language, assembly language, high-level language and their advantages and disadvantages; Principles of programming - algorithms and flowcharts.

UNIT III

Operating systems (OS) - definition, basic concepts; Introduction to WINDOWS and LINUX Operating Systems; Local area network (LAN); Wide area network (WAN); Internet and World Wide Web; HTML and IP.

UNIT IV

Introduction to MS Office - Word, Excel, Power Point; Audio visual aids - definition, advantages, classification and choice of A.V. aids; Criteria for selection and evaluation of A.V aids; Video conferencing; Communication process, Berlo's model, feedback and barriers to communication.

Practical

Exercises on binary number system; Algorithm and flow chart; MS Word; MS Excel; MS Power Point; Internet applications: web browsing, creation and operation of email account; Analysis of data using MS Excel; Handling of audio visual equipments; Planning, preparation, presentation of posters, charts, overhead transparencies and slides; Organization of an audio visual programme.

Course No	: **BT-247**	Course Title	: **Introductory Bioinformatics**
Credits	: **3(2+1)**	Semester	: **IV**

Theory

UNIT I

Introduction to bioinformatics; Development and scope of bioinformatics; Applications of computers in bioinformatics: Operating systems, hardware, software, Internet, www resources, FTP.

UNIT II

Primary databases: Nucleotide sequence databases (GenBank, EMBL), protein sequence databases; Secondary databases: SwissProt/TrEMBL, conserved domain database, Pfam;

Structure databases: Protein Data Bank (PDB), MMDB, SCOP, CATH; File formats: Genbank, EMBL, Fasta, PDB, Flat file, ASN.1, XML.

UNIT III

Introduction to sequence alignment and its applications: Pair wise and multiple sequence alignment, concept of local and global alignment; Algorithms: Dot Matrix method, dynamic programming methods (Needleman–Wunsch and Smith–Waterman); Tools of MSA: ClustalW, TCoffee; Phylogeny; Introduction to BLAST and FASTA.

Practical

Basic computing: Introduction to UNIX, LINUX; Nucleotide information resource: EMBL, GenBank, DDBJ, Unigene; Protein information resource: SwissProt, TrEMBL, Uniprot; Structure databases: PDB, MMDB; Search Engines: Entrez, ARSA, SRS; Similarity Searching: BLAST and interpreting results; Multiple sequence alignment: ClustalW; Structure visualization of DNA and proteins using Rasmol.

Course   : **BT-3617**   Course Title   : **Computational Biology**
Credits   : **3(2+1)**   Semester   : **VI**
Theory

UNIT I

Introduction to computational biology; Web based servers and software for genome analysis: Ensembl, UCSC genome browser, MUMMER, BLASTZ; Sequence submission.

UNIT II

Protein interaction databases: BIND, DIP, GRID, STRING, PRIDE; Principles of Protein structure prediction; Fold Recognition (threading); Homology modeling; SCOP, CATH, PDB, PROSITE, PFAM; Methods for comparison of 3D structures of proteins.

UNIT III

Phylogenetic analysis: Evolutionary models, tree construction methods, statistical evaluation of tree methods; PHYLIP, dendroscope, MEGA; DNA barcoding database-BOLD.

Practical

Application of Genome browsers in genomic research; Exploring protein-protein interaction databases; Working with protein structural classification databases; SNP and SSR identification tools; PHYLIP.

Course No   : **BITEL-461** Course Title   : **Programming for Bioinformatics**
Credit   : 4(**2+2**)   Semester   : **VI**

Theory

UNIT I

Introduction: Operating systems, programming concepts, algorithms, flow chart, programming languages, compiler and interpreter; Computer number format: Decimal, Binary, Octal and Hexadecimal.

UNIT II

C-Language: History, constant, variables and identifiers, character set, logical and relational operators, data input and output concepts; Decision making: if statement, if-else   statement, for loop, while loop and do-while loop; Arrays and functions, file handling;   Programs related to arithmetic operations, arrays and file handling in C.

Practical

UNIT I

PERL-Language: Introduction, variables, arrays, string, hash, subroutines, file handling,   conditional blocks, loops string operators and manipulators, pattern matching and regular expressions   in   PERL;   Sequence   handling   in   PERL demonstrating string, array and hash.

UNIT II

Shell Programming: Concepts and types of UNIX shell, Linux variables, if statements, control and iteration, arithmetic operations, concepts of awk, grep and sed; Sequence manipulations using shell scripting.

Text Books:
1. Balagurusamy. 2008. *Programming in ANSI C*. Tata McGraw-Hill Education.
2. James Tisdall. 2003. *Mastering Perl for Bioinformatics*. O'Reilly Media.
3. Tom Christiansen, Brian D Foy, Larry Wall & Jon Orwant. 2012. *Programming Perl.*4thEd. O'Reilly Media.
4. KanetkarYashavant. 2013. *Let Us C*. BPB Publications.

Course No   : **BITEL-462**   Course Title: **Bioinformatics Tools and Biological Databases**
Credit   : **3(2+1)**   Semester   : **VI**
Theory

UNIT I

Introduction: Biological data types, collection, classification schema of biological databases; Biological databases retrieval systems; Sequence and molecular file formats.

UNIT II

Biological databases: Nucleotide database, protein database, structural database, genome databases, metabolic pathway database, literature database, chemical database, gene expression database, crop database with special reference to BTISNET databases.

UNIT III

Bioinformatics Tools: Concept of alignment, scoring matrices, alignment algorithms, heuristic methods, multiple sequence alignment, phylogenetic analysis, molecular visualization tools.

Practical

NCBI; Expasy: SwissProt; EBI; Search engines: ENTREZ and SRS; Perform local alignment using all BLAST variants; Multilple sequence alignment using ClustalW; T Coffee; phylogenetic analysis by PHYLIP; MEGA.

Text Books:
1. Baxevanis AD. & Ouellette BFF. 2001. *Bioinformatics: A practical guide to the analysis of genes and proteins.*John Wiley and Sons.
2. Mount DW. 2001. *Bioinformatics: Sequence and Genome Analysis*. Cold Spring Harbor.
3. Xiong J. 2006. *Essential Bioinformatics.*Cambridge University Pres

Course No   : **BITEL-463**   Course Title   : **Structural Bioinformatics**
Credit   : **3(2+1)**   Semester   **: VI**
Theory

UNIT I

Introduction to structural databases of macromolecules, natural and synthetic small molecules; Structure of amino acids; Protein structure classification, Ramachandran plot; Experimental structure determination methods; Motifs, domain, profiles, fingerprint and protein family databases.

UNIT II

Structural features of RNA, RNA secondary structure predictions; RNA folding; Small RNA prediction.

UNIT III

Structure prediction: Basics of protein folding, protein folding problem, molecular chaperons; Secondary structure prediction methods and algorithms: Homology, *ab initio* and folding based tertiary structure prediction; Structure validation tools, energy minimization techniques; Introduction to molecular dynamics and simulation, Monte-Carlo methods, Markov chain and HMM; Structure visualization and comparison methods.

Practical

Protein structural classification databases, 3D-Structural databases searching and retrieval, Ramchandran Plot, Structural visualization tools, Tools for protein secondary and tertiary structure prediction; RASMOL, Cn3D, CHIMERA, SWISSPDBviewer, CPH, MODELLER, SWISS Model, EasyModeler, Procheck; GROMAC; SANJIVNI; BHAGIRATH.

Text Books:
1. A.Malcolm Campbell & Laurie J.Heyer. 2007. *Discovering Genomics, Proteomics and Bioinformatics*. Benjamin Cummings.
2. Allan Hinchkliffe. 2008. *Modeling for Beginners*. Wiley.
3. Creighton TE. 1993. *Proteins: Structures and Molecular Properties*. W.H. Freeman
4. Mount DW. 2001. *Bioinformatics: Sequence and Genome Analysis*. Cold Spring Harbor.

Reference Book:
1. Setubal Joao &Meidanis Joao. 1997. *Introduction to Computational Molecular Biology*.PWS Publishing Company