Hands-on Research Training in Molecular Docking & Structure-Based Drug Design

Student Training Handbook

Program Duration: 4 Weeks
Class Schedule: 3 Days per Week + 2 Doubt Clearing Sessions
Class Timing: 7:30 PM – 8:30 PM
Mode of Training: Online Live Hands-on Sessions
Training Focus: Practical molecular docking workflow using real protein targets and ligands.

Program Goal

By the end of this training, students will be able to independently perform protein preparation, ligand preparation, molecular docking, interaction analysis, and visualization using commonly used bioinformatics and molecular docking tools.

WEEK 1 — SOFTWARE SETUP & FUNDAMENTALS

DAY 1 — Introduction & Software Installation

- Introduction to molecular docking
- Overview of structure-based drug discovery
- Installing AutoDock Tools
- Installing AutoDock Vina
- Installing PyMOL and Discovery Studio Visualizer
- Basic navigation in PyMOL

DAY 2 — Understanding Protein Structures

- Protein structure basics
- Understanding PDB files
- Chains, residues, ligands, and heteroatoms
- Downloading proteins from RCSB PDB
- Protein cleaning and preprocessing

DAY 3 — Ligand Preparation

- Downloading ligands from PubChem
- Understanding ligand file formats
- Ligand preparation workflow
- Energy minimization basics
- Preparing docking-ready ligand files

WEEK 2 — MOLECULAR DOCKING WORKFLOW

DAY 4 — Protein Preparation for Docking

- Adding hydrogens and charges
- Preparing protein PDBQT files
- Common preprocessing mistakes
- Preparing individual target proteins

DAY 5 — Grid Box Setup & Docking Parameters

- Understanding active sites
- Grid box setup
- Blind docking vs targeted docking
- Docking configuration file preparation
- Optimizing docking search space

DAY 6 — Running Docking Simulations

- Running docking using AutoDock Vina
- Generating docking poses
- Understanding docking output files
- Binding affinity interpretation
- Comparing docking scores

WEEK 3 — VISUALIZATION & INTERACTION ANALYSIS

DAY 7 — Visualization Using PyMOL

- Visualizing docked complexes
- Surface, cartoon, and stick representations
- Binding pocket visualization
- Creating publication-style images

DAY 8 — Interaction Analysis

- Hydrogen bond analysis
- Hydrophobic interaction analysis
- Pi-pi and salt bridge interactions
- Identifying interacting residues
- Comparing strong and weak binders

DAY 9 — Advanced Docking Analysis

- RMSD basics
- Pose comparison
- Selecting best docking conformations
- Ranking ligands based on affinity
- Understanding false positive docking results

WEEK 4 — MINI PROJECT & FINAL ANALYSIS

DAY 10 — Individual Mini Project Work

- Independent docking workflow practice
- Error troubleshooting
- Workflow optimization
- Individual project guidance

DAY 11 — Final Result Analysis

- Binding affinity comparison
- Interaction image preparation
- Docking result interpretation
- Preparing final docking outputs

DAY 12 — Practical Evaluation

- Complete docking workflow demonstration
- Protein preparation
- Ligand preparation
- Docking execution
- Interaction analysis and interpretation

Additional Doubt Clearing Sessions (if required)

- Session 1: Software installation issues and docking troubleshooting
- Session 2: Mini project discussion

Student Learning Outcomes

- Independently prepare proteins and ligands for docking
- Perform molecular docking using AutoDock Vina
- Analyze protein-ligand interactions
- Visualize molecular interactions professionally
- Interpret docking scores and binding affinities
- Understand practical structure-based drug discovery workflow

Recommended Research Papers & Learning Resources

1. Morris GM et al., 2009 — AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility.
2. Trott O and Olson AJ, 2010 — AutoDock Vina: Improving the speed and accuracy of docking.
3. Forli S et al., 2016 — Computational protein–ligand docking and virtual drug screening with AutoDock suite.
4. Seeliger D and de Groot BL, 2010 — Ligand docking and binding site analysis with PyMOL and AutoDock/Vina.
5. Kitchen DB et al., 2004 — Docking and scoring in virtual screening for drug discovery.

Useful Databases & Software Links

- RCSB Protein Data Bank (PDB) — https://www.rcsb.org
- PubChem Database — https://pubchem.ncbi.nlm.nih.gov
- AutoDock Suite — https://autodock.scripps.edu
- PyMOL — https://pymol.org
- Ligplot+ — https://www.ebi.ac.uk/thornton-srv/software/LigPlus/

Final Note to Students:

This training is designed to provide practical exposure to molecular docking and computational drug discovery workflows. Students are encouraged to practice the workflow regularly outside class hours for maximum learning benefit.