

# RENMING (REMY) LIU

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## RESEARCH INTERESTS

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- Network Biology
- Graph Representation Learning
- AI for Health & Science
- Single-Cell Analysis

## EDUCATION

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<b>Michigan State University</b> Ph.D., Computational Mathematics, Science and Engineering	09/2019 - 05/2024
<b>Michigan State University</b> B.S., Chemical Engineering Concentration in Biochemical Engineering Minor in Computer Science	09/2014 - 06/2018

## PROFESSIONAL EXPERIENCE

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<b>Post-doctoral Fellow</b> Ray and Stephanie Lane Computational Biology Department. Carnegie Mellon University. Topic: Machine learning methods and software for single-cell epigenomics.	06/2024 - present
<b>Ph.D. Student and Research Assistant</b> Department of Computational Mathematics, Science and Engineering. Michigan State University. Topic: Biomedical and Molecular Interaction Networks, Graph Representation Learning, Spectral Graph Theory.	09/2019 - 05/2024
<b>Research Assistant</b> Department of Biomedical Informatics. Colorado University Anschutz Medical Campus. Topic: Context-specific biological network embeddings.	06/2023 - 08/2023
<b>Research Assistant</b> Department of Chemical Engineering and Materials Science. Michigan State University. Topic: Thermodynamic modeling of associating systems including alcohols and acetic acids.	05/2017 - 08/2019
<b>Professional Aide</b> Department of Computational Mathematics, Science and Engineering. Michigan State University. Topic: Human gene function prediction using ML with biological networks.	09/2018 - 08/2019

## HONORS & AWARDS

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<b>Silver Medal in Kaggle</b> NeurIPS Multimodal Single-Cell Integration Across Time, Individuals, and Batches.	2022
<b>Outstanding Graduate Student Award</b> Awarded to the most outstanding doctoral student in each program.	2022
<b>Raymond P. and Marie M. Ginther Fellowship</b> Awarded to outstanding incoming Ph.D. students to the CMSE program at MSU.	2019
<b>Maurice G. and Sara V. Larian Scholarship</b>	2017

## OPEN-SOURCE PROJECTS

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<b>OB NB</b> (sole developer)	2023
A Python toolkit for benchmarking biomedical networks using gene annotation resources.	
<b>DANCE</b> (core developer)	2022
An extensive deep learning toolkit for single-cell (multi-)omics data.	
<b>PyGenePlexus</b>	2022
A network-based gene classification service using ML with gene interaction network features.	
<b>PecanPy</b> (sole developer)	2020
A memory efficient and parallel Python implementation of node2vec with an improved version <i>node2vec+</i> for weighted graph.	

## PUBLICATIONS

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*\*indicates (co-)first author*

### Journal and Conference Papers

- Graph Positional and Structural Encoder  
S. Cantürk\*, **R. Liu\***, O. Lapointe-Gagné, V. Létourneau, G. Wolf, D. Beaini, L. Rampásek  
*International Conference on Machine Learning (ICML)*, 2024
- DANCE: A Deep Learning Library and Benchmark Platform for Single-cell Analysis  
J. Ding\*, H. Wen\*, W. Tang\*, **R. Liu\***, Z. Li, J. Venegas, R. Su, D. Molho, W. Jin, W. Zou, Y. Wang, R. Yang, Y. Xie, J. Tang  
*Genome Biology*, 2024
- Deep Learning in Single-Cell Analysis  
D. Molho\*, J. Ding, Z. Li, H. Wen, W. Tang, Y. Wang, J. Venegas, W. Jin, **R. Liu**, R. Su, P. Danaher, R. Yang, Y. Lei, Y. Xie, J. Tang  
*ACM Transactions on Intelligent Systems and Technology*, 2024
- Joint representation of molecular networks from multiple species improves gene classification  
C.A. Mancuso\*, K.A. Johnson, **R. Liu**, A. Krishnan  
*PLOS Computational Biology*, 2024
- SpatialCTD: a large-scale TME spatial transcriptomic dataset to evaluate cell type deconvolution for immuno-oncology  
J. Ding\*, J. Venegas, Q. Lu, Y. Wang, W. Jin, H. Wen, **R. Liu**, W. Tang, Z. Li, W. Zuo, Y. Chang, Y. Lei, P. Danaher, Y. Xie, J. Tang  
*Journal of Computational Biology*, 2024
- Open Biomedical Network Benchmark: A Python Toolkit for Generating Benchmarking Datasets with Biomedical Networks  
**R. Liu\***, A. Krishnan  
*Machine Learning in Computational Biology (MLCB)*. PMLR, 2023
- Single-Cell Multimodal Prediction via Transformers  
W. Tang\*, H. Wen\*, **R. Liu\***, J. Ding, W. Jin, Y. Xie, H. Liu, J. Tang  
*ACM International Conference on Information & Knowledge Management (CIKM)*, 2023
- Accurately modeling biased random walks on weighted networks using *node2vec+*  
**R. Liu\***, M.J. Hirn, A. Krishnan  
*Bioinformatics*, 2023

- PyGenePlexus: A Python package for gene discovery using network-based machine learning  
C.A. Mancuso\*, **R. Liu**, A. Krishnan  
*Bioinformatics*, 2023
- Taxonomy of Benchmarks in Graph Representation Learning  
**R. Liu**\*, S. Cantürk\*, F. Wnkel, S. McGuire, X. Wang, A. Little, L. O’Bray, M. Perlmutter, B. Rieck, M.J. Hirn, G. Wolf, L. Rampásek  
*Learning on Graph (LoG) Conference*, 2022
- GenePlexus: A web-server for gene discovery using network-based machine learning  
C.A. Mancuso\*, P.S. Bills, D. Krum, J. Newsted, **R. Liu**, A. Krishnan  
*Nucleic Acids Research*, 2022
- Applications of an Association Activity Coefficient Model, NRTL-PA, to Alcohol-Containing Mixtures  
A.M. Bala\*, **R. Liu**, L. Peereboom, C.T. Lira  
*Industrial & Engineering Chemistry Research*, 2022
- PecanPy: a fast, efficient and parallelized Python implementation of node2vec  
**R. Liu**\*, A. Krishnan  
*Bioinformatics*, 2021
- Supervised Learning is an accurate method for network-based gene classification  
**R. Liu**\*, C.A. Mancuso\*, A. Yannakopoulos, K.A. Johnson, A. Krishnan  
*Bioinformatics*, 2020

## Preprints and Submissions

- A General Single-Cell Analysis Framework via Conditional Diffusion Generative Models  
W. Tang\*, **R. Liu**\*, H. Wen, X. Dai, J. Ding, H. Li, W. Fan, Y. Xie, J. Tang  
*bioRxiv*
- CONE: COntext Specific Network Embedding via Contextualized Graph Attention  
**R. Liu**\*, H. Yuan\*, K.A. Johnson, A. Krishnan  
*Submitted to MLCB’24*
- Memory-Augmented Pretraining for Single-Cell Multi-Omic Analysis  
X. Dai\*, H. Wen, W. Tang, **R. Liu**, Y. Wu, J. Ding, W. Jin, L. Yu, Y. Xie, J. Tang  
*Submitted to IDCM’24*
- Single Cells Are Spatial Tokens: Transformers for Spatial Transcriptomic Data Denoising  
H. Wen\*, W. Tang, W. Jin, J. Ding, **R. Liu**, F. Shi, Y. Xie, J. Tang  
*arXiv*

## PRESENTATIONS

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### Invited Talks

- Professor Trey Ideker’s lab at University of California San Diego 02/2024
- Professor Jian Ma’s lab at Carnegie Mellon University 02/2024
- Learning on Graphs (LoG) local meetup at Mid-North US 01/2024

### Oral Presentations

- Systematic study of human diseases using graph signal processing 12/2022  
*ISCB-Rocky’22*

- Taxonomy of Benchmarks in Graph Representation Learning 12/2022  
*LoG'22*
- Understanding dataset characteristics via graph diffusion 09/2022  
*SIAM-MDS'22*
- Accurately identify disease genes and contexts using context-specific network embeddings 07/2022  
*ISMB'22*
- Accurate network-based gene classification with ultra-fast context-specific node embeddings 05/2021  
*GLBIO'21*

## Posters

- Open Biomedical Network Benchmark: A Python Toolkit for Generating Benchmarking Datasets with Biomedical Networks 11/2023  
*MLCB'23*
- A Python Toolkit for Generating Benchmarking Datasets for Machine Learning with Biological Networks 03/2023  
*CSHL-NetBio'23*
- PecanPy: a fast, efficient, and parallelized Python implementation for node2vec 07/2020  
*ISMB'20*
- Supervised-learning is an accurate method for network-based gene classification 08/2019  
*CoCoH'19*
- Machine learning outperforms label propagation for network-based gene classification 03/2019  
*CSHL-NetBio'19*

## SERVICES

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### Teaching

- Teaching Assistant for CMSE 201: Introduction to Computational Modeling 2020  
Lecture assistant, office hours, and grading.
- Grader for CHE 804: Foundations in Chemical Engineering 2019
- Grader for CHE 321: Thermodynamics for Chemical Engineering 2019

### Mentoring

- Keenan Manpearl (she/her) 03/2023 - Present  
Ph.D. student at University of Colorado Anschutz Medical Campus  
Ongoing Project: Leveraging ontology embeddings to enable transfer learning for gene classification.

### Conference & Workshop Program Chairs

- The Web Conference 2024 Graph Foundation Model Workshop 2024  
Program Chair

### Journal and Conference Paper Reviews

- Machine Learning in Computational Biology (MLCB) 2024
- NeurIPS Datasets and Benchmarks Track 2024
- Transactions on Knowledge and Data Engineering (TKDE) 2023 - 2024
- Transactions on Knowledge Discovery from Data (TKDD) 2023 - 2024

- F1000 Research 2023
- Cell Systems 2022
- Nature Computational Science 2022
- Bioinformatics 2021
- eLife 2019