Zixuan (Eleanor) Zhang

zzhang39@usc.edu ● 1450 Biggy Street, LA, CA, 90033 ● (530) 979-4001 ● https://zixuanzhang.github.io

EDUCATION

University of Southern California, Keck School of Medicine   Expected 08/2025
PhD candidate in Biostatistics
Advisor: co-advised by Dr. Nicholas Mancuso and Dr. Steven Gazal
GPA: 3.97/4.0

Columbia University, Mailman School of Public Health   05/2020
Master of Science (MS) in Biostatistics
Advisor: Dr. Cheng-Shiun Leu
GPA: 4.0/4.3

University of California, Davis   06/2018
Bachelor of Science (BS) in Genetics & Genomics
- Graduated with high honors. GPA: 3.8/4.0

RESEARCH INTEREST

- Efficient statistical and computational approaches to analyze genetic and genomics data to characterize genetic architectures in human complex traits.
- Molecular QTL mapping using single cell data.

PUBLICATIONS

1. ***Zhang, Z. E.***, Kim, A., Suboc, N., Mancuso, N. & Gazal, S. (2025). Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping. *medRxiv*.
2. ***Zhang, Z.***, Jung, J., Kim, A., Suboc, N., Gazal, S., and Mancuso, N. (2023). A scalable approach to characterize pleiotropy across thousands of human diseases and complex traits using GWAS summary statistics. *Am. J. Hum. Genet*.
3. Wang, J., ***Zhang, Z.***, Lu, Z., Mancuso, N., and Gazal, S. (2024). Genes with differential expression across ancestries are enriched in ancestry-specific disease effects likely due to gene-by-environment interactions. *Am. J. Hum. Genet.*
4. Kim, A., ***Zhang, Z.***, Legros, C., Lu, Z., de Smith, A., Moore, J.E., Mancuso, N., and Gazal, S. (2024). Inferring causal cell types of human diseases and risk variants from candidate regulatory elements. *medRxiv*.

JOURNAL ARTICLES IN PREP

1. Rui, X., Lu, Z., ***Zhang, Z.***, Gazal, S., and Mancuso, N. scFM: An efficient statistical fine-mapping approach for eQTLs using large-scale single-cell data.
2. Zhao, Y., ***Zhang, Z.***, Carr, M., and Mancuso, N. Efficient saddlepoint approximation in generalized linear model for large-scale genetic association studies.

PRESENTATIONS

1. ***Zixuan Zhang***, Artem Kim, Noah Suboc, Nicholas Mancuso, Steven Gazal. (Nov 6, 2024). "Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping." *American Society of Human Genetics conference 2024.* (Poster)

2. ***Zixuan Zhang***, Nicholas Mancuso, Steven Gazal. (July 22, 2024). "Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping." *Computational Genomics Summer Institute (CGSI) 2024.* (**Talk**)

3. ***Zixuan Zhang***, Junghyun Jung, Artem Kim, Steven Gazal, Nicholas Mancuso. (Feb 16, 2024). "A variational Bayesian approach to characterize pleiotropic components across thousands of human diseases and complex traits using GWAS summary statistics." Dr. Xiang Zhou's group at University of Michigan. (**Invited talk**)

4. ***Zixuan Zhang***, Steven Gazal, Nicholas Mancuso. (May 9, 2023). "Scalable count-based models improve power and robustness to detect eQTLs in large-scale single-cell data." *Biology of Genome conference 2024.* (Poster)

5. ***Zixuan Zhang***, Steven Gazal, Nicholas Mancuso. (Nov 2, 2023). "Scalable count-based models improve power and robustness to detect eQTLs in large-scale single-cell data." *American Society of Human Genetics conference 2023.* (Poster)

6. ***Zixuan Zhang***, Steven Gazal, Nicholas Mancuso. (Oct 17, 2023). "Scalable count-based models improve power and robustness to detect eQTLs in large-scale single-cell data." *Program in Quantitative Genomics conference 2023.* (Poster)

7. ***Zixuan Zhang***, Nicole Li, Miao Zang, Huan Cheng. (Aug 17, 2023). "Simulation study for basket trial design." *Statistics in Pharmaceuticals conference 2023.* (Poster)

8. ***Zixuan Zhang***, Junghyun Jung, Artem Kim, Steven Gazal, Nicholas Mancuso. (Aug 1, 2023). "A variational Bayesian approach to characterize pleiotropic components across thousands of human diseases and complex traits using GWAS summary statistics." *Computational Genomics Summer Institute (CGSI) 2023.* (**Talk**)

9. ***Zixuan Zhang***, Junghyun Jung, Artem Kim, Steven Gazal, Nicholas Mancuso. (March 9, 2023). "A variational Bayesian approach to characterize pleiotropic components across thousands of human diseases and complex traits using GWAS summary statistics." *Probabilistic Modeling in Genomics conference 2023.* (Poster)

10. ***Zixuan Zhang***, Junghyun Jung, Steven Gazal, Nicholas Mancuso. (Oct 26, 2022). "A variational Bayesian approach to characterize pleiotropic components across thousands of human diseases and complex traits using GWAS summary statistics." *American Society of Human Genetics conference 2022.* (**Platform Talk**)

11. ***Zixuan Zhang***, Junghyun Jung, Noah Suboc, Steven Gazal, Nicholas Mancuso. (Oct 18, 2021). "A variational Bayesian approach to characterize latent genetic components using GWAS summary statistics." *American Society of Human Genetics conference 2021.* (Poster)

12. ***Zixuan Zhang***, Timothy J. Lewis, Daisuke Sato. (April 27, 2018). "Stochastic ion channel activity in ischemic regions of the heart can cause reflected waves." *Undergraduate Research Conference at UC Davis, CA.* (Poster)

FELLOWSHIPS & REWARDS

Student Success Scholarship, Department of Population and Public Health Sciences $500	10/2024
Conference Travel Award, Department of Population and Public Health Sciences $500	10/2023
Keck School of Medicine Dean's Fellowship Role: PhD student $36,000	2020-2021

TEACHING EXPERIENCE

Department of Population and Public Health Sciences, Keck School of Medicine, USC *Instructor for R bootcamp workshop*	08/24

- Data wrangling, basic Linux commands and using R on HPC.

Department of Population and Public Health Sciences, Keck School of Medicine, USC *Teaching Assistant, Machine Learning for the Health Sciences*	01/24-05/24

- Machine learning approaches and implementation using R.

Department of Population and Public Health Sciences, Keck School of Medicine, USC *Instructor for R bootcamp workshop*	08/22

- Parallel computing in R, basic Linux commands and batch jobs on HPC.

Department of Biostatistics, Columbia University Medical Center *Teaching Assistant, Biostatistics Method I*	09/19-12/19

- Biostatistics method including hypothesis testing and linear regression.

Department of Biostatistics, Columbia University Medical Center *Teaching Assistant, Data Science I*	09/19-12/19

- Exploratory data analysis, regression methods, build dashboard, visualization, and GitHub Pages using R.

HONORS

Recipient, Dean's Honors List, College of Letters and Sciences,   Fall 2014
Recipient, Dean's Honors List, College of Agricultural and Environmental Sciences,   Winter 2015 and Fall 2015
Recipient, Dean's Honors List, College of Biological Sciences,   Spring 2017 and Spring 2018

SERVICE

Manuscript reviewer
- Nature Genetics
- Nature Communication
- Human Genetics and Genomics (HGG) Advances
- PLOS Genetics
- Cell Genomics
- Frontier in Neuroscience
- PeerJ Computer Science

President   08/22-08/24
Graduate Society of Biostatistics and Epidemiology (GSBE) at Keck School of Medicine, USC
- Organized academic and career development events such as book clubs, workshops, and social events.
- Collaborated with PhD program directors on social events such as "greet and meet" between faculty member and students.
- Represented GSBE to give celebration speech for graduation ceremony and welcoming talk for school orientation.

President   01/18-01/20
Career China Club at Columbia University Mailman School of Public Health
- Planned events for student panel talk of internship experience.
- Invited speakers from pharmaceutical industries to visit campus and share working experience with students.

UNDERGRADUATE AND GRADUATE (OR OTHER) MENTORSHIP

2021-	Noah Suboc	Undergraduate at USC	Generated figures for scientific publication
2023-	Yu Zhao	MS, Biostatistics	Creating efficient saddlepoint approximation for generalized linear models
2024-	Yunqing Ke	MS, Biostatistics	Cis- and trans-eQTL mapping using single cell data for GWAS risk variants
2024-	Hongbo Wang	MS, Biostatistics	Factor analysis using FactorGo on GWAS summary statistics data

SKILLS

- Softwares: R, Python (*Numpy, Panda, JAX*), Linux, shell scripting, HPC, Git & GitHub
- Relevant coursework: Machine learning, Deep learning, Advanced statistical computing, High dimensional data, Generalized linear models, Mixed effects modeling

REFERENCES

Nicholas Mancuso, PhD
Associate Professor in Biostatistics at the Center for Genetic Epidemiology,
Department of Population and Public Health Sciences at USC Keck School of Medicine
1450 Biggy Street
Los Angeles, CA, US, 90033
Email: Nicholas.Mancuso@med.usc.edu

Steven Gazal, PhD
Assistant Professor of Biostatistics at the Center for Genetic Epidemiology,
Department of Population and Public Health Sciences at USC Keck School of Medicine
1450 Biggy Street
Los Angeles, CA, US, 90033
Email: gazal@usc.edu

Na Cai, PhD
Assistant Professor in Computational Medical Genomics, ETH, Zurich,
Rämistrasse 101, 8092 Zürich, Switzerland
Email: na.cai@bsse.ethz.ch