Martin Jinye Zhang

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Position

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

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

My research focuses on developing statistical methods for high-throughput sequencing data analysis like GWAS, RNA-Seq, and single-cell RNA-seq. I am also interested in general statistical and machine learning algorithms, particularly those involving data integration, adaptive sampling, and empirical Bayes modeling.

Publications

(* equal contributions)

1. 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", under review in *NeurIPS*, 2020.

2. **Martin Jinye Zhang**, Angela Oliveira Pisco, Spyros Darmanis, James Zou. "Mouse Aging Cell Atlas Analysis Reveals Global and Cell Type Specific Aging Signatures", under review in *eLife*, 2020.

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

4. **Martin Jinye Zhang***, Vasilis Ntranos*, and David Tse. "Determining sequencing depth in a single-cell RNA-seq experiment", *Nature Communications*, 2020.

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

6. **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.

7. 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.

8. 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.

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

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

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

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

Talks

1. "Adaptive Monte Carlo Multiple Testing via Multi-armed Bandits", ICML 2019.

2. "AdaFDR: a Fast, Powerful and Covariate-Adaptive Approach to Multiple Hypothesis Testing", RECOMB 2019.

3. "Optimal sequencing-budget allocation for single-cell RNA-seq", CISS 2019.

4. "Adaptive Monte Carlo Multiple Testing via Multi-armed Bandits", ITA 2019.

Professional Services

1. Reviewer for *Nature Communications*, *BMC Biology,*, *Bioinformatics*, *Biometrics*, *Journal of Genetics and Genomics*, *NeurIPS 2020*, *ICML 2020*, *NeurIPS 2019*, *NeurIPS 2019*.

2. 2015 - 2019: organizer for Information Systems Laboratory Colloquium, EE, Stanford.

Internships

- **Grail, Inc. (early cancer detection via cell-free DNA)** — Menlo Park, CA
  Bioinformatician — *Jun - Sep, 2018*
  - **Project**: cancer patient classification via cell-free RNA.
- **Genapsys, Inc. (next generation high-throughput sequencer)** — Redwood city, CA
  Research Scientist — *Jun - Sep, 2017*
  - **Project**: sensor signal clustering.
- **Baidu, Inc.** — Beijing, China
  R & D Engineer, Department of Natural Language Processing — *Sep 2013 - Feb 2014*
  - **Project**: query-parsing or Baidu's voice assistant.

Distinctions

1. RECOMB 2019 Best Paper Award (Research in Computational Molecular Biology)

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

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

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

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

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

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