

Chang Su

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Employment

2023- Assistant Professor, Department of Biostatistics and Bioinformatics, Emory University

Education

2018-2023 Ph.D., Biostatistics, Yale University
Advisors: Hongyu Zhao and Zhou Fan
2014-2018 B.S., Statistics, Sun Yat-sen University

Research Interests

Fields: Statistical methods for single cell genomics and genetics

Topics: Gene networks, Gene regulation, Transcriptome-wide association studies, Confounder adjustment, Quantitative trait loci mapping

Publications

Statistical Methodologies

- [1] Biao Cai, Jingfei Zhang, Hongyu Li, **Chang Su** and Hongyu Zhao (2024). Statistical inference of cell-type proportions estimated from bulk expression data. *Journal of the American Statistical Association*. [[paper](#)]
- [2] **Chang Su**, Jingfei Zhang, Hongyu Zhao (2024). Estimating cell-type-specific gene co-expression networks from bulk gene expression data with an application to Alzheimer's disease. *Journal of the American Statistical Association*. [[paper](#)] [[code](#)] [[R package](#)]
- [3] **Chang Su**, Zichun Xu, Xinning Shan, Biao Cai, Hongyu Zhao, Jingfei Zhang (2023). Cell-type-specific co-expression inference from single cell RNA-sequencing data. *Nature Communications*. [[paper](#)] [[R package](#)] [[Python package](#)]
- [4] Xinyi Zhong*, **Chang Su***, Zhou Fan (2022). Empirical Bayes PCA in high dimensions. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. [[paper](#)] [[software](#)]
*: equal contribution

Collaborative Work

- [1] Hussain Bukhari*, **Chang Su***, Elvisha Dhamala, Zijin Gu, Keith Jamison, Amy Kuceyeski (2023). A graph-matching based metric of functional connectome distance between pairs of individuals varies with their ages, cognitive performances and familial relationships. *Human Brain Mapping*. [[paper](#)]
*: **equal contribution**
- [2] Le Zhang, Chuan Hua He, Sarah Coffey, ..., **Chang Su**, ..., David A Hafler, Hongyu Zhao, Stephen M Strittmatter (2023). Single-cell transcriptomic atlas of Alzheimer’s disease middle temporal gyrus reveals region, cell type and sex specificity of gene expression with novel genetic risk for MERTK in female. *Under revision at Nature Communications*. [[preprint](#)]
- [3] Biqing Zhu, Jae-Min Park, Sarah Coffey, ..., **Chang Su**, Hongyu Zhao, David A Hafler, Sreeganga S Chandra, Le Zhang (2022). Single-cell transcriptomic and proteomic analysis of Parkinson’s disease brains. *Under revision at Science Translational Medicine*. [[preprint](#)]

Talks and Presentations

† *Indicates scheduled*

- 2024 Sydney Precision Data Science Centre at The University of Sydney (virtual) †
- 2024 STATGEN 2024: Conference on Statistics in Genomics and Genetics, Pittsburgh, PA
Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data
(Invited session)
- 2024 DBIDS Informatics seminar, the University of Alabama at Birmingham
Statistical inference of cell-type-specific gene co-expression networks with single cell and bulk RNA-seq data
- 2024 MCBIOS 2024: MidSouth Computational Biology and Bioinformatics Society Annual Conference, Atlanta, GA
Statistical inference of cell-type-specific gene co-expression networks with single cell and bulk RNA-seq data
- 2023 Biology of Genomes, Cold Spring Harbor
Cell-type-specific co-expression inference with single cell RNA sequencing data. (Selected talk)
- 2022 Annual Meeting of American Society of Human Genetics, Los Angeles, CA
CS-CORE: cell-type-specific co-expression inference with single cell RNA sequencing data. (Poster)
- 2022 Join Statistical Meeting, Washington DC
Estimating cell-type-specific gene co-expression networks from bulk gene expression data with an application to Alzheimer’s disease.
- 2022 ENAR, Houston, TX
Estimating cell-type-specific gene co-expressions from bulk RNA-seq data.

Grants

2024-2025	PI: Georgia CTSA BERD pilot grant <i>Title: Mapping the genetic control of gene expression with single-cell omics data</i>
2023-	Co-I: NIH R01GM141074 (Hu), 4.2 calendar months <i>Title: Novel Statistical Methods for Analyzing Complex Microbiome Data</i>
2023-	Co-I, NIH R01HL166455 (Hu), 1.2 calendar months <i>Title: Cadmium and Arsenic Effects on Pyrimidine Biosynthesis in Early Airway Development</i>

Teaching

Instructor

2024 Fall	BIOS 555: High Throughput Data Analysis Using R & Bioconductor, Emory University
2024 Spring	BIOS 590 & 790: Seminar in Biostatistics, Emory University
2023 Fall	BIOS 590 & 790: Seminar in Biostatistics, Emory University
2023 Fall	BIOS 516: Introduction to Large-scale Biomedical Data Analysis (Guest lecture), Emory University

Teaching Fellow

2019 Fall	BIS 557: Computational Statistics, Yale University
2020 Spring	S&DS 240: An Introduction to Probability Theory, Yale University
2020 Summer	BIS 515: Accelerated Biostatistics, Yale University

Mentorship

Ph.D. students

2024 -	Yutong Liu, Emory Rollins School of Public Health (Ph.D. in Biostatistics)
2023-	Dongsoo Lee, Emory Rollins School of Public Health (Ph.D. in Biostatistics)

Master and undergraduate students

2024-	Xinyi Chen, University of Washington (MS in Statistics)
2023-	Xuebo Wang, Emory Rollins School of Public Health (MSPH in Biostatistics)
2023-2024	Jessica Chan, Emory Rollins School of Public Health (MSPH in Biostatistics)
2022-2023	Zichun Xu, Yale School of Public Health (M.S. in Biostatistics)
2022-2023	Xinning Shan, Yale School of Public Health (M.S. in Biostatistics)
2022-2023	Karen Li, Yale School of Public Health (M.S. in Biostatistics)
2022-2023	Xinyi Chen, University of Toronto (B.S. in Statistics and Computer Science)

Professional Services & Activities

Committee

2024-	Broad member, MidSouth Computational Biology and Bioinformatics Society (MCBIOS)
2023-2024	Co-chair, Organizing committee, 2024 MCBIOS Annual Conference
2023-2024	Departmental seminar, Department of Biostatistics and Bioinformatics, Emory University
2023-	Computation and Data Science Advisory Group, Emory Rollins School of Public Health

Conference

2024 JSM	Session chair, <i>Modeling networks with textual edges</i>
2024 JSM	Session chair, <i>Novel statistical and AI methods for single-cell and spatial transcriptomic data analysis</i>

Referee Services

Transactions on Machine Learning Research, Journal of Computational and Graphical Statistics, Plos Genetics, Genome Biology (4), Bioinformatics (2), PLOS Computational Biology, Journal of Genetics and Genomics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, NAR Genomics and Bioinformatics

Membership

American Statistical Association (ASA), American Society of Human Genetics (ASHG), Eastern North American Region (ENAR)

Honors and Awards

2023	JXTX + CSHL Biology of Genomes Scholarship
2023	YSPH Conference Fund Travel Award, Yale School of Public Health
2022,2023	Graduate Student Assembly Conference Travel Fellowship Award, Yale Graduate School of Arts and Sciences
2018	Distinguished Graduate of Sun Yat-sen University
2017	National Scholarship (top 1%)

Academic Experience

2018 Summer	Visiting student, Hong Kong University of Science and Technology
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Industry Experience

2022 Summer Research scientist intern, Meta