Zhenxing Guo

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Google scholar: `https://scholar.google.com.hk/citations?user=hm0mP4EAAAAJ&hl=zh-CN`

Education

- **Ph.D. candidate in Biostatistics and Bioinformatics**   2017 - Present
  Emory University, Laney Graduate School
  — Advisor: Hao Wu

- **M.S. in Operational Research**   2014 - 2017
  Academy of Mathematics and System Science (AMSS)
  Chinese Academy of Sciences (CAS), Beijing, China.
  — Advisor: Shihua Zhang
  — Thesis: *Models and Algorithms for Sparse deep nonnegative matrix factorization*

- **B.S. in Applied Mathematics**   2010 - 2014
  College of Mathematics & Econometrics
  Hunan University, Changsha, China.

Published Methodological work

- **Z. Guo**, A. M. Shafik, P. Jin, H. Wu (202x) *Differential RNA Methylation Analysis for MeRIP-seq Data under General Experimental Design.* **Bioinformatics** *under revision.*

- **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`

Collaborations

- 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* (202x) *Reduced SARS-CoV-2 Vaccine Response in Patients Treated with Biologic Therapies for Asthma.* **In preparation**.

- Y. Pan*, Y. Yang, K. Kathleen, G. Khalil, R. Kelly, B. Switzer, **Z. Guo** (202x) *Simulation Study for Improving Efficacy Estimates for New HIV Treatments.* **In preparation**.

- 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

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**.

- **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 m^{6}A 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

- Guest speaker at 2021 Summer school at Shandong University   July 2021
  — Topic: *Including Historical Data in Clinical Trial Analysis*
  — Invited by **Rong Liu**, Senior Director, Biostatistics, Hematology, Cell Therapy at Bristol Myers Squibb.

Invited talks at other academic institutes

- Statistical method and tools for RNA methylation sequencing analysis. Department of Population and Quantitative Health Sciences, School of Medicine, Case Western Reserve University, Virtual   May 2022

Mentoring Experience

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

- PhD student mentor for 2nd year theory qualifying exam, 2021.

Teaching Experience

- 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.

Work Experience

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

- Oct 2018 – May 2021, Research assistant, Emory University, Department of Biostatistics and Bioinformatics, Atlanta, GA
  Advisor: Prof. Hao Wu
  Role: Research projects on high-throughput genomic sequencing data

Honors and Award

PhD career:

- 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.

- SAS Certified Base Programmer for SAS 9, 2017.

Undergraduate career:

- Outstanding Graduate of Hunan University, 2014.

- First Prize of Dissertation, Hunan University, 2014.

- Merit Student of Hunan University (top 6%), Hunan University, 2011-2012, 2012-2013.

- National Scholarship($<1\%$), Hunan University, 2011-2012.

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

- Operating Systems: Windows, Unix