Ran Zhang

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RESEARCH INTERESTS

My research focuses on harnessing large-scale, high-dimensional genomics data to facilitate biological hypothesis generation, especially in under-characterized data modalities and biological contexts. Specifically, I develop machine learning methods to:

- leverage functional genomics and quantitative genetics data to predict context-specific genes and processes underlying complex diseases
- predict single-cell profiles across modalities and time to provide multi-omics views of cellular regulation
- transfer disease models and single-cell profiles from model organisms to human

EDUCATION

Princeton University *2012 - 2019*
PhD in Molecular Biology
Advisor: Olga Troyanskaya
Dissertation: Context-specific disease gene prediction and functional characterization

Tsinghua University *2008 - 2012*
Bachelor of Science in Biology
Advisor: Li Yu
Thesis: Basal autophagy regulates late endosome and lysosome biogenesis

PROFESSIONAL APPOINTMENTS

The University of North Carolina at Chapel Hill *2025 - present*
Assistant Professor, School of Data Science and Society

University of Washington *2020 - 2025*
Postdoctoral Fellow, Genome Sciences
Advisor: William Stafford Noble

Princeton University *2019 - 2020*
Postdoctoral Research Associate, Lewis-Sigler Institute
Advisor: Olga Troyanskaya

University of Michigan *Summer 2011*
Research Assistant, Life Sciences Institute
Advisor: Daniel Klionsky

PUBLICATIONS

[17] **Ran Zhang**, Chengxiang Qiu, Gala Filippova, Gang Li, Jay Shendure, Jean-Philippe Vert, Xinxian Deng, William Stafford Noble, and Christine Disteche. ”Multicondition and multimodality single-cell temporal profile inference during mouse embryonic development” *Genome Research (2025, in press)*

[16] Gang Li, Hyeon-Jin Kim, Sriram Pendyala, **Ran Zhang**, Christine M. Disteche, Jean-Philippe Vert, Xinxian Deng, Doug Fowler, William Stafford Noble. ”Pseudotime analysis for time-series single-cell sequencing and imaging data” *Genome Biology (2025)*

[15] **Ran Zhang***, Mu Yang*, Jacob Schreiber, Diana R O'Day, James MA Turner, Jay Shendure, Christine M. Disteche, William Stafford Noble, and Xinxian Deng. "Cross-species imputation and comparison of single-cell transcriptomic profiles" *Genome Biology (2025)*

[14] 4D Nucleome Consortium, Job Dekker, Betul Akgol Oksuz, ..., **Ran Zhang**, ..., Jian Ma, William S Noble, Feng Yue. "An integrated view of the structure and function of the human 4D nucleome" *bioRxiv (2024)*

[13] Ruth Dannenfelser, Jeffrey Zhong, **Ran Zhang**, Vicky Yao. "Into the Single Cell Multiverse: an End-to-End Dataset for Procedural Knowledge Extraction in Biomedical Texts" *Accepted (NeurIPS Datasets and Benchmarking Track (2023))*

[12] Daniel Mar, Ilona Babenko, **Ran Zhang**, William Stafford Noble, Oleg Denisenko, Tomas Vaisar, and Karol Bomsztyk. "MultiomicsTracks96: A high throughput PIXUL-Matrix-based toolbox to profile frozen and FFPE tissues multiomes" *Laboratory Investigation (2023)*

[11] Laetitia Meng-Papaxanthos, **Ran Zhang**, Gang Li, Marco Cuturi, William Stafford Noble, Jean-Philippe Vert. "LSMMD-MA: Scaling multimodal data integration for single-cell genomics data analysis" *Bioinformatics (2023)*

[10] **Ran Zhang**, Margarete Knudsen, Pedro Del Cioppo Vasques, Alicja Tadych, Patricia Rodriguez-Rodriguez, Paul Greengard, Jean-Pierre Roussarie, Ana Milosevic#, and Olga Troyanskaya#. "Identifying genes and pathways linking astrocyte regional specificity to Alzheimer's disease susceptibility" *bioRxiv (2022) [Under Revision]*

[9] **Ran Zhang**, Laetitia Meng-Papaxanthos, Jean-Philippe Vert, William Stafford Noble. "Multimodal Single-Cell Translation and Alignment with Semi-Supervised Learning" *Journal of Computational Biology (2022)*

[8] **Ran Zhang**, Laetitia Meng-Papaxanthos, Jean-Philippe Vert, William Stafford Noble. "Semi-supervised single-cell cross-modality translation using Polarbear" *International Conference on Research in Computational Molecular Biology (2022)*

[7] Xi Chen, Jian Zhou, **Ran Zhang**, Aaron K Wong, Christopher Y Park, Chandra L Theesfeld, Olga G Troyanskaya. "Tissue-specific enhancer functional networks for associating distal regulatory regions to disease" *Cell Systems (2021)*

[6] Jose Henrique Ledo, **Ran Zhang**, Luka Mesin, Diego Mourão-Sá, Estefania P. Azevedo, Olga G. Troyanskaya, Victor Bustos, Paul Greengard. "Lack of a site-specific phosphorylation of Presenilin 1 disrupts microglial gene networks and progenitors during development" *PLoS One (2020)*

[5] Jose Henrique Ledo, Thomas Liebmann, **Ran Zhang**, Jerry C. Chang, Estefania P. Azevedo, Eitan Wong, Hernandez Moura Silva, Olga G. Troyanskaya, Victor Bustos, Paul Greengard. "Presenilin 1 phosphorylation regulates amyloid-β degradation by microglia" *Molecular Psychiatry (2020)*

[4] Arjun Krishnan*, **Ran Zhang***, Victoria Yao, Chandra L Theesfeld, Aaron K Wong, Alicja Tadych, Natalia Volfovsky, Alan Packer, Alex Lash, Olga G Troyanskaya. Genome-wide autism gene prediction and functional characterization" *Nature Neuroscience (2016)*

[3] Casey S Greene, Arjun Krishnan, Aaron K Wong, Emanuela Ricciotti, Rene A Zelaya, Daniel S Himmelstein, **Ran Zhang**, Boris M Hartmann, Elena Zaslavsky, Stuart C Sealfon, Daniel I Chasman, Garret A FitzGerald, Kara Dolinski, Tilo Grosser, Olga G Troyanskaya. "Understanding multicellular function and disease with human tissue-specific networks" *Nature Genetics (2015)*

[2] Qian Zhu, Aaron K Wong, Arjun Krishnan, Miriam R Aure, Alicja Tadych, **Ran Zhang**, David C Corney, Casey S Greene, Lars A Bongo, Vessela N Kristensen, Moses Charikar, Kai Li, Olga G Troyanskaya. "Targeted exploration and analysis of large cross-platform human transcriptomic compendia" *Nature Methods (2015)*

[1] JunYa Peng, **Ran Zhang**, YiTong Cui, HaoDong Liu, XiaoXin Zhao, Lei Huang, MingXu Hu, XiaoXi Yuan, BenYu Ma, XiaoWei Ma, Ueno Takashi, Komatsu Masaaki, XingJie Liang, Li Yu. "Atg5 regulates late endosome and lysosome biogenesis" *Science China Life Sciences (2014)*

GRANTS

NIH Pathway to Independence Awards (K99/R00, NHGRI) (2024 -)

INVITED TALKS

Cross-species imputation and comparison of single-cell transcriptomic profiles using Icebear.
– UW eScience Seminar (2025)

Decoding Tissue and Cellular Complexity using Network Models and Deep Learning.
– Westlake University (2024)

Multi-condition/modality inference of single-cell profiles during mouse embryonic development.
– 4DN Annual Meeting - 4D Nucleome program (2023)
– 4D-genome meeting (2023)

What we have learned trying to match images and omics in WTC11.
– 4DN IOWG Meeting (2024)
– 4DN IOWG Meeting (2023)

Integration and prediction of genomics data across modality, time, and species.
– Biology Department seminar, Western Washington University (2023)

Integration and imputation of functional genomics data across modality, time, and species.
– Genome Science seminar, University of Washington (2023)

Cross-species imputation and comparison of single-cell transcriptomics profiles.
– 4D-genome meeting (2023)

Modeling single cell profiles across time.
– 4D-genome meeting (2022)

Semi-supervised single-cell cross-modality translation using Polarbear.
– Research in Computational Molecular Biology (RECOMB 2022)
– Machine Learning in Computational Biology (MLCB 2021)
– 4D-genome meeting (2021)

Imputation of HFFc6 & WTC-11 1D profiles using Avocado.
– 4DN JAWG Meeting (2021)

Embedding analysis of WTC-11 single cell Hi-C data
– 4DN NOFIC-AICS Meeting (2020)

Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder.
– Cold Spring Harbor Laboratory (2016)
– Computational Systems for Integrative Genomics (2016)

REVIEWER

Nature Machine Intelligence
Genome Biology
PLOS Computational Biology
Bioinformatics
BMC Bioinformatics
Journal of Molecular Biology
Research in Computational Molecular Biology (RECOMB)
Intelligent Systems for Molecular Biology (ISMB)

Neural Information Processing Systems (NeurIPS)
Workshop on Algorithms in Bioinformatics (WABI)
ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)