Graph Neural Networks for Drug Development

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Stanford | **ENGINEERING** Computer Science

Drug Development



Opportunities for AI in Drug Development





Finding drugs for disease treatments relies on several types of interactions, *e.g.*, drug-target, protein-protein, drug-drug, drug-disease, disease-protein pairs

Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities, Information Fusion 2049

Today's Talk



New tricks for old drugs

Faced with skyrocketing costs for developing new drugs, researchers are looking at ways to repurpose older ones — and even some that failed in initial trials.

Goal: Find which diseases a drug (new molecule) could treat



Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities, Information Fusion 2019

Key Insight: Subgraphs **Disease:** Subgraph of rich **Drug:** Subgraph of rich protein network defined protein network defined on on drug's target proteins disease proteins A drug likely treats a disease if it is **close** to the disease in pharmacological space [Paolini et al., Nature Biotech.'06; Menche et al., Science'15]

Idea: Use the paradigm of embeddings to operationalize the concept of closeness in pharmacological space

Predicting Links Between Drug and Disease Subgraphs

Task: Given drug *C* and disease *D*, predict if *C* treats *D*





We need drug repurposing dataset

Protein-protein interaction network culled from 15



Molecular pathways, disease symptoms, side effects

Predictive Performance

Task: Given a disease and a drug, predict if the drug could treat the disease

AUPRC AUROC

0.888

0.851

Our method (SUGAR)

proach

Graphlets [Bioinformatics'13] PREdicting Drug IndiCaTions [Mol. Sys. Biol.'11]

Bi-directional random walks [Bioinformatics'16] Heterogeneous graph inference [Bioinformatics'14]

Drug-disease closeness [Nat. Commun.'17] Drug-disease dispersion [Nat. Commun.'17] Gene-based network overlap [Nat. Commun.'17] Up to 49% improvement

Up to 172% improvement

Drug Repurposing at Stanford

Drug

N-acetyl-cysteine Xamoterol Plerixafor Sodium selenite Ebselen Itraconazole Bestatin Bestatin Ketaprofen Sildenafil Tacrolimus Benzamil Carvedilol Benserazide Pioglitazone Sirolimus

Disease

cystic fibrosis neurodegenerat cancer cancer C difficile cancer lymphedema pulmonary arterial hypertension lymphedema lymphatic malformation pulmonary arterial hypertension psoriasis Chagas' disease BRCA1 cancer interstitial cystitis dystrophic epidermolysis bullosa

Task: Predict if an existing drug can be repurposed for a new disease

Stanford

Rank:	36/5000
Rank:	10/5000
Rank:	26/5000
Rank:	11/5000
Rank:	16/5000
Rank:	28/5000
Rank:	26/5000
Rank:	46/5000
Rank:	114/5000
Rank:	9/5000
Rank:	41/5000
Rank:	13/5000
Rank:	46/5000

From Rench to Redside

SPARK Translational Research Program

Feedbacks for the AI Loop



Feedbacks for the AI Loop



Explaining GNN Predictions

Key idea:

- Summarize where in the data the model "looks" for ' evidence for its prediction
- Find a small subgraph most influential for the prediction



GNNExplainer: Key Idea

- Input: Given prediction f(x) for node/link x
- Output: Explanation, a small subgraph M_x together with a small subset of node features:
 - M_x is most influential for prediction f(x)
- Approach: Learn M_x via counterfactual reasoning
 - Intuition: If removing v from the graph strongly decreases the probability of prediction ⇒ v is a good counterfactual explanation for the prediction



GNN Explainer: Generating Explanations for Graph Neural Networks, NeurIPS 2019

GNNExplainer: Results

"Why did you predict that this molecule will have a mutagenic effect on Gram-negative bacterium *S. typhimurium*?"

Input
GNN EXPLAINER

Grad
Att

Grad
Att

GRN
GRN





GNN Explainer: Generating Explanations for Graph Neural Networks, NeurIPS 2019

Today's Talk



Polypharmacy

Patients take multiple drugs to treat complex or co-existing diseases

46% of people over 65 years take more than 5 drugs

Many take more than 20 drugs to treat heart diseases, depression or cancer

15% of the U.S. population affected by unwanted side effects

Annual costs in treating side effects exceed \$177 billion in the U.S. alone

Unexpected Drug Interactions

Co-prescribed drugs

Side Effects



Why is modeling polypharmacy hard?

Combinatorial explosion

- >13 million possible combinations of 2 drugs
- >20 billion possible combinations of 3 drugs

Non-linear & non-additive interactions

Different effect than the additive effect of individual drugs

Small subsets of patients

- Side effects are interdependent
- No info on drug combinations not yet used in patients







Our Approach: Decagon



2. Decoder: Use the learned embeddings to predict typed edges between nodes



Encoder: Propagate Neighbors

Generate embeddings based on **local network neighborhoods separated by edge type**

1) Determine a node's computation graph for each edge type

''2

 r_3

3

 r_3

 r_2

2) Learn how to transform and propagate information across computation graph



Decoder: Weighted, Typed Edges Output: Predicted edges, new discovered relationships $p(\triangle, \mathbf{r_1}, \triangle) = \sigma(\mathbf{z}_c^T \mathbf{D}_{r_1} \mathbf{R} \mathbf{D}_{r_1} \mathbf{z}_s)$ $p(\triangle, \mathbf{r_2}, \triangle) = \sigma(\mathbf{z}_c^T \mathbf{D}_{r_2} \mathbf{R} \mathbf{D}_{r_2} \mathbf{z}_s)$ \mathbf{Z}_{c} Input: Embeddings of $\mathbf{p}(\mathbf{A}, \mathbf{r}_3, \mathbf{A}) = \sigma(\mathbf{z}_c^T \mathbf{D}_{r_3} \mathbf{R} \mathbf{D}_{r_3} \mathbf{z}_s)$ R two nodes, C and S $\mathbf{p}(\mathbf{A}, \mathbf{r}_4, \mathbf{A}) = \sigma(\mathbf{z}_c^T \mathbf{D}_{r_4} \mathbf{R} \mathbf{D}_{r_4} \mathbf{z}_s)$ \mathbf{Z}_{S} \mathbf{D}_{r_n} Probability that *C* and *S* are linked by an edge of type r_4 **Tensor factorized model** $\mathbf{p}(\mathbf{A}, \mathbf{r}_n, \mathbf{A}) = \sigma(\mathbf{z}_c^T \mathbf{D}_{r_n} \mathbf{R} \mathbf{D}_{r_n} \mathbf{z}_s)$ captures dependences between different edge types

$\mathbf{R}, \mathbf{D}_{r_i}$ Parameter weight matrices Modeling polypharmacy side effects with graph convolutional networks, *Bioinformatics* 2018

We need polypharmacy dataset



A polypharmacy network with over 5 million edges and over 1,000 different edge types

We apply our deep approach to the polypharmacy network

E.g.: How likely will Simvastatin and Ciprofloxacin, when taken together, break down muscle tissue?

Simvastatin Γ_2 (breakdown of muscle tissue) Ciprofloxacin

Results: Side Effect Prediction



Our method (Decagon)

- RESCAL Tensor Factorization [Nickel et al., ICML'11]
- Multi-relational Factorization [Perros, Papalexakis et al., KDD'17]
- Shallow Network Embedding [Zong et al., Bioinformatics'17]

New Predictions

First AI method to predict side effects of drug combinations, even for combinations not yet used in patients

Next: Can the method generate hypotheses and give:

- Doctors guidance on whether it is a good idea to prescribe a particular combination of drugs to a particular patient
- Researchers guidance on effective wet lab experiments and new drug therapies with fewer side effects

New Predictions

Approach:

- 1) Train deep model on data generated **prior to 2012**
- 2) How many **predictions** have been **confirmed after 2012**?



Clinical Validation of New Predictions

Drug interaction markers, lab values, and many other surrogates



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Today's Talk



Complex, interconnected datasets are transforming science and medicine

Graph ML can unlock these datasets





Physical instruments facilitate discoveries

Instruments for modern, data-intensive sciences

Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities, Information Fusion 2019

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> Papers, data & code <u>cs.stanford.edu/~marinka</u> <u>snap.stanford.edu/biodata</u>





Students and postdocs for projects in machine learning on biomedical data

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