

ZHENXING GUO

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Employment

- **Nov. 2022 – Present, Assistant Professor (Tenure-track)** School of Data Science, Chinese University of Hong Kong, Shenzhen, Guangdong, China.

Education

- **Ph.D in Biostatistics** 2017 - 2022
Department of Biostatistics and Bioinformatics
Emory University, Atlanta, USA.
- **M.S. in Operational Research** 2014 - 2017
Academy of Mathematics and System Science (AMSS)
Chinese Academy of Sciences (CAS), Beijing, China.
- **B.S. in Applied Mathematics** 2010 - 2014
College of Mathematics & Econometrics
Hunan University, Changsha, China.

Previous Work Experience

- **June 2020 - August 2020, Statistical Technical Summer Intern** at Bristol Myers Squibb, Summit, NJ 07901, USA
Mentors: Rong Liu
Role: Augmentation of current clinical trial with external real world data using Bayesian techniques.

Research Interests

- Statistical Methodology: Epitranscriptomics and multi-omics data analyses. My detailed research interests lies in the development of statistically principled and computationally efficient method and tools for the analysis of biomedical data, in particular, omics data.

- Applications: Cancer, Alzheimer’s disease, asthma, cardiovascular diseases, obesity.

Publications of methodological works

† for co-first authorship, and * for co-corresponding authorship

- L Chen†, **Z. Guo**†, T Deng, H Wu, scCTS: identifying the cell type specific marker genes from population-level single-cell RNA-seq. **Under review**, 2023.
- **Z. Guo**†, D Duan†, W Tang, J Zhu, W S Bush, L Zhang, X Zhu, F Jin, H Feng (2023), magpie: a power evaluation method for differential RNA methylation analysis in N6-methyladenosine sequencing. **major revision at PLOS Computational Biology**.
- D. Duan, W. Tang, R. Shu, **Z. Guo***, H. Feng* (2023) Evaluation of Differential Epitranscriptome Analysis Methods. **Briefings in Bioinformatics**, 24 (3), bbad139.
- **Z. Guo**, A. M. Shafik, P. Jin, H. Wu (2022) *Differential RNA Methylation Analysis for MeRIP-seq Data under General Experimental Design*. **Bioinformatics**, 38(20): 4705-4712.
- **Z. Guo**, A. M. Shafik, P. Jin, Z. Wu, H. Wu (2021) *Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing*. **Bioinformatics**, 37(18): 2818–2824. <https://doi.org/10.1093/bioinformatics/btab181>
- Z Li, **Z. Guo**, Y Cheng, P Jin, H Wu. Robust partial reference-free cell composition estimation from tissue expression. **Bioinformatics**, (2020), 36(11): 3431-3438. <https://academic.oup.com/bioinformatics/article/36/11/3431/5804977>
- **Z. Guo**†, Y Cui†, X Shi, JA Birchler, I Albizua, SL Sherman, ZS Qin*, T Ji* (2020) *An empirical bayesian approach for testing gene expression fold change and its application in detecting global dosage effects*. **NAR Genomics and Bioinformatics**, 2(3):lqaa072. <https://academic.oup.com/nargab/article/2/3/lqaa072/5908375>
- **Z. Guo**, S Zhang (2020) *Sparse deep nonnegative matrix factorization*. **Big Data Mining and Analytics**, 3(1):13-28. <https://ieeexplore.ieee.org/document/8935092>

Collaborative works

- Y. Pan, K. Kathleen, **Z. Guo**, Y. Yang, G. Khalil, R. Kelly, B. Switzer (202x) *Simulation Study for Improving Efficacy Estimates for New HIV Treatments*. *In preparation*.
- M. C. Runnstrom1, A. Morrison-Porter, M. Ravindran, H. Quehl, R. Ramonell, M. Woodruff, M. Kuruvilla, F. Anam, R. Swerlick, C. Swenson, C. Polito, W. Neveu, R. Patel, C. Kim, l. Hentenaar, **Z. Guo**, H. Wu, N. S. Haddad, J. L. Daiss, I. Sanz, F. E. Lee* (2022), *Reduced SARS-CoV-2 Vaccine Response in Patients Treated with Biologic Therapies for Asthma*. **Journal of Allergy and Clinical Immunology**, 149(2):AB319. [https://www.jacionline.org/article/S0091-6749\(21\)01844-3/fulltext](https://www.jacionline.org/article/S0091-6749(21)01844-3/fulltext)
- A. M. Shafik, F. Zhang, **Z. Guo**, Q. Dai, K. Pajdzik, Y. Li, Y. Kang, B. Yao, H. Wu, C. He, E. G. Allen, R. Duan, P. Jin* (2021) *N6-methyladenosine dynamics in neurodevelopment and aging, and its potential role in Alzheimer’s disease*. **Genome Biology**, 22(1):1-19. <https://link.springer.com/article/10.1186/s13059-020-02249-z>

Book Chapters

- **Z. Guo**, A. Shafik, P. Jin, Z. Wu, H. Wu (2023) Analyzing mRNA epigenetic sequencing data with TRESS. In: H. Oliveira, P. (eds) Computational Epigenomics and Epitranscriptomics. Methods in Molecular Biology, vol 2624. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-2962-8_12.

Software Developed

- **TRESS**: Toolbox for mRNA Epigenetics Sequencing analysis. An R/Bioconductor package for analysis of RNA methylation sequencing data. Available at <https://bioconductor.org/packages/devel/bioc/html/TRESS.html>.
— Software based on publication Guo 2021 **Bioinformatics**; Guo 2022 **Bioinformatics**.
- **Foldseq**: Fold change detection from RNA-seq data. An R package for testing gene expression fold change. Available on github at <https://github.com/cuiyingbeicheng/Foldseq>.
— Software based on publication Guo 2020 **NAR Genomics and Bioinformatics**

Presentations

- Guo, Z. Differential m⁶A Analysis for MeRIP-seq Data under General Experimental Design. Poster Presentation at Georgia Statistics Day, Atlanta, GA Oct 2021
- Guo Z., Shafik A. M., Jin P., Wu Z., Wu H. (2021) Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing. JSM 2021, Virtual Aug 2021

Invited talks / lectures at other academic institutes

- Benchmark of N6-methyladenosine differential analysis methods and a Power Assessment Tool for MeRIP-seq. CSBMB 2023, Tai'an, China. September 2023
- Evaluation of Differential Epitranscriptome Analysis Methods. ICSA China 2023, Chengdu, China. July 2023
- Statistical method and tools for RNA methylation sequencing analysis. Department of Population and Quantitative Health Sciences, School of Medicine, Case Western Reserve University. May 2022
- Statistical method and tools for RNA methylation sequencing analysis. School of Data Science, Chinese University of Hong Kong, Shenzhen. April 2022
- Including Historical Data in Clinical Trial Analysis. Summer school at Shandong University. July 2021

Teaching Experience

At SDS, CUHK-SZ

- Instructor. Spring 2023: STA2004 Mathematical statistics

- Instructor. Spring 2023: STA3002 Generalized Linear Models

At Emory

- Teaching assistant. Fall 2020: BIOS 731 Advanced statistical computing.
- Teaching assistant. Spring 2020: BIOS 545 R programming.
- Teaching assistant. Fall 2019: BIOS 555 High-throughput data analysis using R/Bioconductor.
- Teaching assistant. Spring 2019: BIOS 591P Lab “Biostatistics Methods II”.
- Teaching assistant. Fall 2018: BIOS 500/003: Statistical Methods I Group C.

Service at CUHK-SZ

- 2022-2023 PhD in Data Science Admission Committee
- 2022-2023 MSc in Bioinformatics Admission Committee

Mentoring at Emory

- PhD student mentor for 1st year theory and 2nd year method qualifying exam, 2020.
- PhD student mentor for 2nd year theory qualifying exam, 2021.

Honors and Award

- Honorable Mention, Emory Biostatistics senior PhD student presentation competition, 2022.
- Excellent Poster Award of Georgia Statistics Day, 2021.
- Michael H. Kutner Doctoral Student Award, Emory University, 2021-2022.
- JSM Distinguished Student Paper Award, 2021.

Professional Membership

- American Statistical Association (ASA)
- The International Biometric Society — Eastern North American Region (ENAR)
- International Chinese Statistical Association (ICSA)

Computational Skills

- Programming Languages: R, SAS, Matlab, Python
- Operating Systems: Windows, Unix