Predicting drug-disease associations based on the known association bipartite network

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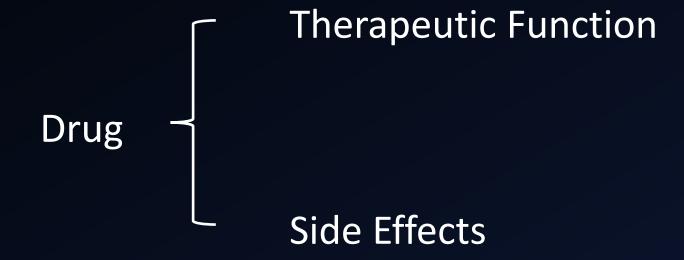
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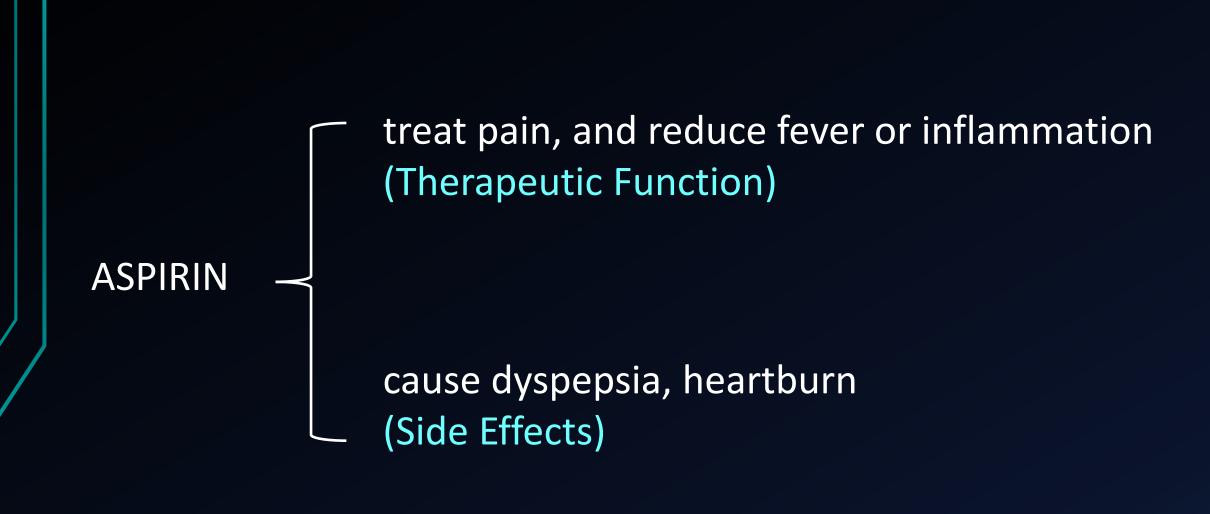
Outline

- Introduction
- Materials and Method
- Experiments and Results
- Conclusion

Background ----- Drug-Disease Associations

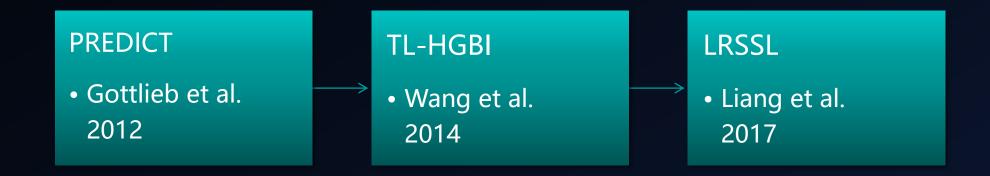






- Motivation
 - Drug-Disease associations provide important information for drug discovery and drug repositioning
 - Wet experimental identification is time-consuming and labor-intensive
 - Computational methods can guide experiments to identify drug-disease associations

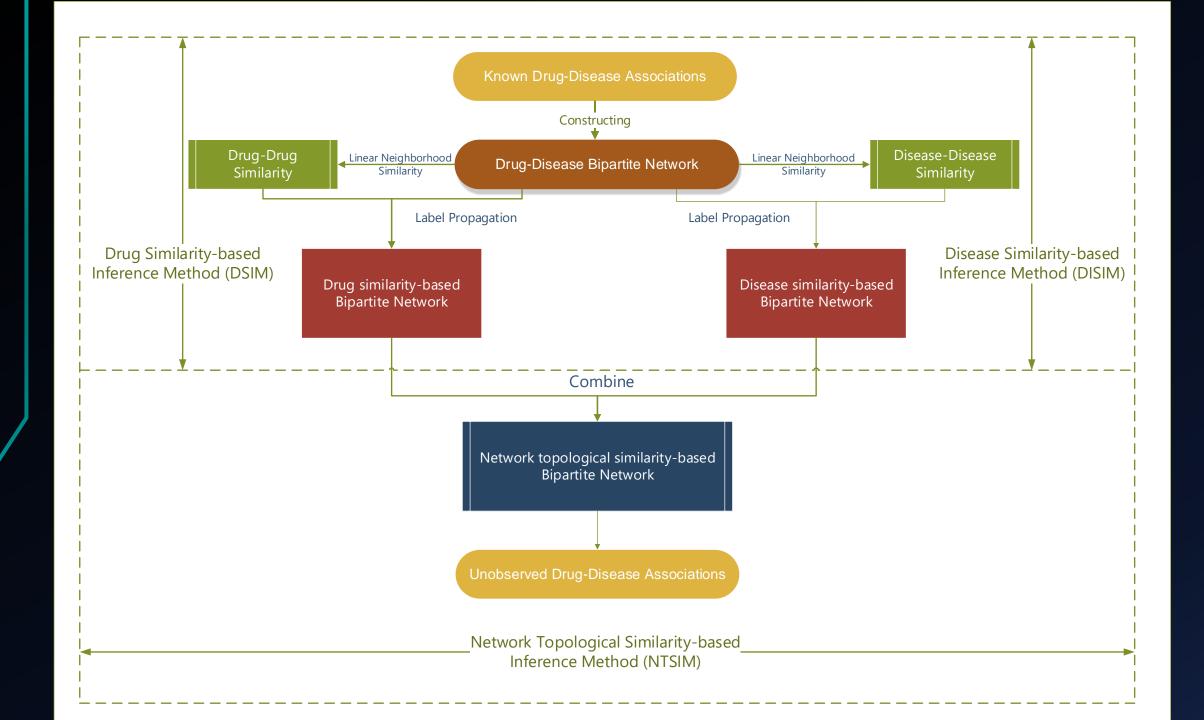
Research Status



- Our Method
- Network topological similarity-based inference method (NTSIM)

Dataset

Name	Drugs	Diseases	Known Associations
Our Dataset	269	598	18416
PREDICT Dataset	593	313	1933
TL-HGBI Dataset	1409	5080	1461
LRSSL Dataset	763	681	3051



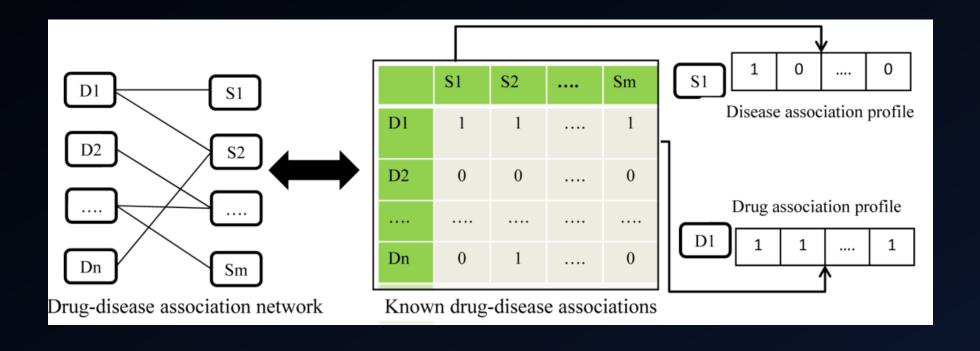
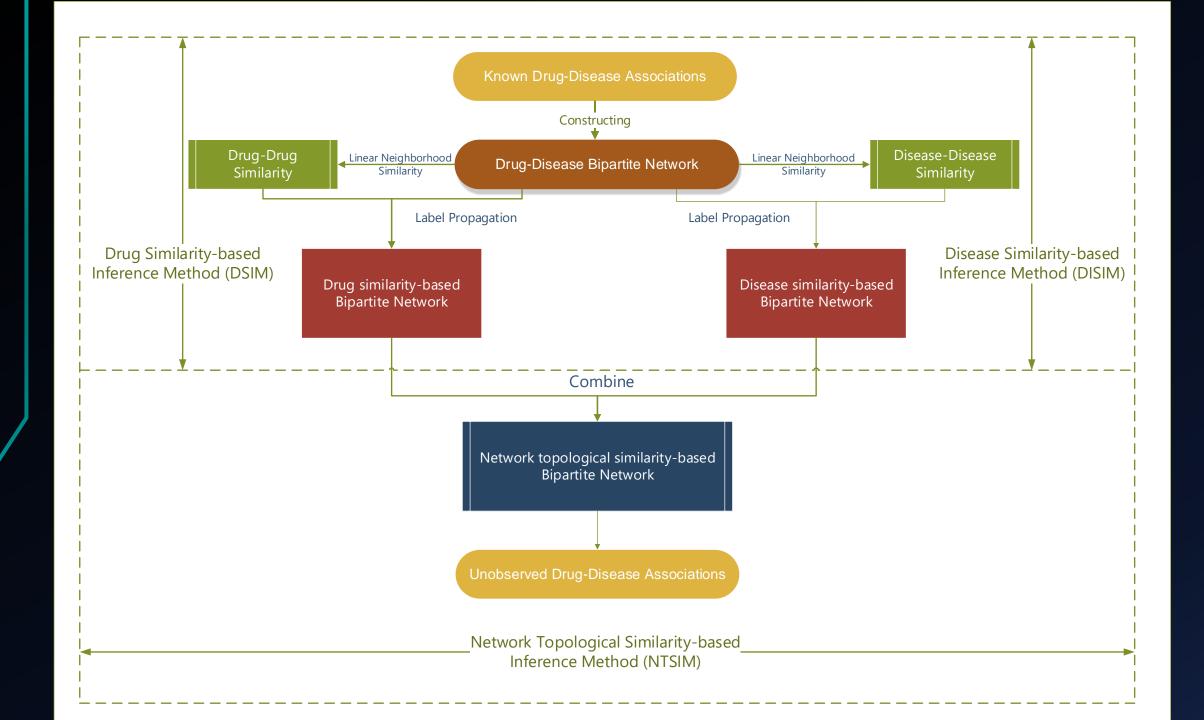
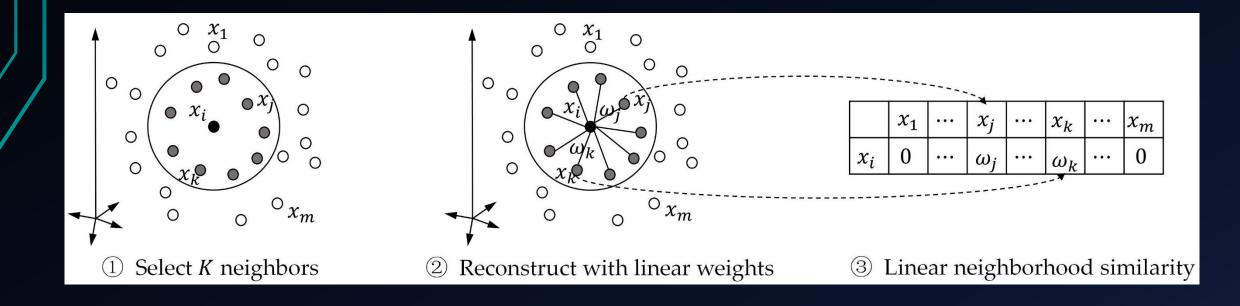


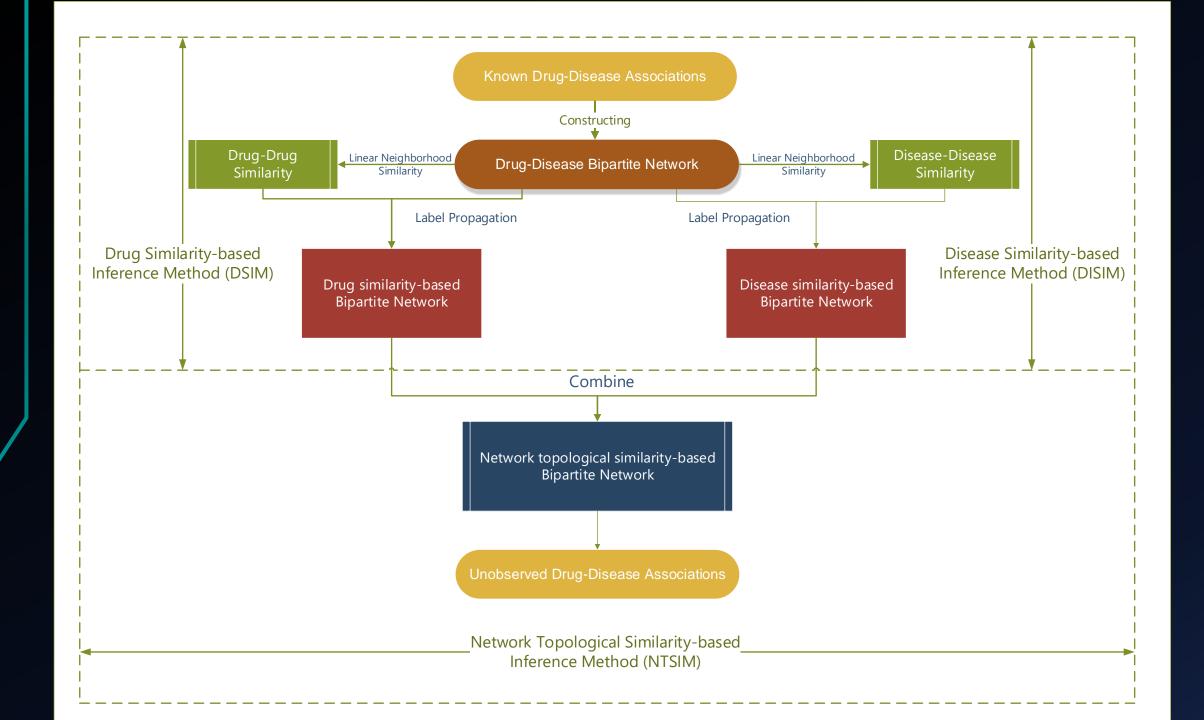
Fig.1. The drug-disease association-based network, disease association profiles and drug association profiles



- Linear Neighborhood Similarity
 - Hypotheses:
 - I) Data points in the feature space can be considered to be linear (S.T Roweis, 2000)
 - II) Each data point can be reconstructed by a linear combination of its neighbors (Wang, 2008)

Linear Neighborhood Similarity





The drug-disease association inference methods

the network topological similarity-based inference method (NTSIM)

$$P_{\text{NTSIM}} = (P_{\text{DSIM}} + P_{\text{DISIM}})/2 \tag{14}$$

Cross Validation and Evaluation Metrics

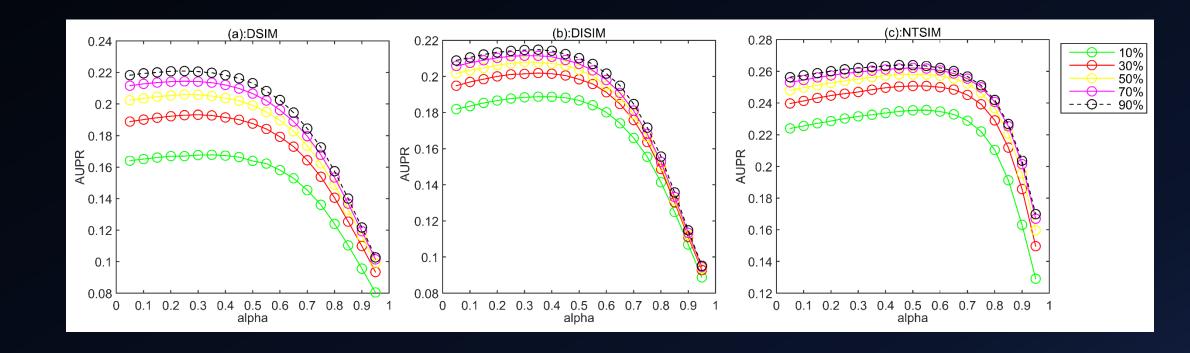
five-fold cross-validation

randomly splits known drug-disease associations into five subsets

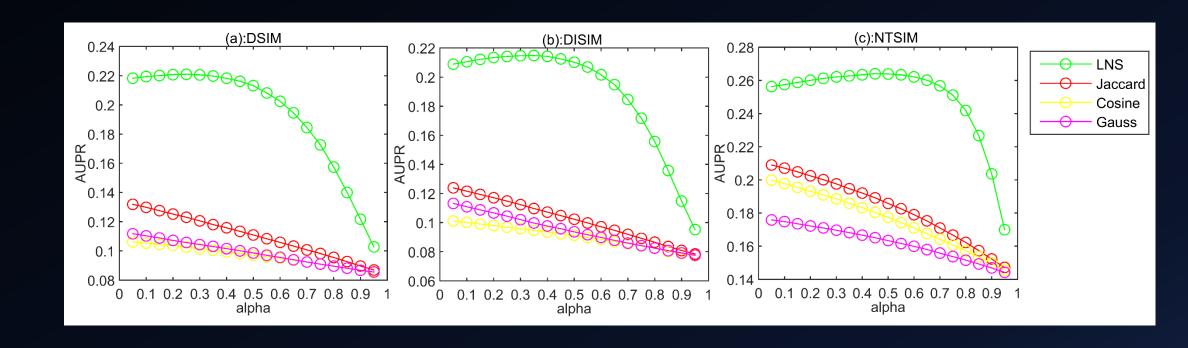
evaluation metrics

(AUC), (AUPR), (SEN) (SPEC), (PRE), (ACC) (F)

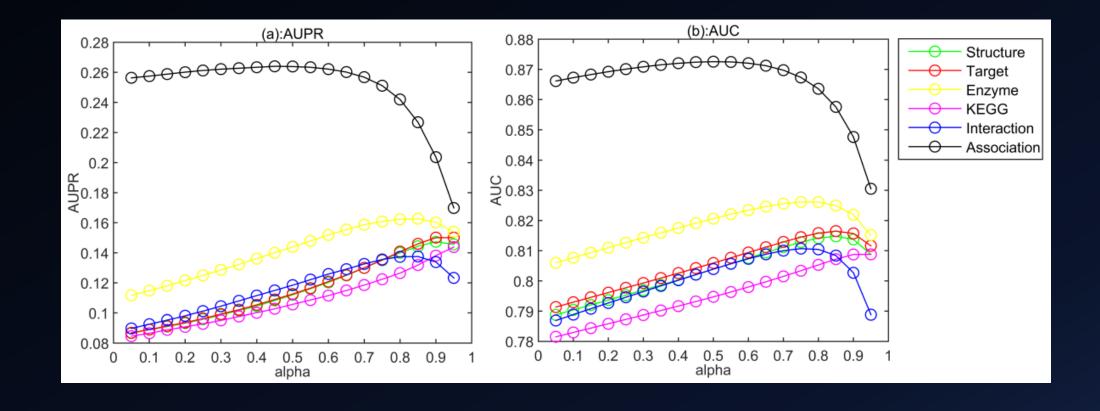
Performances of prediction models



Performances of prediction models



Comparison of Different Features



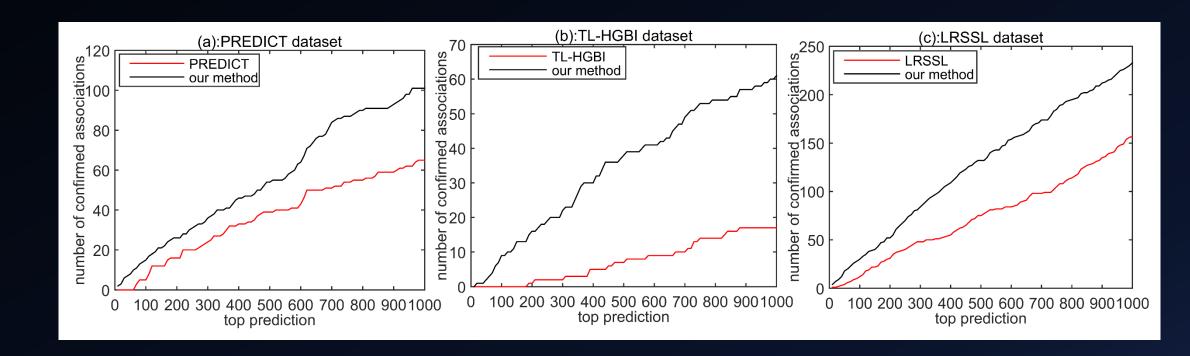
Compared with benchmark methods

Methods	Datasets	AUPR	AUC
Resource allocation	Resource allocation our dataset		0.8408
Our method	our dataset	0.2621	0.8709
Resource allocation	PREDICT dataset	0.3212	0.8462
Our method	PREDICT dataset	0.3376	0.9205
Resource allocation	TL-HGBI dataset	0.0951	0.7747
Our method	TL-HGBI dataset	0.2631	0.9616
Resource allocation	LRSSL dataset	0.2094	0.8059
Our method	LRSSL dataset	0.2693	0.9021

Compared with benchmark methods

Methods	Datasets	AUPR	AUC
PREDICT	PREDICT dataset	0.1507	0.9020
Our method	PREDICT dataset	0.3376	0.9205
TL-HGBI	TL-HGBI dataset	0.0492	0.9584
Our method	TL-HGBI dataset	0.2631	0.9616
LRSSL	LRSSL dataset	0.1789	0.8250
Our method	LRSSL dataset	0.2693	0.9021

Independent Experiments



Case Study

NO.	Drugs	Diseases	Evidence	
1	Methadone	Seizures	https://www.drugs.com/methadone.html	
2	Amiodarone	Hypertension	http://factmed.com/drugcover.php?drugname = Amiodarone	
3	Clozapine	Headache	https://www.drugs.com/clozapine.html	
4	Morphine	Tremor	http://www.medindia.net/doctors/drug_infor mation/morphine.htm	
5	Methamphetamine	Hypotension	https://www.drugbank.ca/drugs/DB01577	
6	Risperidone	Anxiety Disorders	N.A.	
7	Amphetamine	Catalepsy	N.A.	
8	Caffeine	Drug-Induced Liver Injury	N.A.	
9	Chlorpromazine	Nausea	https://www.drugs.com/mtm/chlorpromazine. html	
10	Clozapine	Sleep Initiation and Maintenance Disorders	N.A.	

Conclusion

Strengths:

- I) A novel similarity measure for graph, robust for graph-based similarity method
- II) for large-scale data, fast speed
- III) little input, but high-accuracy performance

Limitations:

- I) Cold start problem
- II) Failing to distinguish two kinds of drug-disease associations

Q&A

Thanks!