

TIANCI SONG

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EDUCATION

Ph.D. in Computer Science at University of Minnesota Sep, 2018 - Aug, 2025
 Advisor: Dr. Rui Kuang
 Thesis: Machine Learning Methods for Reconstructing Spatially Resolved Transcriptomes

M.E. in Computer Science & Technology at Jilin University Sep, 2014 - Jun, 2017
 Advisor: Dr. Yanchun Liang and Dr. Wei Du

B.S. in Computer Science & Technology at Jilin University Sep, 2010 - Jun, 2014

RESEARCH INTEREST

- Design machine learning models for knowledge generalization and representation
- Develop computational models for single-cell and spatial transcriptomics data analysis
- Develop computational models for heterogeneous biomedical data integration

WORK EXPERIENCES

Machine Learning Scientist at [Genentech](#), South San Francisco, CA Sep, 2025 - Now

- Lead development of tensor decomposition models for genome-wide perturbation single-cell datasets, enabling discovery of new biological insights for colon cancer.

Research Assistant at [Kuang Lab](#), Minneapolis, MN Sep, 2018 - Aug, 2025

- Proposed linear and nonlinear tensor completion models guided by both spatial and functional relations to impute missing gene expression signals of in-situ capturing based 2D spatial transcriptomics data to facilitate the downstream analyses;
- Proposed a deep clustering model to group genes based on their spatial expression patterns as well as known functional relations encoded in knowledge graph to reveal gene activities in the underlying morphological context for 2D spatial transcriptomics data;
- Proposed a tensor decomposition model informed by spatial and functional relations to reconstruct 3D gene expression from tomography based 1D spatial transcriptomics data to study gene expression patterns in 3D space for embryonic development.

Research Intern at [NEC Labs America](#), Princeton, NJ Feb, 2025 - May, 2025

- Proposed a graph neural network based model to infer single-cell level spatial gene expression from histopathological images (*Worked with Dr. Jonathan Warrell and Dr. Eric Cosatto*).

Research Intern at [NEC Labs America](#), Princeton, NJ July, 2024 - Oct, 2024

- Proposed a graph neural network based model to learn compartment or cellular level features from digital pathology images associated with bulk gene expression to predict immunotherapy efficacy (*Worked with Dr. Jonathan Warrell and Dr. Eric Cosatto*).

Research Intern at [NEC Labs America](#), Princeton, NJ May, 2023 - Sep, 2023

- Proposed a graph neural network-based model to predict spatial resolved transcriptomics data from histopathological images (*Worked with Dr. Jonathan Warrell*).

Research Assistant at [Neuro Trauma Research Lab](#), Minneapolis, MN Jun, 2020 - Dec, 2021

- Developed an ensemble classification model to identify the severity of brain injury based on both features from deep learning models on CT images and serum biomarker data (*Worked with Dr. Uzma Samadani*).

Research Intern at [Infervision](#), Beijing

Mar, 2018 - Aug, 2018

- Developed capsule network based models for lung nodule detection based on 2D CT images and intracerebral hemorrhage volume measurement based on 3D CT images (*Worked with Dr. Rongguo Zhang*).

Research Assistant at [Computational System Biology Lab](#), Athens, GA

Oct, 2015 - Jan, 2017

- Investigated cell-type specific contributions to breast cancer based on multi-omics data with dictionary learning (*Worked with Dr. Sha Cao*);
- Explored the competitive relationship between DNA methylation, nucleotide synthesis, and anti-oxidation in cancers with dynamic modeling on multi-omics data (*Worked with Dr. Sha Cao and Dr. Ying Xu*).

Research Assistant at [Machine Learning Lab](#), Changchun, Jilin

Sep, 2013 - Jun, 2015

- Developed a computational model with multiple kernel learning to integrate multi-omics data to improve breast cancer grade classification (*Worked with Dr. Wei Du and Dr. Yanchun Liang*);
- Developed a computational model with the local principal curve to quantify the abnormalities of altered biological pathways or processes in pan-cancers based on their bulk gene expression and demonstrated its potential in clinical applications (*Worked with Dr. Wei Du and Dr. Yanchun Liang*).

FULL PUBLICATION

JOURNAL AND CONFERENCE PAPERS

1. 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) [[Paper](#)] [[Code](#)]
2. **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*. **Bioinformatics** (2024) (*The 23rd European Conference on Computational Biology (ECCB 2024)*, Accept rate: 12%) [[Paper](#)] [[Code](#)]
3. Charles Broadbent, **Tianci Song**, and Rui Kuang. *Deciphering High-order Structures in Spatial Transcriptomes with Graph-guided Tucker Decomposition*. **Bioinformatics** (2024) (*The 32nd International Conference on Intelligent Systems for Molecular Biology (ISMB 2024)*, Accept rate: 16%, 🏆 Outstanding Student Paper) [[Paper](#)] [[Code](#)]
4. **Tianci Song**, Charles Broadbent, and Rui Kuang. *GNTD: Reconstructing Spatial Transcriptomes with Graph-guided Neural Tensor Decomposition Informed by Spatial and Functional Relations*. **Nature communication** (2023) [[Paper](#)] [[Code](#)]
5. Kai Tian, Jiefeng Zeng, **Tianci Song**, Zhuliu Li, Asenso Evans, and Jiuhaio Li. *Tomato Leaf Diseases Recognition based on Deep Convolutional Neural Networks*. **Journal of Agricultural Engineering** (2023) [[Paper](#)]
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) [[Paper](#)] [[Code](#)]
7. Zhuliu Li, **Tianci Song**, Jeongsik Yong, and Rui Kuang. *Imputation of Spatially-resolved Transcriptomes by Graph-regularized Tensor Completion*. **PLoS computational biology** (2021) [[Paper](#)] [[Code](#)]
8. Raphael Petegrosso, **Tianci Song**, and Rui Kuang. *Hierarchical Canonical Correlation Analysis Reveals Phenotype, Genotype, and Geoclimate Associations in Plants*. **Plant Phenomics** (2021) [[Paper](#)] [[Code](#)]
9. Ying Song, **Tianci Song**, and Rui Kuang. *Path Segmentation for Movement Trajectories with Irregular Sampling Frequency using Space-time Interpolation and Density-based Spatial Clustering*. **Transactions in GIS** (2019) [[Paper](#)]

10. Mingxin Tao, **Tianci Song**, Wei Du, Siyu Han, Chunman Zuo, Ying Li, Yan Wang, and Zekun Yang. *Classifying Breast Cancer Subtypes using Multiple Kernel Learning based on Omics Data*. **Genes** (2019) [[Paper](#)]
11. Sen Liang, Rongguo Zhang, Dayang Liang, **Tianci Song**, Tao Ai, Chen Xia, Liming Xia, and Yan Wang. *Multimodal 3D DenseNet for IDH Genotype Prediction in Gliomas*. **Genes** (2018) [[Paper](#)]
12. Sha Cao, Yi Zhou, Yue Wu, **Tianci Song**, Burair Alsaihati, and Ying Xu. *Transcription Regulation by DNA Methylation under Stressful Conditions in Human Cancer*. **Scientific Reports** (2017) [[Paper](#)]
13. **Tianci Song**, Sha Cao, Tao Sheng, Sen Liang, Wei Du, and Yanchun Liang. *A Novel Unsupervised Algorithm for Biological Process-based Analysis on Cancer*. **Scientific Reports** (2017) [[Paper](#)]
14. **Tianci Song**, Yanchun Liang, Zhongbo Cao, Wei Du, and Ying Li. *Computational Analysis of Specific microRNA Biomarkers for Noninvasive Early Cancer Detection*. **BioMed Research International** (2017) [[Paper](#)]
15. Wei Du, Zhongbo Cao, **Tianci Song**, Ying Li, and Yanchun Liang. *A Feature Selection Method based on Multiple Kernel Learning with Expression Profiles of Different Types*. **BioData Mining** (2017) [[Paper](#)]
16. **Tianci Song**, Yan Wang, Wei Du, Sha Cao, Yuan Tian, and Yanchun Liang. *The Method for Breast Cancer Grade Prediction and Pathway Analysis based on Improved Multiple Kernel Learning*. **Journal of Bioinformatics and Computational Biology** (2017) [[Paper](#)]

PREPRINTS

1. **Tianci Song**, Quoc Nguyen, Charles Broadbent, and Rui Kuang. *Reconstructing 3D Spatial Structures of RNA-Tomography Transcriptomes by Collapsed Tensor Factorization*. **In submission**
2. Thomas Karl Atkins, **Tianci Song**, and Rui Kuang. *FIST-nD: A Tool for N-dimensional Spatial Transcriptomics Data Imputation via Graph-regularized Tensor Completion*. **bioRxiv** (2022) [[Rx Preprint](#)]
3. Daniel Rafter, Zhuliu Li, Tory Schaaf, Kristen Gault, Maxwell Thorpe, Shivani Venkatesh, Radhika Edpuganti, **Tianci Song**, Rui Kuang, and Uzma Samadani. *Machine Learning with Objective Serum Markers and Algorithmic Deep Learning Computed Tomography Scan Analysis for Classification of Brain Injury*. **medRxiv** (2021) [[Rx Preprint](#)]

SKILLS

ML/AI: Deep learning, tensor modeling, representation learning, graph neural networks, transformers, generative models, foundation models, and multi-agent systems.

Applications: Spatial transcriptomics, single-cell omics, multi-omics integration, computational pathology, biomedical imaging.

Programming/Framework: Python, R, C/C++, Matlab, PyTorch, TensorFlow, Tensorly, scikit-learn.

Tool/Platform: Unix/Linux, Git, LaTeX, high-performance clusters, and cloud environments, and high performance clusters.

Language: Mandarin (native), English (fluent)

TALKS

- **Machine Learning Methods for Reconstructing Spatially Resolved Transcriptomes**
Genentech, South San Francisco, CA, Sep, 2025
- **Machine Learning Methods for Reconstructing Spatially Resolved Transcriptomes**
Oak Ridge National Laboratory, Oak Ridge, TN, Aug, 2025
- **Machine Learning Methods for Reconstructing Spatially Resolved Transcriptomes**
Yale University, Remote, July, 2025
- **Predicting Spatially Resolved Gene Expression via Tissue Morphology**
NEC Labs America, Princeton, NJ, Sep, 2024

AWARDS AND HONORS

- John T. Riedl Memorial Graduate Teaching Assistant Award 2023, University of Minnesota
- Computer Science and Engineering Graduate Fellowship 2018 and 2019, University of Minnesota
- National Excellent Student Scholarship 2012 and 2013, Jilin University

TEACHING

- CSCI 5521 - Machine Learning Fundamentals/Introduction to Machine Learning, University of Minnesota (Teaching Assistant, Fall 2019, Spring 2020, Spring 2023)
- CSCI 5461 - Functional Genomics, Systems Biology, and Bioinformatics, University of Minnesota (Teaching Assistant, Spring 2021)
- Computational Biology, Jilin University (Guest Lecturer, Spring 2015)
- Introduction to Bioinformatics, Harbin Medical University (Guest Lecturer, Fall 2014)

ACADEMIC SERVICES

- **Journal Reviewer/Co-Reviewer:** Bioinformatics, Biomarker Research, BMC Genomics, BMC Cancer, Computational and Structural Biotechnology Journal, Engineering Applications of Artificial Intelligence, Genome Biology, Journal of Cancer Research and Clinical Oncology, Nature Communications, Nature Methods, npj Digital Medicine, and Scientific Reports
- **Conference Co-Reviewer:** ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2020, 2021, 2022, 2023, and 2024, 2025 International Conference on Intelligent Systems for Molecular Biology (ISMB) 2025