Morigaon College (Autonomous)
Morigaon: Assam

SYLLABUS

Zoology

(MA 1st Semester)

Evolution, Chronobiology and Bioinformatics

Course Code: ZLG-PG-MCA-1014 (Total Marks: 80+20=100)

4 Credits

Course Description

This course provides an integrated understanding of evolutionary biology, chronobiology, and bioinformatics, emphasizing the mechanisms that drive biological diversity and adaptation. The course explores the origin and evolution of life, molecular evolution, genetic variation, and speciation processes. It introduces the principles of biological timing systems, circadian rhythms, their molecular basis, and applications in human health and medicine. The bioinformatics component focuses on sequence analysis, molecular phylogeny, protein structure prediction, and computational approaches used to study evolutionary relationships and biological systems. The course equips students with theoretical knowledge and analytical skills necessary for modern biological research.

Course Objectives (COB)

1. To understand the origin of life and the fundamental mechanisms driving biological evolution, including mutation, genetic drift, natural selection, and speciation.
2. To explain the principles of molecular evolution and the application of molecular tools in phylogenetic analysis and classification.
3. To understand the organization, regulation, and significance of biological clocks and biological rhythms in living organisms.
4. To examine the molecular basis and physiological applications of circadian rhythms in health, behavior, and medicine.
5. To develop knowledge of bioinformatics tools and techniques for sequence analysis, phylogenetic tree construction, and protein structure prediction.

Course Outcomes (CO)

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

1. Explain major evolutionary theories and analyze the roles of genetic variation, mutation, genetic drift, and isolation mechanisms in evolution and speciation.
2. Interpret concepts of molecular evolution, molecular clocks, gene duplication, and phylogenetic relationships using molecular data.
3. Describe the mechanisms and significance of biological clocks and various biological rhythms in organisms.
4. Evaluate the molecular basis and practical applications of circadian rhythms in human health, chronotherapy, and chronopharmacology.
5. Apply bioinformatics approaches for sequence alignment, phylogenetic analysis, and prediction of protein secondary and tertiary structures.

Course Content:

1. Origin of life: Modern theories, Changes in hereditary instructions in relation to evolution.
2. Notion of selectively neutral mutations, evolutionary gene duplication, the founder principle, bottleneck effect of genetic drift.
3. Factors and forces of evolution: Mutation, Genetic variation, Isolation mechanisms and their role in speciation.
4. Emergence of the theory of Neo-Darwinism.
5. Molecular evolution : Concept of neutral evolution (Kimura), molecular divergence and molecular clock, molecular tools in phylogeny, classification and identification, Origin of new genes and proteins, gene duplication and divergence
6. Biological clocks, Significance of Biological time keeping
7. Biological rhythms: Types of rhythms- Circadian, Circatidal, Circalunar, Circannual; Centres of biological rhythms – Suprachiasmatic nuclei, Pinealgland, Opticlobes; Factors influencing biological rhythms- Environmental, Photoperiod, Temperature, Other Zeitgebers.
8. Molecular basis of circadian rhythms: Clock genes: Drosophila and Mouse.
9. Applied Chronobiology: Human circadian rhythms, Application of circadian rhythms and principles; Jet-lag/shift work; Depression and sleep disorders; Chronopharmacology and Chronotherapy.
10. Theoretical aspects of sequence analysis. Needleman-Wunsch and Smith-Waterman methods of global and local alignments for a pair of sequences.
11. Molecular phylogeny and evolution: Properties and types of phylogenic trees; Tree building methods- Distance based: UPGMA (Unweighted pair group method using arithmetic mean), Neighbor-joining, minimum evolution and least square methods; Character-based: Maximum parsimony, maximum likehood.
12. Levels of protein structures and visualization: Protein secondary and tertiary structures prediction methods (Description of machine learning methods for secondary structures, homology/comparative modeling, fold recognition or threading and ab infitio methodsfor tertiary structure prediction)

Referred Books:-

1. **Nelson, R. J., & Kriegsfeld, L. J. (2023).** *An Introduction to Behavioral Endocrinology* (6th Edition). Oxford University Press.
2. **Binkley, S. A. (1990).** *The Clockwork Sparrow: Time, Clocks, and Calendars in Biological Organisms*. Prentice Hall.
   (No newer edition appears to be available; the 1990 edition remains the standard reference.)
3. **Chandrashekaran, M. K. (1985).** *Biological Rhythms*. Madras Science Foundation, Chennai.
   (No revised or later edition is currently available and the original edition continues to be cited.)
4. **Mount, D. W. (2004).** *Bioinformatics: Sequence and Genome Analysis* (2nd Edition). Cold Spring Harbor Laboratory Press.
   (The 2nd edition remains the latest published edition.)

5. **Pevsner, J. (2015).** *Bioinformatics and Functional Genomics* (3rd Edition). Wiley-Blackwell.

Genetics, Cytogenetics and Instrumentation

Course Code: ZLG-PG-MCA-1024 (Total Marks: 80+20=100)

4 Credits

Course Description

This course provides a comprehensive understanding of chromosome organization, chromatin structure, mitochondrial genetics, bacteriophage biology, and the genetic basis of cancer. It introduces fundamental concepts of gene mapping, sex determination, and dosage compensation mechanisms in different organisms. The course also emphasizes modern cytogenetic, molecular, and biochemical techniques, including microscopy, chromatography, electrophoresis, blotting methods, autoradiography, ELISA, chromosome banding, and fluorescence in situ hybridization (FISH). Students will gain theoretical knowledge of chromosome biology and practical applications of molecular and cellular techniques used in genetics, biotechnology, biomedical research, and disease diagnosis.

Course Objectives

1. To understand the structure, organization, and functional significance of eukaryotic chromosomes, chromatin, and mitochondrial DNA.
2. To explain the genetic and chromosomal basis of cancer, including the roles of oncogenes, tumor suppressor genes, and chromosomal abnormalities.
3. To develop an understanding of gene mapping techniques, sex determination systems, and dosage compensation mechanisms in different organisms.
4. To familiarize students with advanced microscopy, immunological assays, and molecular separation techniques used in biological research.
5. To understand the principles and applications of cytogenetic and molecular techniques such as electrophoresis, blotting methods, chromosome banding, and FISH.

Course Outcomes

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

1. Describe the organization of chromatin, chromosome structure, mitochondrial DNA, and bacteriophage morphology and relate them to cellular functions.
2. Analyze chromosomal abnormalities and explain the genetic mechanisms underlying cancer development, including the roles of oncogenes and tumor suppressor genes.
3. Apply principles of gene mapping, linkage analysis, sex determination, and dosage compensation in genetic studies.

4. Explain the principles, applications, and limitations of modern microscopy, immunological techniques, and chromatographic methods used in biological investigations.
5. Interpret and evaluate molecular and cytogenetic data generated through electrophoresis, blotting techniques, chromosome banding, and FISH for research and diagnostic purposes.

Course Content:

1. Eukaryotic chromatin structure and chromosome organization: Classes of DNA Chromosomal proteins: histones and their modifications, non-histone proteins, scaffold/ matrix proteins, levels of chromatin condensation at interphase and metaphase stage.
2. Organization and functions of mitochondrial DNA
3. Bacteriophage: Type, structure and morphology
4. Chromosome anomalies and diseases: chromosomal anomalies in malignancy(chronic myeloid leukemia, Burkitt's lymphoma, retinoblastoma and Wilm's tumor)
5. Genetics and cancer: oncogenes-tumour inducing retroviruses and viral oncogenes, chromosome rearrangements and cancer, tumour suppressor genes, cellular roles of tumour suppressor genes, PRB, P 53, PAPC, genetic pathways to cancer.
6. Methodsofgenemapping:3 point test cross in Drosophila, gene mapping in human by Linkage analyses in pedigrees.
7. Sex determination and dosage compensation gap of X-linked genes, hyperactivation of X linked genes in Drosophila, Inactivation of X-linked gene in female mammals, Hypoactivation of X-linked genes in Caenorhabditis elegans.
8. Microscopy: Principles and applications of phase contrast, Fluorescence and confocal Microscopy.
9. Principles and application of autoradiography, radio immunoassay, Enzyme linked Immuno-absorbant assay (ELISA)
10. Molecular separation Techniques: Ion-Exchange, Absorption, partition, gel filtration, affinity chromatography, and HPLC.
11. Electrophoresis- Principle and applications, Agarose, SDS, SDS-PAGE, Pulsed gel and Disc electrophoresis, determination of molecular weight by SDS-gel electrophoresis
12. Southern, Northern and Western Blotting
13. Chromosome banding, FISH-chromosome painting technique

Referred Books:-

1. **Lodish, H., Berk, A., Kaiser, C. A., et al. (2021).** *Molecular Cell Biology* (9th Edition). W.H. Freeman.
2. **Alberts, B., Johnson, A., Lewis, J., et al. (2022).** *Molecular Biology of the Cell* (7th Edition). Garland Science.
3. **Brown, T. A. (2023).** *Genomes 5* (5th Edition). Garland Science.
4. **Snustad, D. P., Simmons, M. J., & Jenkins, J. B. (2024).** *Principles of Genetics* (9th Edition). Wiley.

Biochemistry and Biostatistics

Course Code: ZLG-PG-MCA-1034 (Total Marks: 80+20=100)

4 Credits

Course Description

This course provides a comprehensive understanding of the biochemical basis of life and the statistical tools essential for biological research. It covers energy metabolism, bioenergetics, enzyme kinetics, protein structure, and major metabolic pathways involving carbohydrates, lipids, and amino acids. The course also introduces fundamental concepts of biostatistics, including sampling techniques, measures of variation, probability distributions, correlation, regression, hypothesis testing, and analysis of variance. Students will develop the ability to interpret biochemical processes and apply statistical methods for the analysis and interpretation of biological data.

Course Objectives

1. To understand the principles of bioenergetics, ATP synthesis, oxidative phosphorylation, and the role of energy-rich compounds in cellular metabolism.
2. To explain the structural organization of proteins and the relationship between protein structure and function.
3. To understand enzyme kinetics, enzyme regulation, and major metabolic pathways of carbohydrates, lipids, and amino acids.
4. To develop knowledge of fundamental statistical concepts, sampling methods, probability distributions, and measures of variation used in biological research.
5. To apply statistical tools for data analysis, hypothesis testing, and interpretation of biological and experimental data.

Course Outcomes

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

1. Explain the mechanisms of cellular energy production, ATP generation, oxidative phosphorylation, and chemiosmotic coupling.
2. Describe the structural organization of proteins and evaluate the factors governing protein folding and stability.
3. Analyze enzyme kinetics and interpret the biochemical pathways involved in carbohydrate, lipid, and amino acid metabolism.
4. Apply appropriate statistical methods to summarize, analyze, and interpret biological data using measures of variation, probability distributions, and sampling techniques.
5. Perform and interpret statistical tests including correlation, regression, Chi-square test, t-test, ANOVA, Kruskal–Wallis test, and Mann–Whitney U test for biological research applications.

Course Content:

1. Energy rich compound, role of ATP/ADP cycle in transfer of high energy phosphate
2. Important respiratory complex of ATP synthesis and oxidative phosphorylation, chemiosmotic hypothesis
3. Secondary structure: α-helix, β-pleated sheet& bends, Prediction of secondary structure, Ramachandran plot
4. Tertiary structure: Forces stabilizing tertiary structure, Domains and motifs, Quaternary Structure of proteins.
5. Enzyme kinetics, lowering of activation energy, Derivation of Michaelis-Menten equation and determination of Km and Vmax using MM & LB plots, Concepts of regulation of enzyme activity.
6. Concept of metabolic pathways, Glycolysis and Gluconeogenesis, Glycogenesis and Glycogenolysis; Kreb cycle.
7. Hexose monophosphate shunt pathway and Its significance
8. β-oxidation of fats and synthesis of fatty acids.
9. Amino acid: Structure and chemistry of amino acid, Amino acid catabolism: Transamination, Transdeamination and oxidative deamination, Urea cycle.
10. Applications of Biostatistics, Sampling methods: Random sampling, Stratified sampling and Sub-sampling
11. Measurement of variations: Standard error, standard deviation and co-efficient of variation, Quartile and percentiles, probability and distribution, Binomial, poison and normal distributions.
12. Correlation and regression: Linear regression equation and line of best fit, Coefficient of correlation, Coefficient of regression
13. Chi-square test value of statistics, Confidence limit, t-test, Introduction to one way and two ways ANOVA and F-test.
14. Kruskal-Wallis test, Man-Whitney U test

Referred Books:-

1. Hall, J. E., & Hall, M. E. (2020). Guyton and Hall textbook of medical physiology
2. **Zar, J. H. (2021).** *Biostatistical Analysis* (6th Edition). Pearson.

Ecology, Environmental Biology, and Biosystematics

Course Code: ZLG-PG-MCA-1044 (Total Marks: 80+20=100): 4 Credits

1. Structure of ecosystem – Salient features of aquatic and terrestrial ecosystem and their biotic communities
2. Biotic community concept– organization, population density, relative abundance, frequency, dominance, carrying capacity, species richness and species diversity
3. Community development: Types of community changes, causes and examples of ecological succession, Climax community and stability
4. The Niche concept, ecological niche, niche overlap and separation
5. Population ecology- growth pattern, life tables & survivorship curve and density dependent & independent factors. Life history strategies: K-or r-selection, Age and sex ratio.
6. Trophic structure, food chain and food webs, energy flow and Lindeman's trophic dynamics concept, Food web pattern and measurement in ecosystem energy flowmodel, concept of productivity and measurement of primary productivity.
7. Environmental concerns–greenhouse effect, global warming and environmental pollution. Anthropogenic Impact on Environment.
8. Environmental Impact assessment. Environmental monitoring and documentation.
9. Concept of species: Species, Polytypic species, Importance of recognition of Polytypic species, taxa.
10. Infraspecific categories, subspecies, temporal sub species , race and cline
11. Speciation: Sympatric, Parapatric and allopatric speciation, Speciation in time, sibling species.
12. Taxonomic characters: Molecular, Behavioural, Ecological and geographical characters, weighing of characters, characters with low and high taxonomic weight.

Referred Books:-

1. Odum, E. P., & Barrett, G. W. (2006). Fundamentals of ecology.
2. Smith & Smith (2021). Elements of ecology.
3. Mayr, E. (2015). Principles of systematic zoology.

Systematics, Genetics, Biochemistry, and Bioinformatics

Course Code: ZLG-PG-MCA-1054 (PRACTICAL)

(Total Marks: 80+20=100): 4 Credits

1. Identification of invertebrates, larval forms of invertebrates, protista and vertebrates.
2. Determination of biodiversity indices: Shannon-Weiner Index, Similarity and Dissimilarity index and association index.
3. Calculation of Standard error, standard deviation, analysis of variation, Coefficient of variation, t-test, chi-square test and two way ANOVA.
4. Extraction of biomolecules (carbohydrates, proteins, lipids) from fish liver.
5. Estimation of protein extracted from fish liver by Biuret/Lowry/Bradford method.
6. Estimation of glycogen extracted from fish liver by Anthrone reagent method.
7. Estimation of DNA
8. Estimation of RNA
9. Study of sex chromatin in buccal smear and hair bud cells (Human).
10. Preparation and study of metaphase chromosomes from mouse bone marrow.
11. Preparation of human karyotype and study of chromosomal aberrations with respect to number, translocation, deletion etc from the pictures provided.
12. Study of Hardy-Weinberg equilibrium in human population by taking the example of blood group system (ABO).
13. Nucleic acid and protein sequence databases
14. Data mining for sequence analysis
15. Web based tools for sequence searches and homology screening
16. Construction for phylogenetic trees for proteins using UPGMA or Neighbor joining method(no software to be used)
17. Reproduction of the same phylogeny using MEGA software for the given set of sequences
18. Prediction and validation of protein structure using homology modeling (use of Swissmodel)