

# Kang Jin, Postdoc

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## RESEARCH INTEREST

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I am driven by a passion for leveraging advanced computational techniques to uncover the intricate biological mechanisms underlying **spatial transcriptomics** and **single-cell sequencing** data, with a particular emphasis on image-based spatial profiling technologies such as MERFISH. My current research focuses on the development of spatial epigenomics and **deep learning** approaches to elucidate cis-regulatory elements and **gene regulatory dynamics** during neurogenesis and other developmental processes.

In previous work, I contributed to the development of a graph neural network model to decipher spatial colocalization patterns ([Jin et al., bioRxiv, 2023](#)) and a generalized linear model for revealing temporal perturbation patterns in single-cell experiments ([Jin et al., Briefings in Bioinformatics, 2022](#)). My extensive experience in data mining spans single-cell and spatial data across diverse biological systems and diseases, including placenta ([Ounadjela\\*,...,Jin\\* et al., Nature Medicine, 2024](#)), HLHS ([Xu, Jin et al., Cell Stem Cell, 2022](#)), and schizophrenia ([Sebastian\\*, Jin\\* et al. Nature Communications, 2023](#)).

I am particularly captivated by groundbreaking bioengineering innovations, including image-based spatial transcriptomics and high-throughput CRISPR screening technologies. With expertise in computational biology and a keen interest in integrating molecular technologies, my ultimate goal is to advance our understanding of neuroscience and cancer biology by pioneering computational methods that harness emerging tools and techniques.

## EDUCATION

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Harvard University/HHMI, Boston, USA	<b>Postdoc</b>	2023-Present
Massachusetts General Hospital, Harvard Medical School, Boston, USA	<b>Visiting Student</b>	2022-2023
Cincinnati Children's Hospital, Cincinnati, USA	<b>Ph.D. in Biomedical Informatics</b>	2018-2023
Zhejiang University, Hangzhou, China	<b>B.Sc. in Biology</b>	2014-2018

## RESEARCH EXPERIENCE

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<b>Department of Chemistry and Chemical Biology, Harvard University</b>	2023-Present
<i>Postdoctoral Researcher in Dr. Xiaowei Zhuang's lab</i>	
<ul style="list-style-type: none"><li>Developed an innovative epigenomic MERFISH technique to map epigenetic profiles in high spatial resolution</li></ul>	
<b>Massachusetts General Hospital, Harvard Medical School</b>	2022/05-2023/11
<i>Visiting student in Dr. Jian Shu's lab</i>	
<ul style="list-style-type: none"><li>Developed transfer learning model for segmentation and cell annotation in image-based spatial transcriptomics data.</li><li>Image processing and pipeline design for STARmap data in Placenta.</li></ul>	
<b>Department of Biomedical Informatics, Cincinnati Children's Hospital</b>	2018/09-2023/11
<i>Ph.D. student in Dr. Bruce Aronow's lab</i>	
<ul style="list-style-type: none"><li>Developed CellDrift, a generalized linear model to analyze single cell perturbation effects. Applied functional data analysis (FDA) to infer temporal perturbational patterns.</li><li>Interrogated temporal impact of NRXN1 deletion in schizophrenia patients using single-cell data from patient-derived brain organoids.</li></ul>	

- 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.

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## SKILLS

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

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

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## 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

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## PUBLICATIONS

*Journal Publications:*

**Jin, K\***, Zhang Z.\*, Zhang K., Viggiani F., Callahan C., Tang J., Aronow B., Shu J. (2023). Bering: joint cell segmentation and annotation for spatial transcriptomics with transferred graph embeddings. *bioRxiv*.

Ounadjela, J. R\*, Zhang, K.\*, Kobayashi-Kirschvink, K. J.\*, **Jin, K.\***, JC Russell\*, A., Lackner, A. I.\*, ... & Shu, J. (2024). Spatial multiomic landscape of the human placenta at molecular resolution. *Nature Medicine*, 1-14.

Guo, M., Morley, M. P., Wu, Y., Du, Y., Zhao, S., Wagner, A., Kouril, M., **Jin, K.**, ... & Xu, Y (2023). "Guided construction of single cell reference for human and mouse lung." *Nature Communications* 14.1: 4566.

Sebastian, R.\*, **Jin, K.\***, Pavon, N., Bansal, R., Potter, A., Song, Y., ... & Pak, C. (2023). Single cell transcriptomic profiling of human brain organoids reveals developmental timing-and cell-type-specific vulnerabilities induced by NRXN1 CNVs in schizophrenia. *Nat Communications*, 14(1), 3770.

**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*: 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**.

McSweeney, D., Gabriel, R., **Jin, K.**, Pang, Z. P., Aronow, B., & Pak, C. (2022). CASK loss of function differentially regulates neuronal maturation and synaptic function in human induced cortical excitatory neurons. **Science**, 25(10), 105187.

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.**, ....., (2022). LungMAP Portal Ecosystem: Systems-Level Exploration of the Lung. **American Journal of Respiratory Cell and Molecular Biology**.

**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. **Science**, 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:*

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.

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.