Molecular Modeling and Drug Design CSE 874 (3-0)

1. **Rationale:**

Drug discovery has traditionally been a lengthy, costly, and high-risk process, often requiring over 12 years and $2.5 billion to achieve a single successful drug from approximately 100,000 candidate compounds. However, the landscape is rapidly evolving. Advances in artificial intelligence, machine learning, and molecular modeling particularly those leveraging structural data are transforming the process. Tools such as AlphaFold and structure-based virtual screening now allow for precise prediction of protein-ligand interactions, reducing reliance on trial- and-error and enhancing target specificity. Predictive algorithms and integrative multi-omics are enabling a more rational, data-driven approach to drug design. As the field becomes increasingly digital and structure-centric, this course has also evolved. While most of the content remains current, selected topics require updates to reflect the recent paradigm shift toward structural informatics and AI-powered modeling in drug discovery.

2. **Educational Objectives**

a. To develop skills for the prediction and analysis of bimolecular structures to design drug candidates using information from proteomics data.
b. To develop and understand integrated molecular models and AI guided workflows that utilize structural data to identify and optimize lead compounds more efficiently and cost-effectively.
c. Enable students to interpret and assess structural biology data (e.g., X-ray crystallography, cryo-EM, AlphaFold models) for drug target selection, validation, and rational optimization of drug-like molecules.

3. **Course Outcomes**

a. After completing this course, student will be able to understand development and validation of
b. Students will be able to develop virtual screening pipelines integrating structures and machine learning based methodologies.
c. Students will be able to construct, optimize and validate the hit identification and lead optimization using proteomics data.

4. **Recommended Reading:**

a. Computational Drug Discovery: Methods and Applications by Vasanthanathan Poongavanam, Vijayan Ramaswamy, DOI:10.1002/9783527840748, 2024

b. Protein-Protein Docking, Methods and Protocols by Agnieszka A. Kaczor, 2024,

c. Virtual Screening for Bioactive Molecules by in Methods and Principles in Medicinal Chemistry, Edited by Hans-Joachim Bohm and Gisbert Schneider, Volume 10, 2000.

d. Pharmacophore and Pharmacophore Search in Methods and Principles in Medicinal Chemistry, Edited by Thierry Langer and Rémy D. Hoffmann, Volume 32, 2006.