Kang Jin

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EDUCATION

Cincinnati Children's Hospital Medical Center, Cincinnati, United States
Ph.D, **Biomedical Informatics**   *Aug 2018 to May 2023 (expected)*
- Advisor: Dr. Bruce Aronow

Zhejiang University, Hangzhou, China
B.S., **Biological Science**   *Aug 2014 to Jun 2018*
- Advisor: Dr. Chen Xin
- GPA: 87.3/100 (3.88/4.0), **Rank: 2/25 (total); 1/25(3rd year)**

RESEARCH INTEREST

Probabilistic Modeling, Single Cell Analysis, Spatial Transcriptomics, System Biology, Biomedical Informatics, Computational Neuroscience

PUBLICATION   (sort by time)

[9] 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.

[8] 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.

[7] 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.

[6] **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.

[5] 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.

[4] 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.

[3] Pak C, Danko T, Mirabella VR, Wang J, Liu Y, Vangipuram M, Grieder S, Zhang X, Ward T, Huang YA, **Jin K**, Dexheimer P, Bardes E, Mitelpunkt A, Ma J, McLachlan M, Moore JC, Qu P, Purmann C, Dage JL,

Swanson BJ, Urban AE, 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 U S A. **2021** Jun 1;118(22):e2025598118. doi: 10.1073/pnas.2025598118. PMID: 34035170.

[2] 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.

[1] 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.

RESEARCH EXPERIENCE

Research Assistant   *Aug 2018 to present*
Aronow Research Lab   Mentor: Dr. Bruce Aronow
- Participated in the development of ToppCell, a hierarchical differential analysis framework for single cell datasets with complex metadata [paper]. Constructing gene signature atlases for COVID-19 patients [paper] and human tissues, including lung [paper], brain, GI [paper] and others.
- Analyzed transcriptomic variance between human hepatoblastoma and xenograft counterpart in mice and found upregulated pathways for xenograft tumors. [paper]
- Build a generalized-linear-model-based method to analyze single cell perturbation effects. Applied Gaussian process and function principal component analysis (fPCA) to interpret temporal perturbation patterns.

Research Internship   *Nov 2016 to July 2018*
Synergy Laboratory for Biomedicine   Mentor: Dr. Chen Xin
- Measured a gene set annotation tool in Arabidopsis: Gene Set Linkage Analysis (GSLA) [paper]
- Participated in a precision medicine project and designed a part of decision support system for cancer patients based on gene mutations and expressional level.

Research Internship   *Jul 2015 to Oct 2016*
Developmental Biology Key Laboratory, Zhejiang University   Mentor: Dr. Chen Jun
- Selected scoliosis zebrafishes with introduced genetic mutations. Used CRISPR technology in zebrafishes with double gRNAs to knock in long DNA fragments with higher precision and specificity.

HONORS & AWARDS
- Second Place in Graduate Student Research Forum (GSRF) in University of Cincinnati, 2020
- Best Application Award of Zhejiang Bioinformatics Competition,2017
- China National Award (1.8%), 2017
- First Scholarship for Excellent Students, 2017
- Tang Lixin Scholarship for Excellent Model Student, 2017
- Zhejiang Provincial Government Scholarship, 2016

Only one student awarded among around 80 students in Biology Department
- Second Prize, Physics Innovation Competition in Zhejiang Province, 2015

SKILLS

Programming: Python, Pytorch, Pyro, R, C++, Linux shell
Skills: Probabilistic modeling**,** single-cell analysis, bulk-RNA sequencing.