School of Pharmaceutical Sciences & Technology

Curriculum for

Fellowship Program in

COMPUTER AIDED DRUG DESIGN

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Course Title: COMPUTER-AIDED DRUG DESIGN
Course Type: FELLOWSHIP
Duration: 360 Hours (can be structured as 24 Credits)
Mode: Lectures, Practicals/Hands-on, Project

Overview

The Fellowship in Computer-Aided Drug Design (CADD) is an intensive, short-term postgraduate program designed to equip participants with the essential computational skills to accelerate the drug discovery process. CADD employs various computational methodologies to identify, design, and optimize biologically active compounds *in silico*, significantly reducing the time and cost associated with traditional wet-lab research. This interdisciplinary field integrates bioinformatics, cheminformatics, molecular modeling, and machine learning to predict how potential drug candidates interact with biological targets and to filter out inefficient compounds early in the pipeline.

Objectives:

Upon completion of the course, the fellow shall be able to:

- Understand the role of rational drug design within the entire drug discovery pipeline.
- Design and optimize potential lead molecules using both structure-based and ligand-based approaches.
- Apply concepts of QSAR, molecular docking, and molecular dynamics simulations to real-world problems.
- Predict key properties of drug candidates, including ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) profiles.
- Utilize state-of-the-art software tools for modeling, visualization, and virtual screening.

Course Outcome:

CO No.	Course Outcome
CO1	Explain the drug discovery and development pipeline and the strategic role of Computer-Aided Drug Design (CADD), target identification, structural biology fundamentals, biological databases, and ADME-Toxicity principles.
CO2	Understand and apply the principles of structure-based drug design, including protein–ligand interactions, molecular docking methodologies, scoring functions, de novo drug design, fragment-based approaches, and QM/MM force-field concepts.
CO3	Analyze and utilize ligand-based drug design techniques, including QSAR modeling, molecular descriptor selection, pharmacophore generation, and virtual screening strategies for lead identification.
CO4	Interpret the theoretical principles of advanced simulations and computational intelligence, including molecular dynamics simulations, free-energy calculations, AI/ML applications in CADD, and network/polypharmacology concepts.

Teaching & Learning Methods:

The program emphasizes a hands-on, problem-based approach. This includes interactive lectures with case studies, mandatory computer lab sessions using CADD software, webinars and talks by industry experts, assignments and quizzes for evaluation, and discussion forums for collaboration.

Syllabus

Theory - 10 Credits (150 Lecture Hours)

Module 1: Introduction to Drug Discovery & CADD (45 hours)

- The complete drug discovery pipeline and the strategic role of CADD.
- Fundamentals of structural biology: protein structure organization and DNA basics.
- Identification of biological targets, binding pockets, and druggable sites.
- Overview of key chemical and biological databases (PDB, PubChem, ChEMBL).
- ADME-Toxicity principles and predictive rules (Lipinski, Veber, etc.).

Module 2: Structure-Based Design Principles (45 hours)

- Theoretical principles of protein-ligand interactions and molecular docking.
- Understanding different types of scoring functions used in docking software.
- Concepts of *de novo* drug design and fragment-based lead discovery.
- Introduction to Quantum Mechanics (QM) and Molecular Mechanics (MM) force fields.

Module 3: Ligand-Based Design Principles (30 hours):

- Quantitative Structure-Activity Relationships (QSAR): underlying theory, molecular descriptors, and statistical correlation methods.
- Pharmacophore modeling and mapping techniques.
- Strategies for effective virtual screening.

Module 4: Advanced Simulations & ML Theory (30 hours):

- Principles of Molecular Dynamics (MD) simulations and free energy calculations (MM/GBSA).
- Theoretical overview of Artificial Intelligence (AI) and Machine Learning (ML) applications in CADD (e.g., ADMET prediction, *de novo* design).
- Concepts of network pharmacology and polypharmacology.

Practical/Hands-on Component: 8 Credits (120 Lab Hours)

1. Database Navigation & Visualization (15 hours):

- Practical exercises using NCBI, PDB, and UniProt for data retrieval.
- Hands-on protein visualization and active site identification using visualization software (e.g., PyMOL, UCSF Chimera).

2. Molecular Docking Simulations (30 hours):

- Step-by-step preparation of macromolecules and ligands for docking.
- Execution of docking runs using open-source tools (e.g., AutoDock Vina).
- Detailed analysis of binding poses and interaction mapping post-docking.

3. QSAR & Virtual Screening Labs (45 hours):

- Generating and calculating relevant molecular descriptors for QSAR studies.
- Building and validating 2D-QSAR models with provided datasets and software.
- Developing pharmacophore models and executing virtual screening protocols against chemical libraries.

4. Advanced Simulation & ML Tools (30 hours):

- Setting up and initiating basic Molecular Dynamics simulations for protein-ligand complexes.
- Using introductory ML/cheminformatics platforms (e.g., KNIME) for ADMET prediction tasks.

Project: 6 Credits (90 Self Study/Research Hours)

A mandatory Project (6 credits) provides practical application. Projects typically involve identifying a drug target, developing a CADD workflow from virtual screening to molecular dynamics simulations, and producing a report, presentation, and *in silico* results

References:

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