

Kang Jin, Ph.D. student

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Date of Birth: Jan 11th, 1997
Updated on Aug 30th, 2022

RESEARCH FOCUS

My long-term research interest is to deconvolute complex biological data using advanced and robust computational methods. I have developed a probabilistic model to study the temporal perturbational patterns and in single-cell experiments, as well as a user-friendly framework to disentangle multiplexed gene signatures in complex single-cell data. I'm also actively involved in single-cell analysis across multiple tissues, including cancer, lung, immune systems, and brain organoids. I aim to improve our understanding of emerging spatial transcriptomics and multi-omics data with the development of innovative computational methods.

EDUCATION

Cincinnati Children's Hospital, Cincinnati, USA	Ph.D. in Biomedical Informatics	2018-2023 (Expected)
Zhejiang University, Hangzhou, China	B.Sc. in Biology	2014-2018

RESEARCH EXPERIENCE

Massachusetts General Hospital, Harvard Medical School 2022/05-Present

Visiting student in Dr. Jian Shu's lab

- Developed deep learning-based methods to improve subcellular analysis in spatial transcriptomics data
- Designed transcriptomics probes for in situ sequencing technologies.

Department of Biomedical Informatics, Cincinnati Children's Hospital 2018/09-Present

Ph.D. student in Dr. Bruce Aronow's lab

- Developed CellDrift, a generalized linear model to analyze single cell perturbation effects. Applied functional data analysis (FDA) to infer temporal perturbational patterns.
- Interrogated temporal impact of NRXN1 deletion in schizophrenia patients using single-cell data from patient-derived brain organoids.
- Analyzed single cell data of human hepatoblastoma and mouse xenograft tumors. Identified tumor clusters with distinct transcriptional profiles.
- Developed ToppCell, a hierarchical differential analysis framework for single cell datasets with complex metadata. Constructed gene signature atlases for COVID-19 patients and multiple human tissues, including lung, brain, GI, and others.

Institute of Pharmaceutical Biotechnology, Zhejiang University 2016/11-2018/07

Undergraduate Student in Dr. Xin Chen's lab

- Benchmarked Gene Set Linkage Analysis (GSLA), a gene set annotation tool in Arabidopsis.
- Participated in the design of decision support system for cancer patients based on gene mutations and transcriptional levels.

Department of Life Science, Zhejiang University 2015/07-2016/10

Undergraduate Student in Dr. Jun Chen's lab

- Selected scoliosis zebrafishes with genetic mutations. Used CRISPR technology in zebrafishes with double gRNAs to knock in long DNA fragments with higher precision and specificity.

SKILLS

Programming: Python, PyTorch, Pyro, R, Linux shell

Skills: Deep learning, Probabilistic modeling, Single-cell analysis, Cloud computing

AWARDS

Second Place, Best Poster Award, ISMB 2022 (SysMod Meeting)	2022
Second Place, Graduate Student Research Forum (GSRF), University of Cincinnati,	2020
Best Application Award, Zhejiang Bioinformatics Competition	2017
China National Award (1.8%)	2017
First Prize Scholarship for Excellent Students, Zhejiang University	2017
Tang Lixin Scholarship for Excellent Model Student	2017
Zhejiang Provincial Government Scholarship	2016
Second Prize, Physics Innovation Competition in Zhejiang Province	2015

PUBLICATIONS

Journal Publications:

Jin, K., Schnell, D., Li, G., Salomonis, N., Prasath, S., Szczesniak, R., & Aronow, B. J. (2022). CellDrift: Inferring Perturbation Responses in Temporally-Sampled Single Cell Data. **Briefings in Bioinformatics** (2022): bbac324.

Xu, X., **Jin, K.**, Bais, A. S., Zhu, W., Yagi, H., Feinstein, T. N., ... & Lo, C. W. (2022). Uncompensated mitochondrial oxidative stress underlies heart failure in an iPSC-derived model of congenital heart disease. **Cell Stem Cell**.

Jin, K., Bardes, E.E., Mitelpunkt, A., Wang, J.Y., Bhatnagar, S., Sengupta, S., Krummel, D.P., Rothenberg, M.E. and Aronow, B.J., 2021. An interactive single cell web portal identifies gene and cell networks in COVID-19 host responses. **IScience**, 24(10), p.103115.

Bondoc A*, Glaser K*, **Jin K***, Lake C, Cairo S, Geller J, Tiao G, Aronow B. Identification of distinct tumor cell populations and key genetic mechanisms through single cell sequencing in hepatoblastoma. **Commun Biol**. 2021 Sep 8;4(1):1049. doi: 10.1038/s42003-021-02562-8. PMID: 34497364.

Sun, X., Perl, A.K., Li, R., Bell, S.M., Sajti, E., Kalinichenko, V.V., Kalin, T.V., Misra, R.S., Deshmukh, H., Clair, G., Kyle, J.,..., **Jin, K.**,... NHLBI LungMAP Consortium, 2022. A census of the lung: CellCards from LungMAP. **Developmental Cell**, 57(1), pp.112-145.

Pak C, Danko T, Mirabella VR, Wang J, Liu Y, Vangipuram M, Grieder S, Zhang X, Ward T, Huang YA, **Jin K**, ..., Aronow BJ, Pang ZP, Levinson DF, Wernig M, Südhof TC. Cross-platform validation of neurotransmitter release impairments in schizophrenia patient-derived NRXN1-mutant neurons. **Proc Natl Acad Sci USA**. 2021 Jun 1;118(22):e2025598118. doi: 10.1073/pnas.2025598118. PMID: 34035170.

Yao H, Wang X, Chen P, Hai L, **Jin K**, Yao L, Mao C, Chen X. Predicted Arabidopsis Interactome Resource and Gene Set Linkage Analysis: A Transcriptomic Analysis Resource. **Plant Physiol**. 2018 May;177(1):422-433. doi: 10.1104/pp.18.00144. Epub 2018 Mar 12. PMID: 29530937; PMCID: PMC5933134.

Preprint:

Sebastian, R.*, **Jin, K.***, Pavon, N., Bansal, R., Potter, A., Song, Y., ... & Pak, C. (2022). Single cell transcriptomic profiling of human brain organoids reveals developmental timing-and cell-type-specific vulnerabilities induced by NRXN1 CNVs in schizophrenia. bioRxiv.

Guo, M., Morley, M. P., Wu, Y., Du, Y., Zhao, S., Wagner, A., Kouril, M., **Jin, K.**, ... & Xu, Y. (2022). Guided construction of single cell reference for human and mouse lung. bioRxiv.

Mihalas, A., Arora, S., O'Connor, S., Feldman, H., Bassett, J., Mitchell, K., ..., **Jin, K.**, ..., & PADDISON, P. (2022). KAT5 activity regulates G0-like states in human gliomas. bioRxiv.

McSweeney, D., Gabriel, R., **Jin, K.**, Pang, Z.P., Aronow, B.J. and Pak, C., (2022). Loss of Neurodevelopmental Gene CASK Disrupts Neural Connectivity in Human Cortical Excitatory Neurons. bioRxiv.

Gaddis, N., Fortriede, J., Guo, M., Bardes, E.E., Kouril, M., Tabar, S., Burns, K., Ardini-Poleske, M.E., Loos, S., Schnell, D., **Jin, K.**,, (2021). LungMAP Portal Ecosystem: Systems-Level Exploration of the Lung. bioRxiv.

Prates, E. T., Garvin, M. R., Pavicic, M., Jones, P., Shah, M., Alvarez, C., ... **Jin.K.**, ... Aronow. B.J. & Jacobson, D. (2020). Functional immune deficiency syndrome via intestinal infection in COVID-19. BioRxiv.