

# Blood Brain Barrier Permeability

Bioinformatics Society and TJML



# Drug Discovery

- The process of discovering new medicine to treat disorders
- Predicting properties of molecules
  - Toxicity, blood brain barrier permeability, determining IC50 concentrations, etc.



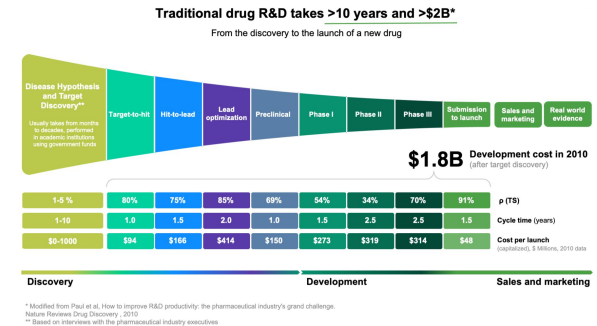
# Current Approaches

1. Identify a critical target protein that modulates a disease
  - a. Requires bioinformatics and expression analysis
2. Screen for molecules that can inhibit the target protein
  - a. Requires combinatorial chemistry, structure-based drug design, and in vitro screening
3. Optimization
  - a. Requires traditional medicinal chemistry & rational drug design
4. Evaluate pharmacokinetic properties
  - a. effects on absorption, distribution, metabolism, and excretion
5. Clinical trials
6. Government registration
  - a. FDA approval



# Problems

- Current drug discovery approaches very expensive and time-consuming
  - Costs upwards of 2 billion dollars and can take a decade of research and development
  - Trial and error
  - 15% of drugs make it through clinical trials

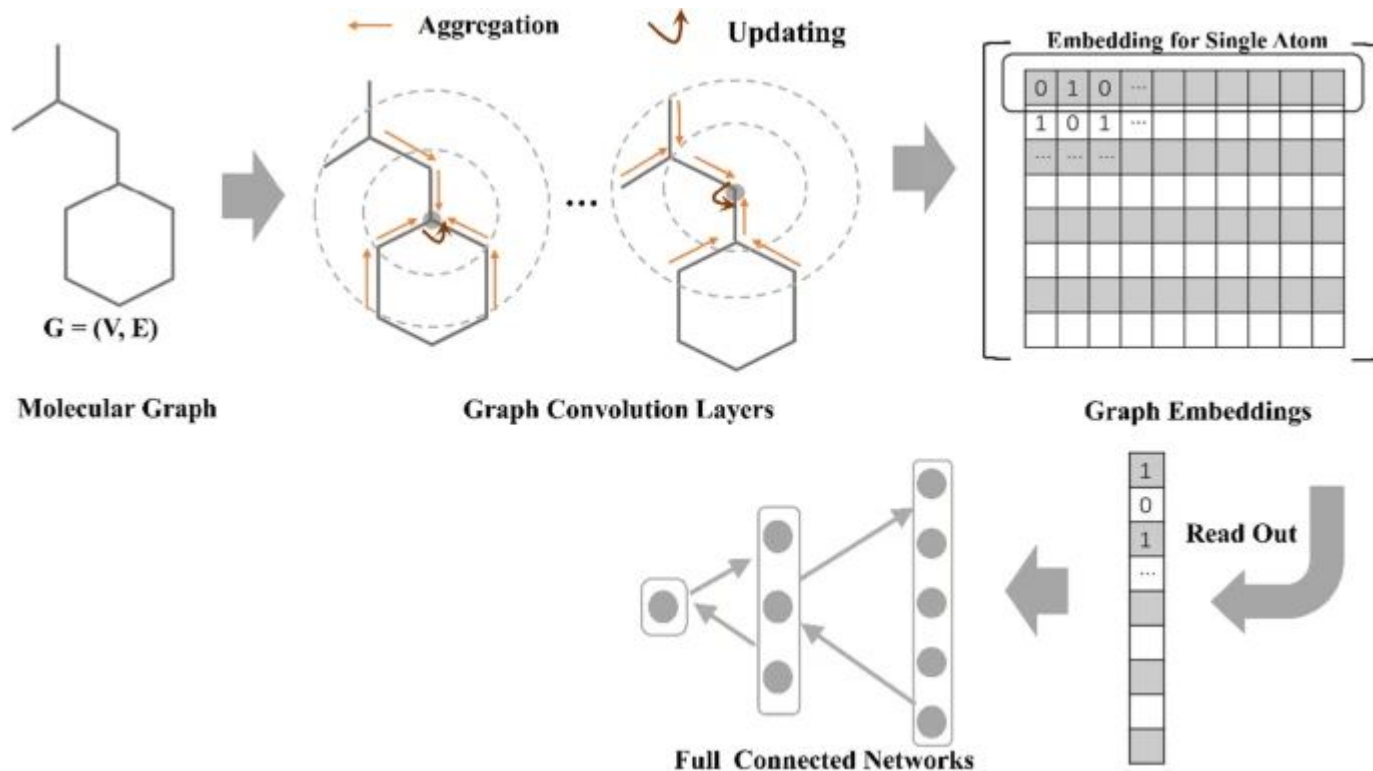


# ML-Based Approaches

- Extract features from molecules to better predict how they interact with the body (toxic, permeable, can bind to specific proteins)
- Predict properties of discovered molecules
- Although prior research extracts features from molecules, current research focuses on learning molecule representations using neural networks
  - Graph neural networks, variational autoencoders



# Graph Neural Networks



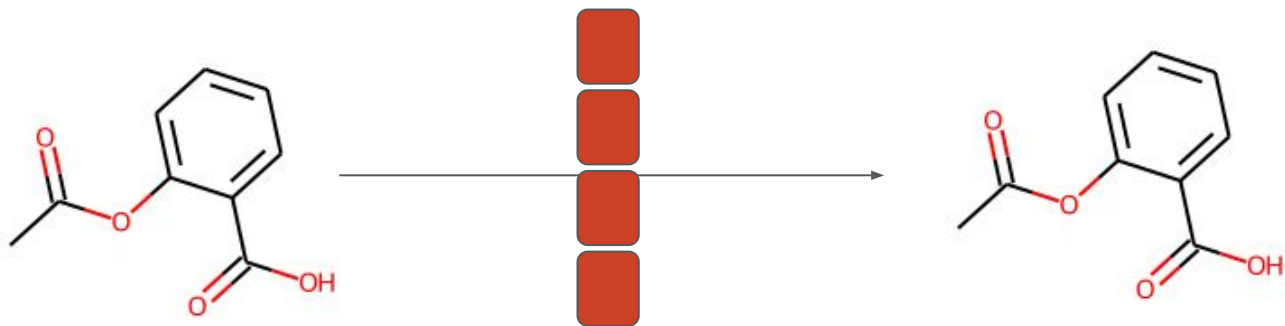
# Implementation Details

- DeepChem library has open source implementations for many neural network architectures tailored for learning representation of molecule datasets
- Abstracts complex implementation details
  - Molecules have more constraints than typical nodes in graphs



## Lab Objective

**Determine whether a certain molecule/drug can permeate the blood brain barrier**





# Data Format

- CSV File → 3 Columns
  - Drug Name
  - SMILES: Simplified molecular-input line-entry system
  - OUTPUT: Permeable or Non-Permeable

name	p_np	smiles
Propranolol	1	<chem>[Cl].CC(C)NCC(O)COc1cccc2ccccc12</chem>
Terbutylchlorambucil	1	<chem>C(=O)(OC(C)(C)C)CCCc1ccc(cc1)N(CC(Cl)CC(Cl)C)C</chem>
40730	1	<chem>c12c3c(N4CCN(C)CC4)c(F)cc1c(c(C(O)=O)cn2C(C)CO...</chem>
24	1	<chem>C1CCN(CC1)Cc1cccc(c1)OCCNC(=O)C</chem>
cloxacillin	1	<chem>Cc1onc(c2ccccc2Cl)c1C(=O)N[C@H]3[C@H]4SC(C)(C)...</chem>



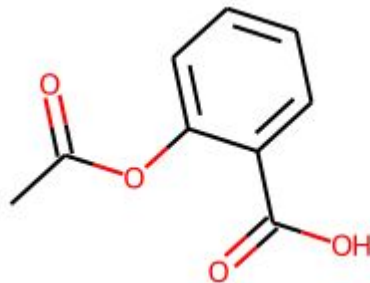
# Drug Representation - SMILES

- Single line representation of molecular structure
- Commonly used in bioinformatics
- ASCII strings with characters representing bonds
  - Example: “=” represents double bond

## SMILES Representation

```
CC(=O)Oc1ccccc1C(=O)O
```

## Structural Representation



# Step-by-Step Process

1. Load in the data
2. Use DeepChem to represent SMILE molecule as adjacency list
3. Initialize GNN model
4. Train Model
5. Evaluate

**ACCESS LAB: [tjmachinelearning.com](http://tjmachinelearning.com) → Lectures → Advanced**

