

CONTACT INFORMATION	San Francisco, CA, USA https://github.com/qinzhu	<i>E-mail:</i> qin.zhu@ucsf.edu <i>Scholar:</i> Google Scholar
SUMMARY	Computational and Experimental Biologist specializing in Algorithm Development and Single-cell Genomics. My research integrates dry-lab expertise in Machine Learning and Statistics (CONCORD, VisCello) with wet-lab proficiency in immunology and pharmacology. I focus on developing and applying high-dimensional frameworks to solve fundamental problems in Cancer Immunology and Developmental Biology. Proven track record of high-impact research published in journals including <i>Science</i> , <i>Nature Biotechnology</i> , and <i>Blood</i> .	
EDUCATION	University of Pennsylvania , Philadelphia, PA, USA Ph.D., Genomics and Computational Biology , August 2021 - Advisers: Dr. Kai Tan, Dr. Junhyong Kim M.B., Master of Biotechnology , May 2015 Nanjing University , Nanjing, Jiangsu, China B.S., Biological Science , March 2013 - Thesis Adviser: Dr. Ling-Dong Kong	
TECHNICAL SKILLS	Languages & Frameworks: Python, R, C/C++, SQL, PyTorch, TensorFlow, cuML, cuGraph, Bash/Unix, Git, HTML/CSS. AI-Assisted Research & Development: Daily use of multi-agent coding workflows (Claude Code, Codex) for algorithm prototyping, pipeline building, code review and hypothesis generation. Machine Learning & Statistics: Contrastive Learning, Representation Learning, Manifold Learning, Differential Geometry, Dimensionality Reduction, Generative Models, Deep Learning (Transformers/CNNs), Expectation Maximization. Computational Biology: Single-cell Multi-omics (scRNA-seq, scATAC-seq, Spatial Multi-omics), Data Integration, High-dimensional Data Visualization, Drug Target Discovery. Experimental Biology: Single-cell Sequencing, Drug Perturbation, Molecular Biology (PCR, Western Blot), Cell Culture, In Vivo Models. Cloud & Infrastructure: AWS (EC2/S3), Docker, HPC (Slurm).	
PROFESSIONAL APPOINTMENTS	University of California, San Francisco (UCSF) , San Francisco, CA Postdoctoral Scholar - Adviser: Dr. Zev Gartner CRI Immuno-Informatics Postdoctoral Fellow University of Pennsylvania , Philadelphia, PA Research Specialist, Lab of Dr. Junhyong Kim	2021 - Present 2023 - 2026 2015 - 2016
FELLOWSHIP & AWARDS	Anthropic's AI for Science Program, 2026. Cancer Research Institute Immuno-Informatics Postdoctoral Fellowship, 2023. Tom Kadesch Prize in Genetics Research, 2021. Blavatnik Family Fellowship in Biomedical Research, 2020.	

Google scholar profile: <https://scholar.google.com/citations?user=AAFQgmQAAAAJ&hl=en>
 MyBibliography: : <https://www.ncbi.nlm.nih.gov/myncbi/167Tjj3Tso6Q8y/bibliography/public/>

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Zhu Q[†], Jiang Z, Zuckerman B, Weinberger L, Thomson M, Gartner Z[†]. Revealing a coherent cell-state landscape across single-cell datasets with CONCORD. *Nature Biotechnology*. 2026 Jan 5:1-5.

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Foyt D, Brown D, Zhou S, Moser B, **Zhu Q**, Gartner ZJ, et al. Foyt D, Brown D, Zhou S, Moser B, Zhu Q, Gartner ZJ, Huang B. HybriSeq: probe-based device-free single-cell RNA profiling. *Communications Biology*. 2025 Aug 19;8(1):1250.

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Zhu Q[†], Conrad DN, Gartner ZJ[†]. deMULTiplex2: robust sample demultiplexing for scRNA-seq. *Genome Biology*. 2024 Jan 30;25(1):37.

Li N*, **Zhu Q***, Tian Y, Ahn KJ, Wang X, Cramer Z, Jou J, Folkert IW, Yu P, Adams-Tzivelekidis S, Sehgal P. Mapping and modeling human colorectal carcinoma interactions with the tumor microenvironment. *Nature Communications*. 2023 Nov 30;14(1):7915.

Yang Y, Mumau M, Tober J, **Zhu Q**, Bennett L, Hong C, Sung D, Keller T, Uzun Y, Gao P, Shewale S. Endothelial MEKK3-KLF2/4 signaling integrates inflammatory and hemodynamic signals during definitive hematopoiesis. *Blood*. 2022 May 12;139(19):2942-57.

Chen C*, Yu W*, Alikarami F, Qiu Q, Chen CH, Flournoy J, Gao P, Uzun Y, Fang L, Hu Y, **Zhu Q**, et al. Single-cell multi-omics reveals elevated plasticity and stem-cell-like blasts underlying the poor prognosis of KMT2A-rearranged leukemia. *Blood*. 2021 Dec 5.

Chen GM*, Chen C*, Das RK*, Gao P, Chen CH, Bandyopadhyay S, Ding YY, Uzun Y, Yu W, **Zhu Q**, Myers RM. Integrative bulk and single-cell profiling of pre-manufacture T-cell populations reveals factors mediating long-term persistence of CAR T-cell therapy. *Cancer Discovery*. 2021 Jan 1.

Gao P, Chen C, Howell ED, Li Y, Tober J, Uzun Y, He B, Gao L, **Zhu Q**, Siekmann AF, Speck NA. Transcriptional regulatory network controlling the ontogeny of hematopoietic stem cells. *Genes & Development*. 2020 Jun 4.

Zhu Q*, Gao P*, Tober J*, Bennett L, Chen C, Uzun Y, Li Y, Howell ED, Mumau M, Yu W, He B, Speck NA, Tan K. Developmental trajectory of pre-hematopoietic stem cell formation from endothelium. *Blood*. 2020 May 11.

Yu W, Uzun Y, **Zhu Q**, Chen C, Tan K. scATAC-pro: a comprehensive workbench for single-cell chromatin accessibility sequencing data. *Genome biology*. 2020 April 20.

Rozenblatt-Rosen O, Regev A, Oberdoerffer P, Nawy T, Hupalowska A, Rood JE, Ashenberg O, Cerami E, Coffey RJ, Demir E, Ding L. The Human Tumor Atlas Network: charting tumor transitions across space and time at single-cell resolution. *Cell*. 2020 Apr 16;181(2):236-49.

Bellissimo DC, Chen CH, **Zhu Q**, Bagga S, Lee CT, He B, Wertheim GB, Jordan M, Tan K, Worthen GS, Gilliland DG. Runx1 negatively regulates inflammatory cytokine production by neutrophils in response to Toll-like receptor signaling. *Blood advances*. 2020 Mar 24;4(6):1145-58.

Peng T, **Zhu Q**, Yin P, Tan K. SCRABBLE: single-cell RNA-seq imputation constrained by bulk RNA-seq data. *Genome biology*. 2019 Dec 1;20(1):88.

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Ransick A*, Lindström NO*, Liu J*, **Zhu Q**, Guo JJ, Alvarado GF, Kim AD, Black HG, Kim J, McMahon AP. Single-cell profiling reveals sex, lineage, and regional diversity in the mouse kidney. *Developmental cell*. 2019 Nov 4;51(3):399-413.

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Liu YL, Pan Y, Wang X, Fan CY, **Zhu Q**, Li JM, Wang SJ, Kong LD. Betaine reduces serum uric acid levels and improves kidney function in hyperuricemic mice. *Planta medica*. 2014 Jan;80(01):39-47.

Wang X, Zhang DM, Gu TT, Ding XQ, Fan CY, **Zhu Q**, Shi YW, Hong Y, Kong LD. Morin reduces hepatic inflammation-associated lipid accumulation in high fructose-fed rats via inhibiting sphingosine kinase 1/sphingosine 1-phosphate signaling pathway. *Biochemical pharmacology*. 2013 Dec 15;86(12):1791-804.

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Yi LT, Zhang L, Ding AW, Xu Q, **Zhu Q**, Kong LD. Orthogonal array design for antidepressant compatibility of polysaccharides from Banxia-Houpu decoction, a traditional Chinese herb prescription in the mouse models of depression. *Archives of pharmacological research*. 2009 Oct 1;32(10):1417.

† Co-correspondence. * Equal contribution.

OPEN SOURCE SOFTWARE

CONCORD (Python, PyTorch): A scalable machine learning framework using contrastive learning for batch integration and dimensionality reduction of massive single-cell datasets (>1M cells).

deMULTiplex2 (R): A probabilistic algorithm for robust sample demultiplexing and doublet detection in scRNA-seq using Expectation Maximization and generalized linear models.

ChemCello (R, Shiny, SQL): A tool for designing drug screen libraries based on compound-target affinity databases, expression level, and polypharmacology.

VisCello (R, Shiny): An interactive software for large-scale single-cell data visualization. <https://github.com/qinzhu/VisCello>

PIVOT (R, Shiny): Platform for Interactive analysis and Visualization Of Transcriptomics data. <https://github.com/qinzhu/PIVOT>

Kidney Cell Explorer (R, Shiny, HTML/CSS): Interactive web portal for exploring kidney single-cell landscapes. <https://cello.shinyapps.io/kidneycellexplorer/>

SCRABBLE (R, MATLAB): Single-cell RNA-seq imputation constrained by bulk RNA-seq data. <https://github.com/software-github/SCRABBLE>

scATAC-pro (Bash, R): A comprehensive workbench for single-cell chromatin accessibility sequencing data processing. <https://github.com/wbaopaul/scATAC-pro>

VERSE (C): A versatile and efficient RNA-seq read assignment tool. <https://github.com/qinzhu/VERSE>

Single Cell Embryogenesis Explorer (R, Shiny): <https://cello.shinyapps.io/celegans/>

Single Cell EHT Explorer (R, Shiny): <https://cello.shinyapps.io/sceht/>

Invited talks

BCH & Harvard Medical School (HMS) Digital Science Seminar Series, May 2026. “[Revealing a coherent cell-state landscape across single-cell datasets with CONCORD](#)”. [\[Recording\]](#).

Institute for Regenerative Medicine Stem Cell Club Seminar, University of Pennsylvania, Dec 2025. "Revealing a coherent cell state landscape across single cell datasets with CONCORD".

AI Biology & Translation (AIBT) Seminar, Genentech, Sept 2025. "Revealing a coherent cell state landscape across single cell datasets with CONCORD".

Tom Kadesch Prize Award Presentation, University of Pennsylvania, Jan 2022. "Understanding gene regulation in development and differentiation using single cell multi-omics".

Conference/Workshop presentations

AI Applications in Biology Symposium, Feb 2026. "Revealing a coherent cell-state landscape across single-cell datasets with CONCORD".

Janelia AI Revolution Meets 4D Cellular Physiology Conference, April 2025. “Contrastive Learning for Cross-domain Reconciliation and Discovery”.

Chang Zuckerberg Single Cell Group Meeting, Nov 2024. “Illuminating the cell state manifold with single cell RNA sequencing and CONCORD”.

CICON24, CRI-ENCI International Cancer Immunotherapy Conference: Translating Science into Survival, Sep 2024. “Mapping the T cell state manifold across time and perturbation”.

CZI Single-Cell 2023 Annual Meeting, Nov 2023. “Tools for mapping the immune cell landscape”.

Penn Single Cell Workshop, 2021. "Single cell RNA-Seq and multiplexed imaging reveal heterogeneity and cell-cell communication in tumor microenvironment of colorectal cancer".

RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges, Nov 2020. “Developmental trajectory of pre-hematopoietic stem cell formation from endothelium.”

Single Cell Analysis Meeting, Cold Spring Harbor Laboratory Meetings, 2019. “Developmental bottleneck and two waves of blood progenitor formation from arterial endothelium.”

Progenitor Cell Translational Consortium (PCTC) Meeting, Harvard Medical School, 2019. “Developmental bottleneck and population heterogeneity in hematopoietic cluster formation from hemogenic endothelium.”

Rebuilding a Kidney (RBK) Consortium Meeting, National Institutes of Health, 2019. “Viscello: interactive visualization tool for large-scale single cell data.”

Penn Worm Club, 2018. “Single cell analysis of *C. elegans* embryogenesis.”

Penn Single Cell Workshop, 2017. “Divide and Combine: Dissecting Hematopoietic Stem Cell (HSC) Ontogeny at Single Cell Resolution.”

Penn Stem Cell Club, 2017. “Transcriptome dynamics during embryonic hematopoiesis at single-cell resolution.”

Poster presentations & Flash talks

Flash talk & Poster presentation at Biohub SF Inter-lab Confab, Oct 2025. “Revealing a coherent cell state landscape across single cell datasets with CONCORD”.

Poster presentation at UCSF Inaugural postdoc specialist and researcher (PSR) symposium, April 2023. “deMULTIplex2: robust sample demultiplexing for scRNA-seq”.

Poster presentation at Cell Symposium: Conceptual Power of Single-Cell Biology, Aug 2023. “deMULTIplex2: robust sample demultiplexing for scRNA-seq”.

Flash talk at Human Cell Atlas Asia Meeting, 2020. “Developmental trajectory of pre-hematopoietic stem cell formation from endothelium.”

Poster presentation at Keystone Single Cell Meeting, 2019. “Developmental bottleneck and population heterogeneity during the formation of hematopoietic stem cells.”

Flash talk & poster presentation at Penn CDB Retreat, 2018. “Transcriptome dynamics during embryonic hematopoiesis at single-cell resolution.”

Poster presentation at NIH Single Cell Meeting, 2017. “PIVOT: platform for interactive analysis and visualization of transcriptomics data.”

Flash talk & poster presentation at Cold Spring Harbor Single Cell Analysis Conference, 2017. “Transcriptome dynamics during embryonic hematopoiesis at single-cell resolution.”

Poster presentation at Penn GCB graduate program retreat, 2017-2020.

TEACHING & MENTORING EXPERIENCE

Teaching and Guest Lectures

Guest lecture for BIOL425: Biochemistry and Molecular Genetics Superlab December 2020
Lecture title: Intro to single cell data analysis.

Teaching assistant (BIOL437: Intro to Computational Biology) August - December 2019
Responsibilities include hosting office hours, grading homework and co-design course material.

Guest lecture for BIOL437 November 2019
Lecture title: Single cell technology and data analysis.

Mentoring

Rotation student & PhD Candidate: Zuzhi Jiang, Tetrad Graduate Program, UCSF Fall 2024 - 2025

Rotation student: Wudi Fan, joint Bioengineering program of UC-Berkeley/UCSF Fall 2023

Rotation student: Caleb Tong, joint Bioengineering program of UC-Berkeley/UCSF Fall 2023

Workshop

Workshop for Penn Program in Single Cell Biology October, 2019
Lecture title: Sequencing data analysis using VisCello.

Workshop for Penn Program in Single Cell Biology January, March & August, 2017
Lecture title: RNA-seq data analysis using PIVOT.

Workshop for Penn Program in Single Cell Biology March, 2015
Lecture title: RNA-seq data analysis using KimLabIDV.

PROFESSIONAL SERVICE

Editorial Boards

Associate editor of Journal *Frontiers in Medicine*. 2023 - 2025

Review editor of Journal *Frontiers in Oncology*. 2021 - Present

Journal Peer Review

Peer review for the following journals:

Genome Biology, JEM, Plos One, BMC Genomics, Frontiers in Medicine, Frontiers in Oncology, Frontiers in Genetics.

Institutional Service

Volunteer for student recruitment event of the Graduate Program in Genomics and Computational Biology, University of Pennsylvania (2016, 2017, 2018).

- Customer discovery and value proposition design; ~20 stakeholder interviews
- Problem–solution fit, market sizing, and commercialization pathways for *in vitro* intestine model