

# Kang Jin, Ph.D. student

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Date of Birth: Jan 11<sup>th</sup>, 1997  
*Updated on April 3<sup>rd</sup>, 2022*

## RESEARCH FOCUS

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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 multi-omics data with the development of innovative computational methods.

## EDUCATION

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

## RESEARCH EXPERIENCE

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**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 Gaussian process and function principal component analysis (fPCA) to infer temporal perturbational patterns (*Manuscript in preparation, ProbGen22 poster*).
- Interrogated temporal impact of NRXN1 deletion in schizophrenia patients using single-cell data from patient-derived brain organoids (*Manuscript in preparation*).
- 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

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

**Skills:** Probabilistic modeling, single-cell analysis, bulk-RNA-seq analysis.

## AWARDS

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Second Place, Graduate Student Research Forum (GSRF), University of Cincinnati,	2020
Best Application Award of 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

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### *Journal Publications:*

**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. *Isience*, 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.

Xu, X., **Jin, K.**, Bais, A. S., Zhu, W., Yagi, H., Feinstein, T. N., ..., Lo, C. W. (2021). iPSC modeling shows uncompensated mitochondrial mediated oxidative stress underlies early heart failure in hypoplastic left heart syndrome. bioRxiv. **(Accepted by Cell Stem Cell)**

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.