Chang Su

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Employment

2023-	Assistant Professor, Department of Biostatistics and Bioinformatics, Emory University
2024-	Assistant Professor, Department of Human Genetics, Emory University (secondary)

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 regulation, Genetic basis of gene expression, Confounder adjustment
Diseases: Alzheimer’s disease, lung diseases, HIV

Publications

***: equal contribution** **†: corresponding author** ___: **trainees**

Statistical Methodologies

[1] **Chang Su**†, Dongsoo Lee, Peng Jin, Jingfei Zhang† (2024). Cell-type-specific mapping of enhancers and target genes from single-cell multimodal data. *Under revision at Nature Communications.* [preprint] [R package]

[2] **Chang Su**, Mengyu He, Vanessa Van Doren, Colleen Kelley, Yi-Juan Hu (2024). TestNet: A Testing Method for Inferring Microbial Networks Using Compositional Data with FalseDiscovery Rate Control. *Under review.*

[3] Biao Cai, Jingfei Zhang, Hongyu Li, **Chang Su**, Hongyu Zhao (2024). Statistical inference of cell-type proportions estimated from bulk expression data. *Journal of the American Statistical Association.* [paper]

[4] **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]

[5] **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]

[6] 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]

Collaborative Work

[1] 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. *Science Translational Medicine.* [preprint]

[2] 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]

[3] 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]

Talks and Presentations

† *Indicates scheduled*

2025	STATGEN, Minnesota, Minneapolis (Invited session)† *Investigating genetic regulation of gene expression using single-cell data* *A powerful statistical framework for single-cell transcriptome-wide association studies* (presented by Zhaotong Lin)
2024	ASHG, Denver, Colorado (Poster, Reviewers' Choice Abstracts) *Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data*
2024	Georgia Statistics Day, Atlanta, Georgia (Invited session) *Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data*
2024	Sydney Precision Data Science Centre at The University of Sydney (Invited, virtual) *Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data*
2024	JSM 2024, Portland, Oregon (Invited session) *Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data*
2024	STATGEN 2024, Pittsburgh, PA (Invited session) *Cell-type-specific mapping of enhancer-gene pairs from multimodal single cell data*
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 (Selected talk) *Cell-type-specific co-expression inference with single cell RNA sequencing data.*
2022	ASHG, Los Angeles, CA (Poster) *CS-CORE: cell-type-specific co-expression inference with single cell RNA sequencing data.*
2022	JSM, 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**: NIH R01GM141074 (Su), 4.2 calendar months *Title: Novel Statistical Methods for Analyzing Complex Microbiome Data*
2024-2025	**PI**: Georgia CTSA BERD pilot grant *Title: Mapping the genetic control of gene expression with single-cell omics data*
2024-	**Co-I**, NIH R01AI174933 (Smith), 0.6 calendar months *Title: Defining Sex-Specific Systemic and Gut inflammatory Profiles in People Living with HIV*
2024-	**BIOS Core member**, NIH P30AI050409 (Carlos), 0.84 calendar months *Title: Center for AIDS Research at Emory University*
2023-	**Co-I**, NIH R01HL166455 (Hu), 1.2 calendar months *Title: Cadmium and Arsenic Effects on Pyrimidine Biosynthesis in Early Airway Development*
2023-2024	**Co-I**: NIH R01GM141074 (Hu), 4.2 calendar months *Title: Novel Statistical Methods for Analyzing Complex Microbiome Data*

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 University (Ph.D. in Biostatistics, co-mentor with Steve Qin)
2023-	Dongsoo Lee, Emory University (Ph.D. in Biostatistics)

Master and undergraduate students

2024-	Weiwei Wu, Emory University (MSPH graduate in Biostatistics, staff)
2024-	Zhengyi Ou, Emory University (MSPH in Biostatistics)
2024-	Guanru Chen, Sun Yat-sen University (Undergrad in Statistics)
2024-	Xinyi Chen, University of Washington (MS in Statistics)
2023-	Xuebo Wang, Emory University (MSPH in Biostatistics)
2023-2024	Jessica Chan, Emory University (MSPH in Biostatistics)
2022-2023	Zichun Xu, Yale University (M.S. in Biostatistics)
2022-2023	Xinning Shan, Yale University (M.S. in Biostatistics)
2022-2023	Karen Li, Yale University (M.S. in Biostatistics)
2022-2023	Xinyi Chen, University of Toronto (B.S. in Statistics and Computer Science)

Professional Services & Activities

Conference

2025 JSM	Session co-chair, *Innovative Statistical Methods and AI for unlocking the power of spatial omics* (Invited session)[†]
2025 STATGEN	Session chair, *Addressing emerging challenges in population-scale single-cell RNA-Seq studies: new statistical and machine learning methods* (Invited session)[†]
2024 JSM	Session chair, *Modeling networks with textual edges*
2024 JSM	Session chair, *Novel statistical and AI methods for single-cell and spatial transcriptomic data analysis*
2024 MCBIOS	Session chair, *Statistical methods for integrative analysis of genetics and omics data*
2024 MCBIOS	Conference co-chair, 2024 MCBIOS Annual Conference

Committee

2024-	Broad member, MidSouth Computational Biology and Bioinformatics Society
2023-	Computation and Data Science Advisory Group, Emory University
2023-2024	Departmental seminar, Department of Biostatistics and Bioinformatics, Emory University

Referee Services

Nature Communications, Cell Systems, Genome Biology, Bioinformatics, Biometrics, Plos Genetics, PLOS Computational Biology, Genomics, Proteomics & Bioinformatics, NAR Genomics and Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of Genetics and Genomics

Journal of Computational and Graphical Statistics, Transactions on Machine Learning Research

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 University
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

Industry Experience

2022 Summer	Research scientist intern, Meta