



## **B.S. Abdur Rahman Crescent Institute of Science and Technology**

### **School of Life Sciences**

# **Introduction to Molecular Modeling and Graphics**

#### **Course Description**

This course is targeted at undergraduate level but is also suitable for graduate students wanting a background in modern computational and modeling approaches to solve biophysical/ biochemical problems in modeling.

#### **Objectives**

The course is designed to introduce future Biochemists, Biophysicists and Bioinformaticians to a wide range of techniques and applications in molecular modeling and computational drug design. Upon successful completion of the course, students will be able to:

1. Recognize the basics of Molecular Modeling
2. Create Molecular visualization images of publication quality
3. List the modeling tools available to study Protein – ligand interactions
4. Explain various steps involved in Molecular Docking and Dynamics
5. Design a mini project to combine the proper application of modeling tools.

#### **Books and References**

1. Molecular Modeling – Principles and Applications, 2nd Ed., Andrew Leach, 2001.
2. C. Mura, C. M. McCrimmon, J. Vertrees, M. R. Sawaya; "An Introduction to Biomolecular Graphics"; PLoS Computational Biology 8 (2010) Vol. 6, pp 1-11

#### **Prerequisites:**

3. We will assume some background in Chemistry, Biochemistry and Physics. There are no computer science prerequisites for this course.

#### **Lecture (Topics covered):**

Introduction to Molecular Modeling; Potential Energy Surfaces and Optimization Methods; Molecular mechanics; Force fields, Types of force fields; Finding equilibrium structures: Geometry optimization; Conformational search; Solvation; Visualization and molecular properties; Molecular Docking and Molecular Dynamics

#### **Hands-on Session:**

1. Introduction to PDB and small molecule databases.
2. Introduction to computational visualization with PyMol and Generating publication images
3. Working with Chimera for performing analysis and modeling experiments
4. Molecular Docking using AutoDock VINA
5. Macromolecular structure preparation: Modeling missing loops, Homology Modeling
6. Molecular dynamics using NAMD and analysis

### **Course Instructors**



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