

# Graph learning for prediction of drug-disease interactions

Preliminary results

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- 1. Motivation
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# **Motivation**

- Node classification
  - Predict type of a given node

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- Network similarity
  - How similar are two (sub) networks
- Link prediction
  - Predict weather two nodes will be linked
  - Knowledge graph completition

## Link prediction task



Training network  $[t_1, t_2]$ 



Test network  $[t_3, t_4]$ 

## Bipartite network



# Methods

#### Methods overview



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#### Example

Second phase of a double-blind study clinical trial on Sibutramine for the treatment of patients suffering essential obesity

(PMID: 11360159)

#### SemRep

• Output:

```
(Sibutramine) - [:TREATS] - > (Obesity)
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• UMLS Concept

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## Semantic MEDLINE



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## Baseline predictors for bipartite networks

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1. Common neighbors:

$$s_{CN'}(u,v) = |\Gamma(u) \cap \Gamma'(v)|$$

2. Jaccard coefficient:

$$s_{JC'}(u,v) = rac{|\Gamma(u) \cap \Gamma'(v)|}{|\Gamma(u) \cup \Gamma'(v)|}$$

3. Adamic/Adar:

$$s_{AA'}(u,v) = rac{1}{\log(|\Gamma(u) \cap \Gamma'(v)|)}$$



#### Machine learning workflow II



#### Word embeddings: word2vec



king - man + woman = queen













## DeepWalk (Perozzi et al., 2013)

- 1. Simulate many short random walks starting from each node
- 2. For each node u, get nearby nodes as a sequence of nodes visited by random walks starting at u
- 3. For each node *u*, learn its embedding by predicting which nodes are in the neighborhood

## node2vec (Grover & Leskovec, 2016)

#### Main idea

Use flexible, biased random walks that can trade off between local and global views of the network.



## From node vectors (embeddings) to link vectors (embeddings)

#### Definition

Define binary operator over node vectors f(u) and f(v) to generate composite link representation g(u, v). We consider:

1. Concatenation:

 $u_i + v_i$ 

2. Average:

$$\frac{u_i \oplus v}{2}$$

3. Hadamard product:

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#### Example (Hadamard)

$$\begin{pmatrix} 1 \\ 2 \end{pmatrix} \odot \begin{pmatrix} 3 \\ 4 \end{pmatrix} = \begin{pmatrix} 1 \cdot 3 \\ 2 \cdot 4 \end{pmatrix} = \begin{pmatrix} 3 \\ 8 \end{pmatrix}$$

# Results

## Classification performance

Method	Binary operator	AUROC	AUPR	Prec <i>k</i>	mAP
CN	_	0.86	0.86	0.86	0.64
JC	_	0.85	0.84	0.86	0.62
AA	_	0.81	0.74	0.82	0.54
DeepWalk	Co	0.83	0.86	0.96	0.79
	Av	0.83	0.86	0.97	0.80
	Ha	0.72	0.72	0.82	0.65
node2vec	Co	0.83	0.86	0.96	0.80
	Av	0.83	0.86	0.97	0.81
	Ha	0.72	0.73	0.83	0.65

*Note:* CN = Common Neighbors, JC = Jaccard Coefficient, AA = Adamic/Adar; (Co)ncatenate, (Av)erage, and (Ha)damard binary operator; AUROC = area under ROC curve, AUPR = area under PR curve, Prec@k = precision at k, mAP = mean average precision

Conclusions

#### Summary

- We investigate the representation learning in bipartite drug-disease network of semantic predications
- We design a deep neural network model that includes the graph structure into the embedding
- We found evidence that DeepWalk and node2vec outperformed baseline predictors in terms of Prec@k and mAP
- Future work:
  - Extend the study to all predication types in SemMedDB
  - Domain expert for results interpretation

