



Xiaojie Qiu

Assistant Professor of Genetics

 Curriculum Vitae available Online

CONTACT INFORMATION

- **Administrative Associate**

Hadley Bickford

Email hadleyb@stanford.edu

Bio

BIO

Dr. Xiaojie Qiu is currently an assistant professor at the Department of Genetics, the BASE program, and the Department of Computer Science at Stanford. Xiaojie's Ph.D. work at University of Washington with Dr. Cole Trapnell made critical contributions to the field of single-cell genomics, exemplified by the development of Monocle 2 & Monocle 3 for pseudotemporal trajectory analysis of scRNA-seq data. In his postdoc at Whitehead Institute and MIT with Dr. Jonathan Weissman, Xiaojie developed Dynamo (<https://github.com/aristoteleo/dynamo-release>) to reconstruct RNA velocity vector field and make reprogramming and in silico perturbation predictions with metabolic labeling enabled single-cell RNA-seq. Recently he also led the development of a powerful toolkit, Spateo (<https://github.com/aristoteleo/spateo-release>), for advanced multi-dimensional spatiotemporal modeling of high definition spatial transcriptomics.

The Qiu lab at Stanford started on Dec. 16, 2023. Xiaojie will continue leveraging his unique background in single-cell genomics, mathematical modeling, and machine learning to lead a research team that bridges the gap between the "big data" from single-cell and spatial genomics and quantitative/predictive modeling in order to address fundamental questions in mammalian cell fate transitions, especially those of heart evolution, development and disease. His research has been supported by the National Human Genome Research Institute, Chan Zuckerberg Institute, Impetus longevity grant, Arc Institute and others.

ACADEMIC APPOINTMENTS

- Assistant Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- NIH Director's New Innovator Award, NIH (10/8/2024)
- Arc Ignite Award, Arc Institute (9/1/2023)
- Pathway to Independence Awards (K99/R00), NHGRI (2/1/2023)

PROFESSIONAL EDUCATION

- Postdoctoral fellow, Whitehead Institute & MIT , single cell and spatial genomics; systems biology (2023)
- PhD, University of Washington , Molecular & cellular biology; genome sciences (2018)
- Masters, East China Normal University , Bioinformatics and systems biology (2012)
- B S, Changchun University of Technology , Bioengineer (2008)

LINKS

- My lab website: <https://www.devo-evo.com/>
- GitHub organization: <https://github.com/aristoteleo>
- Google scholar: https://scholar.google.com/citations?hl=en&user=4lzYRk0AAAAJ&view_op=list_works&sortby=pubdate
- Twitter account: <https://twitter.com/home>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

In the Qiu lab, we are combining advances in machine learning with advances in genomics to understand heart evolution, development and disease. We are pushing boundaries, pioneering research that simply would not have been possible a few years ago.

The research strategies in my lab involve a full cycle of experimentation, computation and predictions. We start with using novel genomics approaches to measure the states of single cells over time and in the physical space. These massive datasets will then be used to train interpretable machine learning models to understand the underlying gene regulatory networks which can be then used to create computer models of hearts to make predictions of congenital heart diseases. Our goal is to achieve a comprehensive understanding of the underlying disease mechanisms of heart disease and when and where disease begins in the heart.

With that knowledge, we can develop therapies to cure or even to prevent disease.

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Tony Zeng

Postdoctoral Faculty Sponsor

Sijie Chen, Nianping Liu, Weize Xu

Publications

PUBLICATIONS

- **Molecular convergence of risk variants for congenital heart defects leveraging a regulatory map of the human fetal heart.** *medRxiv : the preprint server for health sciences*
Ma, X. R., Conley, S. D., Kosicki, M., Bredikhin, D., Cui, R., Tran, S., Sheth, M. U., Qiu, W. L., Chen, S., Kundu, S., Kang, H. Y., Amgalan, D., Munger, et al
2024
- **Storm: Incorporating transient stochastic dynamics to infer the RNA velocity with metabolic labeling information.** *PLoS computational biology*

- Peng, Q., Qiu, X., Li, T.
2024; 20 (11): e1012606
- **Spatiotemporal modeling of molecular holograms.** *Cell*
Qiu, X., Zhu, D. Y., Lu, Y., Yao, J., Jing, Z., Min, K. H., Cheng, M., Pan, H., Zuo, L., King, S., Fang, Q., Zheng, H., Wang, et al
2024
 - **Deciphering cell states and genealogies of human hematopoiesis.** *Nature*
Weng, C., Yu, F., Yang, D., Poeschla, M., Liggett, L. A., Jones, M. G., Qiu, X., Wahlster, L., Caulier, A., Hussmann, J. A., Schnell, A., Yost, K. E., Koblan, et al
2024
 - **Systematic functional interrogation of SARS-CoV-2 host factors using Perturb-seq.** *Nature communications*
Sunshine, S., Puschnik, A. S., Replogle, J. M., Laurie, M. T., Liu, J., Zha, B. S., Nuñez, J. K., Byrum, J. R., McMorro, A. H., Frieman, M. B., Winkler, J., Qiu, X., Rosenberg, et al
2023; 14 (1): 6245
 - **Massively parallel base editing to map variant effects in human hematopoiesis.** *Cell*
Martin-Rufino, J. D., Castano, N., Pang, M., Grody, E. I., Joubran, S., Caulier, A., Wahlster, L., Li, T., Qiu, X., Riera-Escandell, A. M., Newby, G. A., Al'Khafaji, A., Chaudhary, et al
2023; 186 (11): 2456-2474.e24
 - **Spatiotemporally resolved transcriptomics reveals the subcellular RNA kinetic landscape.** *Nature methods*
Ren, J., Zhou, H., Zeng, H., Wang, C. K., Huang, J., Qiu, X., Sui, X., Li, Q., Wu, X., Lin, Z., Lo, J. A., Maher, K., He, et al
2023; 20 (5): 695-705
 - **Single-cell Stereo-seq reveals induced progenitor cells involved in axolotl brain regeneration.** *Science (New York, N.Y.)*
Wei, X., Fu, S., Li, H., Liu, Y., Wang, S., Feng, W., Yang, Y., Liu, X., Zeng, Y. Y., Cheng, M., Lai, Y., Qiu, X., Wu, et al
2022; 377 (6610): eabp9444
 - **Inferring gene regulation from stochastic transcriptional variation across single cells at steady state.** *Proceedings of the National Academy of Sciences of the United States of America*
Gupta, A., Martin-Rufino, J. D., Jones, T. R., Subramanian, V., Qiu, X., Grody, E. I., Bloemendal, A., Weng, C., Niu, S. Y., Min, K. H., Mehta, A., Zhang, K., Siraj, et al
2022; 119 (34): e2207392119
 - **Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution.** *Cell*
Yang, D., Jones, M. G., Naranjo, S., Rideout, W. M., Min, K. H., Ho, R., Wu, W., Replogle, J. M., Page, J. L., Quinn, J. J., Horns, F., Qiu, X., Chen, et al
2022; 185 (11): 1905-1923.e25
 - **Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays.** *Cell*
Chen, A., Liao, S., Cheng, M., Ma, K., Wu, L., Lai, Y., Qiu, X., Yang, J., Xu, J., Hao, S., Wang, X., Lu, H., Chen, et al
2022; 185 (10): 1777-1792.e21
 - **Mapping transcriptomic vector fields of single cells.** *Cell*
Qiu, X., Zhang, Y., Martin-Rufino, J. D., Weng, C., Hosseinzadeh, S., Yang, D., Pogson, A. N., Hein, M. Y., Hoi Joseph Min, K., Wang, L., Grody, E. I., Shurtleff, M. J., Yuan, et al
2022; 185 (4): 690-711.e45
 - **Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq.** *Nature methods*
Qiu, Q., Hu, P., Qiu, X., Govek, K. W., Cámara, P. G., Wu, H.
2020; 17 (10): 991-1001
 - **Inferring Causal Gene Regulatory Networks from Coupled Single-Cell Expression Dynamics Using Scribe.** *Cell systems*
Qiu, X., Rahimzamani, A., Wang, L., Ren, B., Mao, Q., Durham, T., McFaline-Figueroa, J. L., Saunders, L., Trapnell, C., Kannan, S.
2020; 10 (3): 265-274.e11
 - **The single-cell transcriptional landscape of mammalian organogenesis**
Spielmann, M., Cao, J., Qiu, X., Huang, X., Ibrahim, D. M., Hill, A. J., Zhang, F., Mundlos, S., Christiansen, L., Steemers, F. J., Trapnell, C., Shendure, J.

NATURE PUBLISHING GROUP.2019: 1043-1044

- **A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition.** *Nature genetics*
McFaline-Figueroa, J. L., Hill, A. J., Qiu, X., Jackson, D., Shendure, J., Trapnell, C.
2019; 51 (9): 1389-1398
- **Thyroid hormone regulates distinct paths to maturation in pigment cell lineages.** *eLife*
Saunders, L. M., Mishra, A. K., Aman, A. J., Lewis, V. M., Toomey, M. B., Packer, J. S., Qiu, X., McFaline-Figueroa, J. L., Corbo, J. C., Trapnell, C., Parichy, D. M.
2019; 8
- **The single-cell transcriptional landscape of mammalian organogenesis.** *Nature*
Cao, J., Spielmann, M., Qiu, X., Huang, X., Ibrahim, D. M., Hill, A. J., Zhang, F., Mundlos, S., Christiansen, L., Steemers, F. J., Trapnell, C., Shendure, J.
2019; 566 (7745): 496-502
- **Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome.** *Cell systems*
Cacchiarelli, D., Qiu, X., Srivatsan, S., Manfredi, A., Ziller, M., Overbey, E., Grimaldi, A., Grimsby, J., Pokharel, P., Livak, K. J., Li, S., Meissner, A., Mikkelsen, et al
2018; 7 (3): 258-268.e3
- **Cicero Predicts cis-Regulatory DNA Interactions from Single-Cell Chromatin Accessibility Data.** *Molecular cell*
Pliner, H. A., Packer, J. S., McFaline-Figueroa, J. L., Cusanovich, D. A., Daza, R. M., Aghamirzaie, D., Srivatsan, S., Qiu, X., Jackson, D., Minkina, A., Adey, A. C., Steemers, F. J., Shendure, et al
2018; 71 (5): 858-871.e8
- **The cis-regulatory dynamics of embryonic development at single-cell resolution.** *Nature*
Cusanovich, D. A., Reddington, J. P., Garfield, D. A., Daza, R. M., Aghamirzaie, D., Marco-Ferreres, R., Pliner, H. A., Christiansen, L., Qiu, X., Steemers, F. J., Trapnell, C., Shendure, J., Furlong, et al
2018; 555 (7697): 538-542
- **Reversed graph embedding resolves complex single-cell trajectories.** *Nature methods*
Qiu, X., Mao, Q., Tang, Y., Wang, L., Chawla, R., Pliner, H. A., Trapnell, C.
2017; 14 (10): 979-982
- **Comprehensive single-cell transcriptional profiling of a multicellular organism.** *Science (New York, N.Y.)*
Cao, J., Packer, J. S., Ramani, V., Cusanovich, D. A., Huynh, C., Daza, R., Qiu, X., Lee, C., Furlan, S. N., Steemers, F. J., Adey, A., Waterston, R. H., Trapnell, et al
2017; 357 (6352): 661-667
- **Single-cell mRNA quantification and differential analysis with Census.** *Nature methods*
Qiu, X., Hill, A., Packer, J., Lin, D., Ma, Y. A., Trapnell, C.
2017; 14 (3): 309-315
- **Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis.** *Science (New York, N.Y.)*
Hanchate, N. K., Kondoh, K., Lu, Z., Kuang, D., Ye, X., Qiu, X., Pachter, L., Trapnell, C., Buck, L. B.
2015; 350 (6265): 1251-5
- **From understanding the development landscape of the canonical fate-switch pair to constructing a dynamic landscape for two-step neural differentiation.** *PLoS one*
Qiu, X., Ding, S., Shi, T.
2012; 7 (12): e49271
- **A transcriptional dynamic network during Arabidopsis thaliana pollen development.** *BMC systems biology*
Wang, J., Qiu, X., Li, Y., Deng, Y., Shi, T.
2011; 5 Suppl 3 (Suppl 3): S8
- **HCCNet: an integrated network database of hepatocellular carcinoma.** *Cell research*
He, B., Qiu, X., Li, P., Wang, L., Lv, Q., Shi, T.

