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

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

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.