NANOBIOTECHNOLOGY (SOFT CORE COURSE) Hours: 40

Course outcomes:

After successful completion of the course, students will be able to:

CO 1. Compare the types and properties of different nanostructures
CO 2. Understand structure and use of nanoparticles
CO 3. Demonstrate the synthesis of nanoparticles.
CO 4. Apply nanotechnology in different fields of science.

Unit I (13 hrs)

Principles of nanotechnology - Nanostructures, nanoparticles and their properties. Carbon Nano Structures: Introduction; Carbon buckyballs, fullerenes, nanostructures; quantum dots, nanotubes, magnetic nanoparticles, noble metal nanoparticles. Nanoscale properties and applications.

Unit II (13hrs)

Characterization of nanomaterials: UV-Vis Spectroscopy, Scanning Electron Microscopy, Transmission Electron Microscopy, Atomic Force Microscopy. Making nanostructures: Top-down and bottom-up approaches. Biological methods of synthesis of nanoparticles: Use of bacteria, fungi, Actinomycetes, Magnetotactic bacteria and plants.

Unit III (14hrs)

Applications in diverse fields: medicine, dentistry, environment, agriculture etc. Toxic effects of nanoparticles on the environment. Toxicity detection. Nanocomposite biomaterials; teeth and bone substitution, Food packaging - materials and properties. Applications of nanoparticle-based products inhealth-care and hygiene. Hybrid systems: Bioelectronic systems based on nanoparticle-enzyme hybrids; nanoparticle-based bioelectronics biorecognition events. DNA-based nanomechanical devices. Biosensors and biochips. Pharmaceutically important nanomaterials, drug nanoparticles, nanoparticles for crossing biological membranes. Fundamentals of nanosized targeted drug delivery systems.

References

1. Nanostructures and nanomaterials: Synthesis, properties and applications, Cao, G and Wang Y. 2011, World Scientific, Imperial College Press
2. Plenty of Room for Biology at the Bottom, An introduction to Bionanotechnology: Ehud Gazit, Imperial College Press,
3. Nanotechnology Booker R and Boysen E., Wiley Dreamtech Publ. New Delhi
4. Nanotechnology: A gentle introduction to the next big idea. Ratner M and Tatner D. Pearson Edition New Delhi

RESEARCH METHOLOGY AND BIOINFORMATICS (SOFT CORE COURSE) Hours: 40

Course outcome

After successful completion of the course, students will be able to:

CO 1. Acquire knowledge about basic concepts of research, scientific writing and paper publications
CO 2. Use statistical measures such as dispersion, normal, binominal and poisson distribution, student's t-test, ANOVA, chi-square test etc.
CO 3. Use databases, sequence alignment programs, BLAST and FASTA along with algorithms and applications.

CO 4. Construct a phylogenetic tree and carry out protein structure analysis, protein prediction tools

CO 5. Perform Computer Aided Drug Design (CADD) and apply it to design new drugs.

UNIT I (13 hrs)

Empirical science, scientific method, literature review, research gaps, questions, objectives, design, lab notebook. Search engines. Sampling - Experiments and controls. Data collection, quantitative and qualitative analysis. Determining outcomes and results. Ethics in research, scientific misconduct. Plagiarism. Technical writing skills, scientific papers. Referencing. Statistics – Definition, application of statistics in Biosciences, Classification and tabulation, Graphical representation of data, Histogram, frequency polygon, frequency curve. Measures of central tendency, Measures of dispersion. Normal distribution, Binomial, Poisson, Probability, non-parametric statistics, Correlation and regression; Sign test, Rank sum test, Rank correlation. Testing of hypothesis: Significance of t-test and ANOVA, Multiple range test, Chi-square test. Experimental designs. Diversity measures and evenness (e.g. Simpson and Shannon-Wiener). Statistical packages.

UNIT II (13 hrs)

Introduction to Bioinformatics. Basics of UNIX OS and PERL Programming. Biological databases: Nucleotide and protein sequence and structure (primary and secondary) databases, File formats, Molecular visualization softwares. Sequence analysis. Sequence Alignment: Gap penalties, scoring matrices, Alignment algorithms - Global and Local alignments, Dynamic programming and Heuristic methods (BLAST, FASTA). Multiple Sequence Alignment: Tree alignment, Star alignment, Progressive alignment methods and tools. Stand alone packages for sequence alignment: GCG Wisconsin and EMBOSS package.

UNIT III (14hrs)

Phylogenetics. Representation of phylogeny. Methods of phylogeny: Maximum Parsimony, Maximum Likelihood, Distance method, UPGMA. Softwares for phylogenetic analysis: PHYLIP, CLUSTAL, Tree viewing and editing softwares. Nucleotide sequence and structure prediction methods and tools: Promoter Scan, Gen Scan, CENSOR, Repeat Masker. Whole genome analysis. Genome sequencing strategies, Restriction mapping, Primer designing. Gene Expression analysis - microarray techniques. Protein sequence and structure prediction, Molecular modeling softwares and servers, Protein folding, Threading. Computer-aided Drug Designing: Molecular Docking. Distributed computing approach: Genome@home, Folding@home.

References

1. Research Methodology Methods and Techniques. Kothari, C.R., New Age Publishers, New Delhi 2004
2. Beginning Perl for Bioinformatics. Tisdall, J.D., San Val Pub., 2001
3. Bioinformatics: Sequence and Genome Analysis. Mount, D.W., CSHL Press, 2004
4. Bioinformatics: Methods and protocols. Misener, S., &Krawetz,S. A., Humana Press, 2000
5. Fundamental Concepts of Bioinformatics. Krane, D.E.& Raymer, M.L., Pearson Ed., 2002
6. Introduction to Protein Structure. Branden,C.-I. & Tooze,J., Garland Pub., 1999
7. Introduction to Bioinformatics. Attwood, T.& Parry-Smith, D., Prentice Hall Pub., 1999
8. Introductory Statistics for Biology. Parker, R.E., Hodder Arnold Pub., 1979
9. Statistics for Biological Sciences. Schefler,W. C., Addison Wesley Pub., 1979
10. Biostatistical Analysis. Zar, J. H. Prentice Hall, 2010
11. Biostatistics. Lewis,A. E.. Prentice Hall, 2010