Kang Jin, Postdoc

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RESEARCH INTEREST

As an enthusiastic researcher, I am passionate about harnessing advanced computational techniques to unveil the biological mechanisms hidden within **high-content imaging and high-throughput sequencing data**, with a specific focus on image-based spatial profiling. My present work primarily centers around the development of cutting-edge **deep learning** models tailored to image-based spatial omics data (Jin et al., bioRxiv, 2023) and the analysis of **temporal perturbation patterns** in single-cell experiments (Jin et al., Briefings in Bioinformatics, 2022). My commitment extends to active involvement in the experimental **design of spatial multi-omics experiments**, and I possess a wealth of experience in exploring single cell data across various biological systems and diseases, including HLHS (Xu, Jin et al., Cell Stem Cell, 2022), schizophrenia (Sebastian*, Jin* et al. Nature Communications, 2023), among others.

I am particularly interested in cutting-edge bioengineering innovations, such as image-based spatial transcriptomics and optical molecular recording.

With expertise in computational biology and a strong interest in bioengineering, my ultimate goal is to advance our understanding of neuroscience and cancer biology by implementing cutting-edge computational methods with emerging new molecular recording technologies.

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
Zhejiang University, Hangzhou, China	***B.Sc.*** *in Biology*	2014-2018

RESEARCH EXPERIENCE

Massachusetts General Hospital, Harvard Medical School   2022/05-2023/11

Visiting student in Dr. Jian Shu' lab

- Developed transfer learning model for segmentation and cell annotation in image-based spatial transcriptomics data.
- Image processing and pipeline design for STARmap data in Placenta.

Department of Biomedical Informatics, Cincinnati Children's Hospital   2018/09-2023/11

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: Imaging Processing, 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*., 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***.

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. ***Iscience***, 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. *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:

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.