

HANSHENG XUE

(+61) 414-266-602 ◇ hansheng.xue@anu.edu.au ◇ <https://xuehansheng.github.io>

The Australian National University, R4.32 HN Bldg 145, Acton ACT 2601, Australia

RESEARCH INTERESTS

My current research includes machine learning and computational biology, with an emphasis on representation learning over graphs, combinatorial optimization and their applications in computational genomics, functional genomics, and multi-omics.

EDUCATION

The Australian National University

Ph.D. in Computer Science

Supervisor: Yu Lin, Vaibhav Rajan(NUS), and Lexing Xie.

Thesis: Representation Learning over Graphs in Genomic Analysis.

Canberra, Australia

Sep. 2019 - Oct. 2023

Harbin Institute of Technology

M.Eng. in Computer Science

Supervisor: Yadong Wang and Jiajie Peng.

Shenzhen, China

Sep. 2015 - Jan. 2018

Nanjing Tech University

B.M. in Electronic Commerce

Thesis: Outstanding Thesis Award, Top 1% in Jiangsu Province, China.

Nanjing, China

Sep. 2011 - Jun. 2015

SELECTED HONORS AND AWARDS

AAAI Student Scholarship	2022
ANU PhD Scholarship (International)	2019
APBC Travel Fellowship	2019
ISBRA Travel Fellowship	2017
IEEE BIBM Student Travel Fellowship	2016
First Prize, Bachelor's Degree Thesis Competition of Jiangsu Province, China (Top 1%)	2015
Meritorious Winner, MCM/ICM: Mathematical Contest in Modeling and Interdisciplinary Contest in Modeling (Top 10%)	2014
First Prize, The 11th Jiangsu Province Mathematics Competition, China (Top 10%)	2012

INTERNSHIP AND TEACHING EXPERIENCE

Research Assistant , School of Computing, National University of Singapore, Singapore. Supervisor: Vaibhav Rajan.	Nov. 2023 - Now
Guest Lecturer for Database Systems, Shandong University (ANU/SDUW Joint Program), China.	Autumn 2023
Visiting Ph.D. Student , School of Computing, National University of Singapore, Singapore. Supervisor: Vaibhav Rajan.	May 2023 - Jun. 2023
Tutor for Statistics Machine Learning, Australian National University, Canberra, Australia. Supervisor: Lexing Xie and Yuan-Sen Ting.	Feb. 2023 - Jun. 2023
Visiting Ph.D. Student , Department of Chemistry, Fudan University, Shanghai, China. Supervisor: Liang Qiao.	Mar. 2021 - Sep. 2021
Research Intern , Alibaba Group, Hangzhou, China. Supervisor: Luwei Yang and Wen Jiang.	May 2020 - Feb. 2021
Research Assistant , Northwestern Polytechnical University, Xi'an, China. Supervisor: Jiajie Peng and Xuequn Shang.	Mar. 2018 - Aug. 2019
Teaching Assistant for Data Mining, Harbin Institute of Technology, Shenzhen, China. Supervisor: Yunming Ye.	Sep. 2016 - Jan. 2017

PUBLICATIONS

(†: Co-first author, ★: Corresponding author.)

[Peer-Reviewed Conference Papers]:

[C.1] **Hansheng Xue**, Vaibhav Rajan, and Yu Lin, "Graph Coloring via Neural Networks for Haplotype Assembly and Viral Quasispecies Reconstruction", *NeurIPS'22*: Thirty-sixth Conference on Neural Information Processing Systems, 2022. [Full paper, Acceptance rate of 25.6%.]

[C.2] **Hansheng Xue**, Vijini Mallawaarachchi, Yujia Zhang, Vaibhav Rajan, and Yu Lin, "RepBin: Constraint-Based Graph Representation Learning for Metagenomic Binning", *AAAI'22*: The Thirty-Sixth AAAI Conference on Artificial Intelligence,

2022. 10.1609/aaai.v36i4.20388 [Full paper, Acceptance rate of 15%, Oral Presentation (<5%).]

[C.3] **Hansheng Xue**, Luwei Yang, Vaibhav Rajan, Wen Jiang, Yi Wei, and Yu Lin, “Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks”, *WWW’21*: The 30th International World Wide Web Conference, 2021. 10.1145/3442381.3449954 [Full paper, Acceptance rate of 20.6%.]

[C.4] **Hansheng Xue†**, Luwei Yang†, Wen Jiang, Yi Wei, Yi Hu, and Yu Lin, “Modeling Dynamic Heterogeneous Network for Link Prediction using Hierarchical Attention with Temporal RNN”, *ECML-PKDD’20*: The European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Database, 2020. 10.1007/978-3-030-67658-2_17 [Full paper, Acceptance rate of 19%.]

[C.5] **Hansheng Xue**, Jiajie Peng, Jiying Li, and Xuequn Shang, “Integrating Multi-Network Topology via Deep Semi-supervised Node Embedding”, *CIKM’19*: The 28th ACM International Conference on Information and Knowledge Management, 2019. 10.1145/3357384.3358164 [Short paper.]

[C.6] Jiajie Peng, **Hansheng Xue**, Yukai Shao, Xuequn Shang, Yadong Wang, and Jin Chen, “Measuring Phenotype Semantic Similarity using Human Phenotype Ontology”, *BIBM’16*: The IEEE International Conference on Bioinformatics and Biomedicine, 2016. 10.1109/BIBM.2016.7822617 [Short paper.]

[C.7] **Hansheng Xue**, Vijini Mallawaarachchi, Yu Lin, Lexing Xie, and Vaibhav Rajan, “Metagenomic Binning using Graph Neural Networks”, *ISMB/ECCB’23 Microbiome*: The 31st Conference on Intelligent Systems for Molecular Biology and the 22nd European Conference on Computational Biology, 2023. [Abstract, Oral and Poster.]

[C.8] **Hansheng Xue**, Jiajie Peng, and Xuequn Shang, “Towards Gene Function Prediction via Multi-Network Representation Learning”, *AAAI’19*: The Thirty-Third AAAI Conference on Artificial Intelligence, 2019. 10.1609/aaai.v33i01.330110069 [Student abstract.]

[C.9] Jiajie Peng, Guilin Lu, **Hansheng Xue**, Tao Wang, Xuequn Shang, “TSGOE: A Web Tool for Tissue-specific Gene Ontology Enrichment”, *BIBM’18 BiOK Workshop*: The IEEE International Conference on Bioinformatics and Biomedicine, 2018. 10.1109/BIBM.2018.8621204 [Workshop.]

[Peer-Reviewed Journal Papers]:

[J.1] Jiajie Peng†, **Hansheng Xue†**, Zhongyu Wei, Idil Tuncali, Jianye Hao, and Xuequn Shang, “Integrating Multi-network Topology for Gene Function Prediction using Deep Neural Networks”, *Briefings in Bioinformatics*, 2020. 10.1093/bib/bbaa036

[J.2] Haijie Liu, Jiaojiao Guan, He Li, Zhijie Bao, Qingmei Wang, Xun Luo, and **Hansheng Xue★**, “Predicting Multiple Sclerosis Disease Genes based on Network Representation Learning”, *Frontiers in Genetics*, 2020.10.3389/fgene.2020.00328

[J.3] **Hansheng Xue**, Jiajie Peng, and Xuequn Shang, “Predicting Disease-related Phenotypes using an Integrated Phenotype Similarity Measurement based on HPO”, *BMC Systems Biology*, 2019. 10.1186/s12918-019-0697-8

[J.4] Jiajie Peng, Guilin Lu, **Hansheng Xue**, Tao Wang, and Xuequn Shang, “TS-GOE: A Web Tool for Tissue specific Gene Set Enrichment Analysis based on Gene Ontology”, *BMC Bioinformatics*, 2019. 10.1186/s12859-019-3125-6

[J.5] Jiajie Peng†, **Hansheng Xue†**, Weiwei Hui, Junya Lu, Bolin Chen, Qinghua Jiang, Xuequn Shang, and Yadong Wang, “An Online Tool for Measuring and Visualizing Phenotype Similarities using HPO”, *BMC Genomics*, 2018. 10.1186/s12864-018-4927-z

[J.6] Jiajie Peng, **Hansheng Xue**, Yukai Shao, Xuequn Shang, Yadong Wang, and Jin Chen, “A Novel Method to Measure the Semantic Similarity of HPO Terms”, *International Journal of Data Mining and Bioinformatics (IJDMB)*, 2017. 10.1504/IJDMB.2017.084268

[J.7] Jiajie Peng, Kun Bai, Xuequn Shang, Guohua Wang, **Hansheng Xue**, Shuilin Jin, Liang Cheng, Yadong Wang, and Jin Chen. “Predicting Disease-related Genes using Integrated Biomedical Networks”, *BMC Genomics*, 2017. 10.1186/s12864-016-3263-4

PROFESSIONAL SERVICE

Journal Reviewer: Briefings in Bioinformatics(x4), IEEE/ACM TCBB(x1), BMC Bioinformatics(x1), PLOS ONE(x1), Frontiers in Neuroscience(x1).

Program Committee/Conference Reviewer: AAAI’24/23, AISTATS’24, NeurIPS-TGL’23, IJCAI’23, RECOMB-CG’21, ECML-PKDD’20, IEEE BIBM-BiOK’21/20/19.

INVITED TALKS AND PRESENTATIONS

1. “Metagenomic Binning using Graph Neural Networks”, ISMB/ECCB’23 Microbiome, Lyon, France, July 2023.
2. “RepBin: Constraint-Based Graph Representation Learning for Metagenomic Binning”, AAAI’22, Virtual, Feb. 2022.
3. “Network Embedding in Computational Biology”, Northwestern Polytechnical University, Xi’an, China, July 2021.
4. “Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks”, WWW’21, Virtual, April 2021.
5. “Predicting Disease-related Phenotypes using an Integrated Phenotype Similarity Measurement based on HPO”, APBC’19, Wuhan, China, Jan. 2019.

6. “An Online Tool for Measuring and Visualizing Phenotype Similarities using HPO”, ISBRA’17, Hawaii, USA, May 2017.
7. “Measuring Phenotype Semantic Similarity using Human Phenotype Ontology”, BIBM’16, Shenzhen, China, Dec. 2016.
8. “Predicting Disease-related Genes using Integrated Biomedical Networks”, GIW’16, Shanghai, China, Oct. 2016.

REFEREES

Referees are available upon request.