JUNJIE TANG

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EDUCATION & APPOINTMENT

Postdoc Research Fellow, Feb 2024 - Present
Ray and Stephanie Lane Computational Biology Department, Kenneth C. Griffin School of Computer Science,
Carnegie Mellon University, Pittsburgh, PA, USA
Advisor: Prof. Jian Ma

Ph.D. in Statistics, 2018–2023
Center for Statistical Science;
School of Mathematical Sciences, Peking University
Advisor: Prof. Ruibin Xi

B.S. in Statistics, Sep 2014 - Jul 2018
School of Mathematical Sciences, South China Normal University

RESEARCH INTERESTS

Fields
Gene Regulation, Gene Programs, Spatial Omics, Cell-Cell Communication, Multimodal Relationships, Cell and Tissue Dynamics

Methods
Hierarchical and Graphical Models, Interpretable Representation Learning, Spatial Statistics, Multimodal Integration, Deep Learning, Dynamic Modeling

RESEARCH EXPERIENCE

Spatial and Temporal Tissue Dynamics
Aug 2026 - Present
I develop computational models to study spatial and temporal tissue dynamics and characterize changes in tissue states.

Foundation Models and Agents for Spatial Biology
Sep 2025 - Present
I develop spatial foundation models to learn reusable tissue representations and analysis agents for reproducible, question-driven biological investigation.

Interpretable Cell-Cell Communication Programs in Spatial Transcriptomics
May 2024 - Present
I lead SpiderNet development to infer directed meta-interactions linking sender regulators, ligand-receptor signals, and receiver targets, with applications to brain aging, cancer, and perturbation responses.

Integrative Gene Module Detection for Spatial Transcriptomics and Histology
Sep 2021 - Jun 2025
I led SpaHDmap, integrating spatial transcriptomics with histology to identify interpretable, high-resolution gene programs and refined tissue structures.

Gene Regulatory Network Inference for Single-Cell RNA-seq
Oct 2018 - Dec 2021
I developed hierarchical graphical models and computational methods for gene network inference from count data and mixed cell populations.

Collaborative Research
I contributed to studies of Alzheimer's disease (Science), spatial niches (SpaNiche), multiscale cellular interactions (Steamboat), and generative spatial transcriptomics modeling (TissueNarrator).

PUBLICATIONS

Zhang, Y.*, Lu, X.*, Kunisky, A. K.‡, Alam, S.‡, **Tang, J.‡**, Zhang, R.‡, Wang, S., Zhang, H., Baroudi, J., Ichcho, W., Jia, D., Ghorbanikalateh, S., Ghorbanikalateh, S., Wang, S., Bennett, D. A., Mathys, H., Duan, Z., Ma, J. (2026). Single-cell multiomics connects 3D genome and transcriptome alterations in Alzheimer's disease. *Science,* 393(6809), eadz1652. [link]

Liang, S., **Tang, J.**, Wang, G., & Ma, J. (2025). Steamboat: Attention-Based Multiscale Delineation of Cellular Interactions in Tissues. *Research in Computational Molecular Biology* (RECOMB), LNCS 15647, 432-436. [link] [preprint] Extended manuscript accepted in principle by *Nature Methods* (2026).

Huang, S.*, Ran, Q.*, **Tang, J.***, Wang, X.*, Xi, J., Ma, S., & Xi, R. (2026). SpaNiche: spatial niche analysis to explore colocalization patterns and cellular interactions in spatial transcriptomics data. *Genome Biology*, 27, 182. [link]

Tang, J.*, Chen, Z.*, Qian, K.*, Huang, S., He, Y., Yin, S., He, X., Ye, B., Zhuang, Y., Meng, H., Xi, J. J., & Xi, R. (2026). The interpretable multimodal dimension reduction framework SpaHDmap enhances resolution in spatial transcriptomics. *Nature Cell Biology*, 28, 363-377. [link]

Huang, Y., Wang, C., **Tang, J.**, Wu, W., & Xi, R. (2025). A Generic Family of Graphical Models: Diversity, Efficiency, and Heterogeneity. *Proceedings of the 42nd International Conference on Machine Learning* (ICML).

Chen, X., Ran, Q., **Tang, J.**, Chen, Z., Huang, S., Shi, X., & Xi, R. (2025). Benchmarking algorithms for spatially variable gene identification in spatial transcriptomics. *Bioinformatics,* 41(4), btaf131. [link]

Tang, J.*, Wang, C.*, Xiao, F., & Xi, R. (2024). Single-cell gene regulatory network analysis for mixed cell populations. *Quantitative Biology*, 12(4), 375-388. [link]

Huang, S., Ouyang, L., **Tang, J.**, Qian, K., Chen, X., Xu, Z., Ming, J., & Xi, R. (2024). Spatial transcriptomics: A new frontier in cancer research. *Clinical Cancer Bulletin*.

Xiao, F.*, **Tang, J.***, Fang, H., & Xi, R. (2022). Estimating graphical models for count data with applications to single-cell gene network. *Advances in Neural Information Processing Systems* (NeurIPS).

Dong, L., Yao, X., Deng, Y., Zhang, H., Zeng, W., Li, X., **Tang, J.**, & Wang, W. (2022). Nitrogen deficiency in soil mediates multifunctionality responses to global climatic drivers. *Science of the Total Environment*.

Dong, L., Zeng, W., Wang, A., **Tang, J.**, Yao, X., & Wang, W. (2020). Response of soil respiration and its components to warming and dominant species removal along an elevation gradient in alpine meadow of the Qinghai-Tibetan plateau. *Environmental Science & Technology*, 54(17), 10472-10482.

* Co-first authors. ‡ Equal contribution within the second author group.

PREPRINTS

Tang, J.†, Liang, S., Alam, S., Cheng, W., Zhang, Y., & Ma, J.† (2026). A meta-interaction basis for cell-cell communication in tissues. *bioRxiv,* 2026.09.21.753369. [link]

Liu, S., **Tang, J.**, Ma, J., & Liang, S. (2025). TissueNarrator: Generative Modeling of Spatial Transcriptomics with Large Language Models. *bioRxiv,* 2025.11.24.690325. [link]

† Corresponding authors.

CONFERENCE PRESENTATION

Tang, J. (2026). Poster presentation, AI4BIO Symposium, Carnegie Mellon University, Pittsburgh, PA, USA. Nov 13, 2026.

Tang, J. (2026). Poster presentation, Spatial Multi-Omics, HHMI Janelia Research Campus, Ashburn, VA, USA. Nov 8-11, 2026.

Tang, J., Liang, S., Alam, S., & Ma, J. (2026). SpiderNet reveals a meta-interaction basis for cell-cell communication in tissues. Oral presentation and poster, RegSys, ISMB 2026. Presenter: Junjie Tang. RegSys Best Poster Award.

Tang, J., Wang, C., Xiao, F., & Xi, R. (2023). Single-cell gene regulatory network analysis for mixed cell populations. Oral presentation, 1st National Joint Conference on Statistics and Data Science in China, Beijing.

Tang, J., Wang, C., Xiao, F., & Xi, R. (2021). Cell-type-specific gene regulatory network inference. Posters, 7th National Academic Conference on Computational Biology and *Bioinformatics,* Yantai (Award for Excellent Poster), and 4th Peking-Tsinghua Statistics Forum, Beijing.

Presentations of Coauthored Work

Huang, Y., Wang, C., **Tang, J.**, Wu, W., & Xi, R. (2025). A Generic Family of Graphical Models: Diversity, Efficiency, and Heterogeneity. Oral, ICML, Vancouver.

Liang, S., **Tang, J.**, Wang, G., & Ma, J. (2025). Steamboat: Attention-Based Multiscale Delineation of Cellular Interactions in Tissues. Oral, RECOMB, Seoul.

Xiao, F., **Tang, J.**, Fang, H., & Xi, R. (2021, 2020). Estimating graphical models for count data with applications to single-cell gene network. Posters, Computational Biology and Bioinformatics conference, Yantai (2021), and 3rd Peking-Tsinghua Statistics Forum, Beijing (2020).

FELLOWSHIPS AND AWARDS

RegSys Best Poster Award, ISMB, 2026

Award for Excellent Poster, Computational Biology and Bioinformatics conference, 2021

Mininglamp Innovation Scholarship, Peking University, 2022

Award for Excellent Academic Performance, Peking University, 2021

Award for Excellent Graduate, South China Normal University, 2018

Individual Grand Prize of Innovation Award, South China Normal University, 2018

National Scholarship, South China Normal University, 2016

National Scholarship, South China Normal University, 2015

RESEARCH SUPERVISION

Undergraduate thesis supervision

Mentored students in statistical modeling, computational effective algorithm implementation, co-designed simulation experiments

Yufei Huang, 2022-2023, Hierarchical graphical model and effective algorithm for cell-type-specific gene regulatory network inference

TEACHING EXPERIENCE

Advanced Mathematics, undergraduate course, teaching assistant, Fall 2020 - Fall 2021

ACADEMIC SERVICE

Ad hoc reviewer

Nature Cell Biology, Nature Communications,

Conference on Research in Computational Molecular Biology (RECOMB),

IEEE transaction Computational Biology, BMC Genomic, BMC Bioinformatics,

Biostatistics and Epidemiology, Artificial Intelligence Review