

HANSHENG XUE

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EDUCATION

Harbin Institute of Technology Sep. 2015 - Dec. 2017
M.S. in Computer Science and Technology
Thesis: Clustering Biomedical Networks using Deep Learning
Advisor: Prof. Yadong Wang
Co-Advisor: Prof. Jiajie Peng

Nanjing University of Technology Sep. 2011 - Jun. 2015
B.S. in E-commerce
GPA:3.41/4

RESEARCH INTEREST

Bioinformatics, Graph Data Analysis, Data Mining, Machine Learning, Deep Learning

EXPERIENCE

Teaching Assistant Sep. 2016 - Jan. 2017
· *Teaching Assistant for Data Mining, School of Computer Science and Technology, Harbin Institute of Technology, Advisor: Prof. Yunming Ye*

Propaganda Minister Sep. 2015 - Sep. 2016
· *Propaganda Minister, School Psychological Association, Harbin Institute of Technology*

Web Developer Sep. 2012 - Jan. 2014
· *Web Developer(internship), Party Propaganda Department, Nanjing University of Technology*

PUBLICATION

- Jiajie Peng, Kun Bai, Xuequn Shang, Guohua Wang, **Hansheng Xue**, Shuilin Jin, Liang Cheng, Yadong Wang*, Jin Chen*, Predicting Disease-related Genes using Integrated Biomedical Networks, **BMC Genomics**, in press, 2016
- Jiajie Peng, **Hansheng Xue**, Yukai Shao, Xuequn Shang, Yadong Wang*, Jin Chen*, Measuring Phenotype Semantic Similarity using Human Phenotype Ontology. **BIBM2016**
- Jiajie Peng, **Hansheng Xue**, Yukai Shao, Xuequn Shang, Yadong Wang*, Jin Chen*, A novel method to measure the semantic similarity of HPO terms, **International Journal of Data Mining and Bioinformatics**, in press, 2017
- **Hansheng Xue**, Jiajie Peng, Bolin Chen, Qinghua Jiang, Xuequn Shang*, Yadong Wang*, PhenoSimWeb: a web tool for measuring and visualizing phenotype similarities using HPO, **IS-BRA2017** (Co-first)
- **Hansheng Xue**, Jiajie Peng, Bolin Chen, Qinghua Jiang, Xuequn Shang*, Yadong Wang*, An online tool for measuring and visualizing phenotype similarities using HPO, **BMC Bioinformatics**, in press, 2017 (Co-first)

PROJECT EXPERIENCE

Phenotype Semantic Similarity Project

**Cooperative with Prof. Jiajie Peng (Associate Professor, Northwestern Polytechnical University, China)*

The goal of this project is to propose a novel similarity measurement to calculate the phenotype similarity and develop an easy-to-use web applicaiton.

Part one: In this part, we propose a new similarity measure called PhenoSim. Our model includes a noise reduction component to model the noisy patient phenotype data, and a path-constrained Information Content-based method for phenotype semantics similarity measurements. PhenoSim has three steps. Firstly, constructs a phenotype network. Secondly, reduce the noise in a patients phenotype set using PageRank algorithm. Thirdly, compute the phenotype similarities by a novel path-constrained Information Content.

Part two: In this part, we develop an easy-to-use web tool, named PhenoSimWeb, which allows researches to conveniently input phenotypes, to measure phenotype similarities, and to visualize the result with an easy-to-use graphical interface. And PhenoSimWeb includes three main functional modules: calculate the pairwise similarities for the input phenotypes, calculate the gene or disease similarities by aggregating the similarities of phenotypes corresponding to the given genes or diseases, identify the most associated genes or diseases with the given phenotype set.

Clustering Biomedical Networks Project

**Cooperative with Prof. Jin Chen (Associate Professor, University of Kentucky, USA)*

This project sources from the National High Technology Research and Development Program (863Program) of China, Biological large data representation index, search and storage access technology. The goal of this project is to propose an improved semi-supervised graph clustering algorithm based on Deep Learning.

This biomedical network has massive nodes, edges and edge weight vectors, which we call it a vector-weighted graph. We consider the semi-supervised clustering algorithm to integrate the prior information into the algorithm to improve the clustering result. However, the computational complexity of spectral clustering is super quadratic to the number of nodes due to eigenvalue decomposition. And we consider to introduce deep learning framework into the semi-supervised graph clustering algorithm.

AWARD

- 2017 ISBRA2017 Travel Fellowship
- 2016 IEEE BIBM2016 Student Travel Award
- 2015 Jiangsu Province's Undergraduate Graduation Design Competition, First Prize
- 2014 Mathematical Contest in Modeling and Interdisciplinary Contest In Modeling (MCM/ICM) Contest, Meritorious Winner
- 2013 China Undergraduate Mathematical Contest in Modeling(CUMCM), Second Prize (Jiangsu Province)
- 2012 The 11th Jiangsu Province's Mathematics Competitions, First Prize
- 2011-2016 Second Prize Scholarship thrice, Third Prize Scholarship twice, Individual Scholarship twice

ACADEMIC EXPERIENCE

Journal Reviewer: IEEE/ACM Transactions on Computational Biology and Bioinformatics(TCBB)

TECHNICAL STRENGTHS

Computer Skills Python, Java, C/C++, MATLAB, Web, Keras, MySQL, Ubuntu