Martin Jinye Zhang

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POSITION

Harvard University Boston, MA
Research Associate, Department of Epidemiology, Advisor: Alkes Price *July 2022 - Present*

Harvard University Boston, MA
Postdoctoral Researcher, Department of Epidemiology, Advisor: Alkes Price *Sept 2019 - June 2022*

EDUCATION

Stanford University Stanford, CA
Doctor of Philosophy (PhD), Department of Electrical Engineering, Advisor: David Tse *Sept 2014 - Sept 2019*

Stanford University Stanford, CA
Master of Science (MS), Department of Electrical Engineering *Sept 2014 - Jul 2017*

Tsinghua University Beijing, China
Bachelor of Engineering (B.Eng.), Department of Electrical Engineering *Sept 2010 - Jul 2014*

RESEARCH INTEREST

1. Integrating GWAS and single-cell RNA-seq data; and understanding how genetic variants impact gene expression levels and diseases in different cellular contexts.

2. Understanding common-and-rare-variant genetic architecture for complex diseases and traits; we are analyzing the UK Biobank WES data for this purpose.

3. Causal inference for multiomics data; distinguishing disease-causing genes from disease-responding genes; and ultimately, understanding how genetic intervention would change the course of diseases.

PUBLICATIONS

(* equal contributions, † corresponding authors)
Publications (as main author)

1. **Martin Jinye Zhang***, Kangcheng Hou*, Kushal K. Dey, Karthik A. Jagadeesh, Kathryn Weinand, Saori Sakaue, Aris Taychameekiatchai, Poorvi Rao, Angela Oliveira Pisco, James Zou, Bruce Wang, Michael Gandal, Soumya Raychaudhuri, Bogdan Pasaniuc†, Alkes L. Price†. "Polygenic enrichment distinguishes disease associations of individual cells in single-cell RNA-seq data", *Nature Genetics*, 2022.

2. **Martin Jinye Zhang**†, Angela Oliveira Pisco†, Spyros Darmanis, James Zou†. "Mouse Aging Cell Atlas Analysis Reveals Global and Cell Type Specific Aging Signatures", *eLife*, 2021.

3. **Martin Jinye Zhang***, Vasilis Ntranos*, and David Tse. "Determining sequencing depth in a single-cell RNA-seq experiment", *Nature Communications*, 2020. Selected as 2020 Top 50 Life and Biological Sciences Articles.

4. **Martin J. Zhang**, James Zou, and David Tse. "Adaptive Monte Carlo Multiple Testing via Multi-armed Bandits", *ICML*, 2019.

5. **Martin J. Zhang**, Fei Xia, and James Zou. "Fast and covariate-adaptive method amplifies detection power in large-scale multiple hypothesis testing", *Nature Communications*, 2019.
Preliminary version, named "AdaFDR: a Fast, Powerful and Covariate-Adaptive Approach to Multiple Hypothesis Testing", received the RECOMB 2019 Best Paper Award, one out of 175 submissions and 37 accepted papers.

6. Abubakar Abid*, **Martin J. Zhang***, Vivek K. Bagaria, and James Zou, "Exploring patterns enriched in a dataset with contrastive principal component analysis", *Nature Communications*, 2018.

7. Vivek Bagaria*, Govinda Kamath*, Vasilis Ntranos*, **Martin J. Zhang***, and David Tse, "Medoids in Almost Linear Time via Multi-armed Bandits", *AISTATS*, 2018.

8. Fei Xia*, **Martin J. Zhang***, James Zou, and David Tse, "NeuralFDR: Learning Discovery Thresholds from Hypothesis Features", *NeurIPS*, 2017 .

9. **Martin J. Zhang**, and Zhijian Ou, "Block-wise MAP Inference for the Determinantal Point Processes with Application to Change Point Detection", *SSP*, 2016.

10. **Jinye Zhang**, Laming Chen, Petros T. Boufounos, and Yuantao Gu, "On the Theoretical Analysis of Cross Validation in Compressive Sensing", *ICASSP*, 2014.

Publications (as supervisor)

1. Antonio Ginart, **Martin Jinye Zhang**, James Zou. "MLDemon: Deployment Monitoring for Machine Learning Systems", *AISTATS*, 2021.

2. Mo Tiwari, **Martin Jinye Zhang**, James Mayclin, Sebastian Thrun, Chris Piech, Ilan Shomorony. "Bandit-PAM: Almost Linear Time k-Medoids Clustering via Multi-Armed Bandits", *NeurIPS*, 2020.

Publications (as contributing author)

1. Xihao Li, Godwin Yung, Hufeng Zhou, Ryan Sun, Zilin Li, Kangcheng Hou, **Martin Jinye Zhang**, Yaowu Liu, Theodore Arapoglou, Chen Wang, Iuliana Ionita-Laza, Xihong Lin. "A multi-dimensional integrative scoring framework for predicting functional variants in the human genome", *The American Journal of Human Genetics*, 2022.

2. M Reza Sailani*, Ahmed A Metwally*, Wenyu Zhou, Sophia Miryam Schüssler-Fiorenza Rose, Sara Ahadi, Kevin Contrepois, Tejaswini Mishra, **Martin Jinye Zhang**, Łukasz Kidziński, Theodore J Chu, Michael P Snyder. "Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California", *Nature Communications*, 2020.

3. The Tabula Muris Consortium. "A single-cell transcriptomic atlas characterizes ageing tissues in the mouse", *Nature*, 2020.

4. Li Gao, Misun Kang, **Martin Jinye Zhang**, M. Reza Sailani, Ryutaro Kuraji, April Martinez, Changchang Ye, Pachiyappan Kamarajan, Charles Le, Ling Zhan, Hélène Rangé, Sunita P. Ho, Yvonne L. Kapila. "Polymicrobial periodontal disease triggers a wide radius of effect and unique virome", *npj Biofilms and Microbiomes*, 2020.

5. Wenyu Zhou*, M. Reza Sailani*, Kévin Contrepois*, Yanjiao Zhou*, Sara Ahadi*, Shana Leopold, **Martin J. Zhang**, · · · , George M. Weinstock, Michael Snyder, "Longitudinal multi-omics of host-microbe dynamics in prediabetes", *Nature*, 2018.

PROFESSIONAL SERVICES

1. Frontiers in Genetics topic editor for the research topic: molecular and genetic heterogeneity of human diseases.

2. Journal reviewer for *Nature Communications*, *BMC Biology*, *Bioinformatics*, *Journal of Machine Learning Research*, *Annals of Applied Statistics*, *Biometrics*, *Scientific Reports*, and *Journal of Genetics and Genomics*.

3. Conference reviewer for *IJCAI* (2021-22), *ICML* (2020-22), *ICLR* (2021), *NeurIPS* (2016, 2019-22)

4. 2015 - 2019: organizer for Information Systems Laboratory Colloquium, EE, Stanford.

Distinctions

1. Postdoctoral Semifinalist for the 2021 Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, ASHG, 2021

2. Reviewers' Choice award for poster "Polygenic enrichment distinguishes disease associations of individual cells in single-cell RNA-seq data", ASHG, 2021

3. Reviewers' Choice award for poster "Transcriptome-wide association studies and fine-mapping at cell-type resolution", ASHG, 2021

4. Top 50 Life and Biological Sciences Articles for the paper "Determining sequencing depth in a single-cell RNA-seq experiment", Nature Communications, 2020

5. Best Paper Award, RECOMB, 2019

6. Travel Awards: RECOMB 2019, NeurIPS 2017, PQG (Program in Quantitative Genomics at Harvard T.H. Chan School of Public Health)

7. Stanford Graduate Fellowship (SGF), Stanford University, 2015

8. Numerical Technologies Award in Electrical Engineering (Numerical Technologies Founders Graduate Fellowship), Stanford University, 2015

9. Ranked 2/79 in the EE Ph.D. qualifying exam, Stanford University, 2015

10. Outstanding Undergraduate Thesis for "Speech Diarization Based on the Determinantal Point Processes", Tsinghua University, 2014

11. Comprehensive Excellence Scholarship in Electronic Engineering, Tsinghua University, 2013