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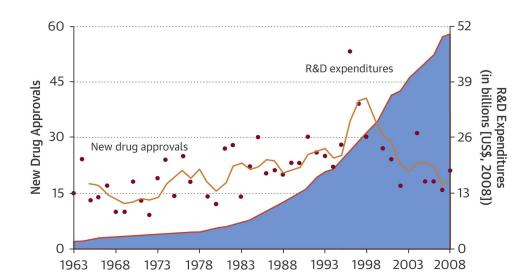
Motivation

- Americans spent \$324.6 Billion on prescription drugs last year
- Drug cost \$2.6B and 17 years to develop on average
- Solving a small portion → big returns

The Present and Future State-of-the-Art Review

Cardiovascular Drug Development: Is it Dead or Just Hibernating?

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Objectives

First Half

- Curate and join drug-receptor databases together from DrugBank, PubChem to establish drug structure to receptor relationships
- Develop a deep binary classifier model to identify potential drugs to repurpose for other receptors

Second Half

- Deeper validation of model
- Create and deploy a web interface for researchers to use that predicts potential receptors for a given drug

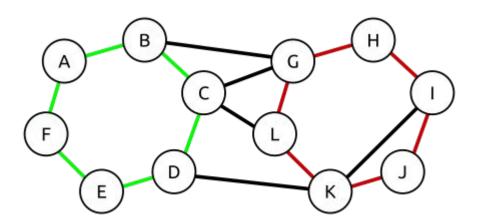
Research Plan: Data

- DrugBank: Drug-target interaction data
 - 6,835 drugs and 4,217 targets
- PubChem: retrieve SMILES (molecular structure in machine readable strings)
- Curated drug reactions
 - Dataset 1: continuous kinase inhibitor reactions with 72 drugs and 422 targets
 - Dataset 2: continuous protein binding scores with 2,116 drugs and 229 targets

Benzaldehyde SMILE C1=CC=C(C=C1)C=O

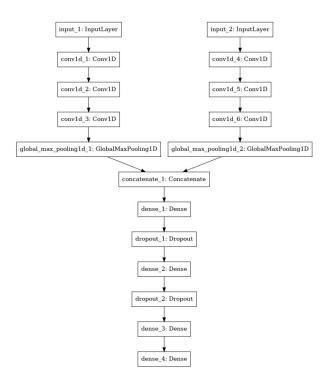
Research Plan: Negative Sampling

Use randomly sampled drugs with a path distance longer than the longest-shortest path

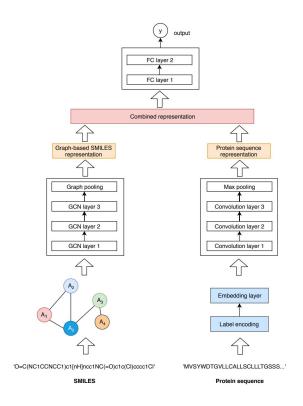


Research Plan: Model

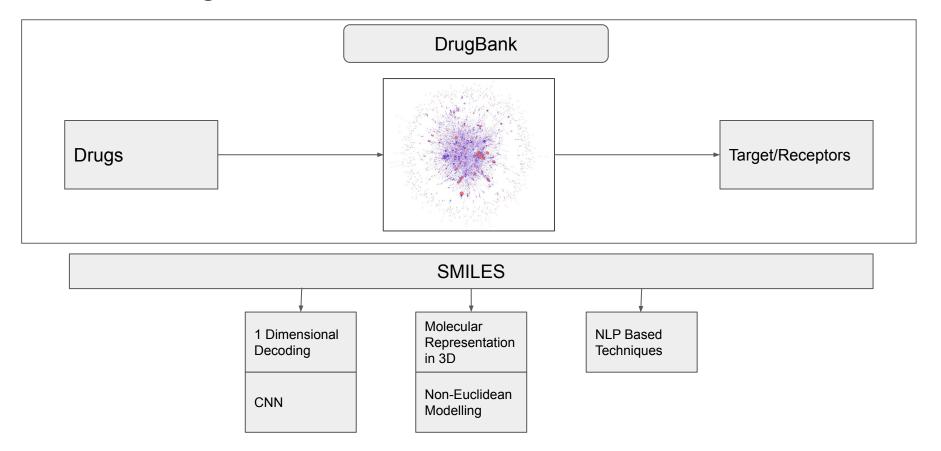
Compound Structure as Strings



Compound Structure as Graph and String



Connecting the Dots



Preliminary Results

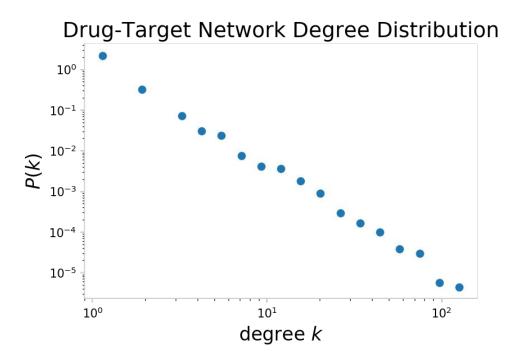


Figure 1: The degree distribution for drugs the FoodBank drug-target interaction network.

- Most drugs have fewer than 10 targets
- Drug with most targets is NADH, a supplement taken for improved cognition and dementia

Preliminary Results

 Large central component does not invalidate sampling technique

Average path size: 7.66

Network diameter: 22

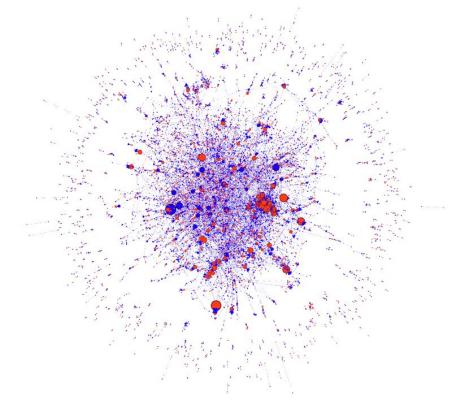


Figure 2: The network layout of the FoodBank drug-target interaction network visualized using the ForceAtlas 2 algorithm. Red nodes represent targets, blue nodes represent drugs, and the node size corresponds with the respective node degree.

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