# Kang Jin, Ph.D. Student

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## RESEARCH INTEREST

As an enthusiastic researcher, my passion lies in leveraging advanced computational methods to unravel high-throughput sequencing data for single cell profiling. My current research endeavors are primarily centered around developing deep learning and probabilistic models to analyze spatial subcellular omics data (*Jin et al., MLCB2022, wrapping up*) and temporal perturbation patterns in single-cell experiments (*Jin et al., Briefings in Bioinformatics, 2022*). I have also contributed to the field by creating an interactive platform called ToppCell for large-scale single cell data exploration (*Jin et al. iScience, 2021*), which enables the investigation of perturbation effects of single cell data in various biological systems and diseases, including HLHS (*Xu et al., Cell Stem Cell, 2022*), schizophrenia (*Sebastian\*, Jin\* et al. Nat Communications, In Revision*), hepatoplastoma (*Bondoc\*, Glaser\*, Jin\* et al. Communications Biology, 2021*), lung fibrosis (*Sun et al. Developmental Cell, 2022*) and COVID-19.

I am particularly interested in cutting-edge bioengineering innovations, such as single-cell multiomics profiling, spatial transcriptomics, pooled CRISPR screens and live-cell imaging. Collaborating with Dr. Jian Shu, I am currently in designing experiments and devising innovative computational approaches to understand cell states and microenvironment perturbations in subcellular resolution using image-based spatial omics technologies.

With expertise in computational biology and a strong interest in bioengineering, my ultimate goal is to advance our understanding of complex cellular states and their changes by implementing cutting-edge computational methods with emerging single-cell and spatial genomics data.

## EDUCATION

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| Massachusetts General Hospital, Harvard Medical School, Boston, USA | *Visiting Student* | 2022-2023 |
| 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' 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, R, Pyro, Linux shell

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

## AWARDS

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| 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.***

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. ***Iscience***, 25(10), 105187.

**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.

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.***

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. (*Nature Communications, In Revision*)

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.

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.