HANSHENG XUE

(+65) 8300-3398 ◇ hansheng.xh@gmail.com ◇ https://xuehansheng.github.io

The National University of Singapore, COM2-04-04, 13 Computing Drive, Singapore 117417

EDUCATION

The Australian National University — Canberra, Australia
Ph.D. in Computer Science — Sep. 2019 - May 2024
Supervisor: Yu Lin, Vaibhav Rajan (NUS), and Lexing Xie.
Thesis: Graph Representation Learning for Structured Data and Genomic Analysis.

Harbin Institute of Technology — Shenzhen, China
M.Eng. in Computer Science — Sep. 2015 - Jan. 2018
Supervisor: Yadong Wang and Jiajie Peng.

Nanjing Tech University — Nanjing, China
B.M. in Electronic Commerce — Sep. 2011 - Jun. 2015
Thesis: Outstanding Thesis Award, Top 1% in Jiangsu Province, China.

RESEARCH AND INDUSTRY EXPERIENCE

Research Assistant, School of Computing, National University of Singapore, Singapore. — Nov. 2023 - Jun. 2024
Supervisor: Vaibhav Rajan.

Research Intern, Alibaba Group, Hangzhou, China. — May 2020 - Feb. 2021
Supervisor: Luwei Yang and Wen Jiang.

PUBLICATIONS

(†: Co-first author, ⋆: Corresponding author.) [Google Scholar, DBLP]

[C.1] **Hansheng Xue**, Vijini Mallawaarachchi, Lexing Xie, and Vaibhav Rajan, "Encoding Unitig-level Assembly Graphs with Heterophilous Constraints for Metagenomic Contigs Binning", *ICLR'24*: Twelfth International Conference on Learning Representations, 2024. [Full paper, Acceptance rate of 31%.]

[C.2] Aishwarya Jayagopal, **Hansheng Xue**, Ziyang He, Robert John Walsh, Krishna Kumar Hariprasannan, David Shao Peng Tan, Tuan Zea Tan, Jason J. Pitt, Anand D Jeyasekharan, and Vaibhav Rajan, "Personalised Drug Identifier for Cancer Treatment with Transformers using Auxiliary Information", *KDD'24*: 30th ACM SIGKDD Conference on Knowledge Discovery and Data Mining, 2024. [Applied Data Science Track, Acceptance rate of 20%.]

[C.3] **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.4] **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. [Full paper, Acceptance rate of 15%, Oral Presentation (<5%).]

[C.5] **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. [Full paper, Acceptance rate of 20.6%.]

[C.6] **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. [Full paper, Acceptance rate of 19%.]

[C.7] **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. [Short paper.]

[C.8] 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. [Short paper.]

[C.9] **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. [Student abstract.]

[C.10] 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. [Workshop.]

[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*, 2021.

[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.

[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.

[J.4] Jiajie Peng, Guilin Lu, **Hansheng Xue**, Tao Wang, and Xuequn Shang, "TS-GOEA: A Web Tool for Tissue specific Gene Set Enrichment Analysis based on Gene Ontology", *BMC Bioinformatics*, 2019.

[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.

[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.

[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 Netoworks", *BMC Genomics*, 2017.

PROFESSIONAL SERVICE

Journal Reviewer: Briefings in Bioinformatics(x4), BMC Genomics(x2), BMC Bioinformatics(x2), Artificial Intelligence Review(x1), IEEE/ACM TCBB(x1), BioData Mining(x1), PLOS ONE(x1), Frontiers in Neuroscience(x1), International Journal of Machine Learning and Cybernetics(x1).

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

TEACHING EXPERIENCE

Guest Lecturer for Database Systems, Shandong University (ANU/SDUW Joint Program), China. Autumn 2023
Tutor for Statistics Machine Learning, Australian National University, Canberra, Australia. Feb. 2023 - Jun. 2023

STUDENT MENTORING

Divyam Pahuja, (co-with Qing Wang), 'Multi-View Graph Representation Learning', Undergrad. at ANU, 02/2024 - Present.
Wei Zhou, (co-with Yu Lin), 'Network Embedding for Metagenomics Binning', Undergrad. at ANU, 02/2022 - 11/2022.
Fenghua Chen, (co-with Yu Lin), 'Representation Learning on Dynamic Graphs', Undergrad. at ANU, 02/2022 - 06/2022.

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

INVITED TALKS AND POSTER PRESENTATIONS

1. "Encoding Unitig-level Assembly Graphs with Heterophilous Constraints for Metagenomic Contigs Binning", ICLR'24, Vienna Austria, May 2024.
2. "Metagenomic Binning using Graph Neural Networks", ISMB/ECCB'23 Microbiome, Lyon, France, Jul. 2023.
3. "Graph Coloring via Neural Networks for Haplotype Assembly and Viral Quasispecies Reconstruction", NeurIPS'22, Virtual, Dec. 2022.
4. "RepBin: Constraint-Based Graph Representation Learning for Metagenomic Binning", AAAI'22, Virtual, Feb. 2022.
5. "Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks", WWW'21,Virtual, Apr. 2021.
6. "Predicting Disease-related Phenotypes using an Integrated Phenotype Similarity Measurement based on HPO", APBC'19, Wuhan, China, Jan. 2019.
7. "An Online Tool for Measuring and Visualizing Phenotype Similarities using HPO", ISBRA'17, Hawaii, USA, May 2017.
8. "Measuring Phenotype Semantic Similarity using Human Phenotype Ontology", BIBM'16, Shenzhen, China, Dec. 2016.
9. "Predicting Disease-related Genes using Integrated Biomedical Networks", GIW'16, Shanghai, China, Oct. 2016.

REFEREES

Referees are available upon request.