Course Title: Computing for Bioinformatics
Course Code BI-801
Course Objectives:

- Apply operating systems concepts to create a test bench to run Bioinformatics Applications
- Apply programming concepts to create bioinformatics pipeline applications from open source utilities
- Use bioinformatics libraries and packages to write programs

Course Outcomes:

After completing this course, the students will be able to:

- Use computational skills to construct and predictive statistical/mathematical/mechanistic models of biological systems.
- Develop advanced computational applications/tools related to bioinformatics
- Understand fundamental methods in probability and statistics and their applications to biological problems
- Understand computational and relevant experimental data.

Course Contents

- Linux Environment, File System and Directory Hierarchy, Command line interface
- Basic System Administration in Linux
- Compiling programs and utilities
- Shell scripting
- Programming Applications for Biologists
- Programming Packages and Libraries for Bioinformatics
- Understanding and encoding data in computer programs, variables, data types
- Selection and Repetition Control structures
- Writing modular programs using functions, Object Oriented programming using classes
- Connectivity with Databases
- Programming Biological Networks using graph libraries
- Project 1: Analysis of Biological Regulatory Networks
- Data Analytics libraries and Packages
- Data visualization using Matplotlib or any other library
- Project 2: Analysis and Visualization of Bioinformatics data
- Selected topics in "Computational Methods in Bioinformatics"

Recommended / Reference Books:

- Richard Petersen, Linux: The Complete Reference
- Magnus Lie, Beginning Python: From Novice to Professional
- James Tisdall, Beginning Perl for Bioinformatics
- Cynthia Gibas, Developing Bioinformatics Computer Skills: An Introduction to Software Tools for Biological App