

TIANCI SONG

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SUMMARY

Ph.D. in Computer Science with over eight years of research experience in ML/AI, specializing in representation learning, tensor modeling, deep learning, and graph neural networks. Experienced in developing scalable and interpretable algorithms for high-dimensional, multimodal data. One year of industry experience implementing ML models in production-like clinical settings and leading cross-functional collaborations. Author of more than ten peer-reviewed publications, including high-impact journals and top venues in computational biology and bioinformatics. Passionate about advancing generative AI, foundation models, and multimodal learning to tackle complex real-world challenges.

EXPERTISE

ML/AI: Deep learning, tensor modeling, representation learning, contrastive learning, graph neural networks, transformers, generative models, multimodal models, foundation models, LLM, and multi-agent systems.
Applications: Spatial/Single-cell transcriptomics, multi-omics integration, digital pathology, biomedical imaging, drug discovery.
Programming/Framework: Python, R, C/C++, Matlab, PyTorch, TensorFlow, Tensorly, Numpy, Pandas, scikit-learn, JAX, Matplotlib, Tidyverse.
Tool/Platform: Unix/Linux, Docker/Singularity, Git, LaTeX, high-performance clusters (Slurm), and cloud computing platforms (AWS, Azure, Google Clouds)

EDUCATION

Ph.D. in Computer Science at University of Minnesota, Twin Cities	Sep, 2018 - Aug, 2025
M.E. in Computer Science & Technology at Jilin University	Sep, 2014 - Jun, 2017
B.S. in Computer Science & Technology at Jilin University	Sep, 2010 - Jun, 2014

EXPERIENCES

Machine Learning Scientist (Contractor) at Genentech , <i>South San Francisco, CA</i>	Sep, 2025 - Now
Representation Learning; Tensor Decomposition; Deep Learning; Knowledge-based Regularization	
Led the development of scalable tensor decomposition models for high-dimensional perturbation single-cell datasets of colon cancer, learning structured latent representations with prior knowledge across diverse experimental conditions, and enabling the discovery of shared and condition-specific structure.	
Research Intern at NEC Labs America , <i>Princeton, NJ</i> (three separate internships)	2023 - 2025
Representation Learning; Graph Neural Networks; Foundation Models; Generative Models; Transformers; Deep Learning; Predictive Modeling	
- Developed an adaptive graph neural network with variational optimization to learn task-dependent graph partitions and representations, improving by 13% prediction accuracy over the best baseline for spatial gene expression prediction from histopathology images. Demonstrated that learned representations capture tumor microenvironment structure in cancers. Work accepted as an oral presentation at ECCB 2024 and published in Bioinformatics. - Extended GNN-based methods to predict compartment-level gene expression to support immunotherapy efficacy studies in triple-negative breast cancer, enabling downstream regression models that improved prognosis accuracy by 44% over the best baseline. Identified predictive biomarkers with translational relevance. Work presented as a poster at AACR 2025.	
Research Assistant at University of Minnesota, Twin Cities , <i>Minneapolis, MN</i>	Sep, 2018 - Aug, 2025

Representation Learning; Tensor Decomposition; Spatial Regularization; Knowledge-based Regularization; Multimodal Model; Contrastive Learning; Deep Learning; LLM; Multi-agent system; Data Imputation

- Proposed a line of graph-guided tensor decomposition models to impute missing gene expression in spatial transcriptomics, improving prediction accuracy by 40% and the accuracy of spatial domain detection based on imputed gene expression by 22% over SOTA methods. Demonstrated robustness and scalability across various datasets. Works published in Nature Communications, Bioinformatics, and PLoS Computational Biology.
- Developed a graph-regularized deep clustering framework for structured representation learning, improving clustering quality under task-specific metrics and enabling interpretable discovery of latent structure in complex spatial gene expression data. Work published in Bioinformatics.
- Co-developed a multi-agent LLM system integrating ML models, knowledge graphs, and literature evidence for drug–target interaction prediction, achieving a 45% F1 improvement over baseline with transparent, interpretable reasoning. Work published as a poster at ICLR 2025 and submitted to Scientific Reports.

SELECTED PUBLICATION

1. **Tianci Song**, Quoc Nguyen, Charles Broadbent, and Rui Kuang. *Reconstructing 3D Spatial Structures of RNA-Tomography Transcriptomes by Collapsed Tensor Factorization*. **Under review with PLoS computational biology**
2. Yoshitaka Inoue, **Tianci Song**, Xinling Wang, Augustin Luna, Tianfan Fu. *DrugAgent: Multi-Agent Large Language Model-Based Reasoning for Drug-Target Interaction Prediction*. **ICLR 2025 Workshop on Machine Learning for Genomics Explorations (MLGenX) (2025) Under review with Scientific Reports**
3. **Tianci Song**, Eric Cosatto, Gaoyuan Wang, Martin Renqiang Min, Rui Kuang, Mark Gerstein, and Jonathan Warrell. *Predicting Spatially Resolved Gene Expression via Tissue Morphology using Graph Neural Networks with Adaptive Spatial Graphs*. **The 23rd European Conference on Computational Biology (ECCB 2024) (2024)**
4. Charles Broadbent, **Tianci Song**, and Rui Kuang. *Deciphering High-order Structures in Spatial Transcriptomes with Graph-guided Tucker Decomposition*. **The 32nd International Conference on Intelligent Systems for Molecular Biology (ISMB 2024) (2024)**
5. **Tianci Song**, Charles Broadbent, and Rui Kuang. *GNTD: Reconstructing Spatial Transcriptomes with Graph-guided Neural Tensor Decomposition Informed by Spatial and Functional Relations*. **Nature communications (2023)**
6. **Tianci Song**, Kathleen K Markham, Zhuliu Li, Kristen E Muller, Kathleen Greenham, and Rui Kuang. *Detecting Spatially Co-expressed Gene Clusters with Functional Coherence by Graph-regularized Convolutional Neural Network*. **Bioinformatics (2022)**
7. Zhuliu Li, **Tianci Song**, Jeongsik Yong, and Rui Kuang. *Imputation of Spatially-resolved Transcriptomes by Graph-regularized Tensor Completion*. **PLoS computational biology (2021)**