

Guanxun Li, Ph.D.

✉ guanxun@stat.tamu.edu

🐙 <https://github.com/guanxunli>

🌐 <https://guanxunli.github.io>

Education

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| Sep. 2022 - Now | 📖 Postdoctoral Research Associate in Statistics, Texas A&M University |
| Sep. 2018 - Aug. 2022 | 📖 Ph.D. in Statistics, Texas A&M University |
| Sep. 2016 - May. 2018 | 📖 M.S. in Computational Mathematics, Texas A&M University |
| Sep. 2013 - Jun. 2017 | 📖 Bachelor of Mathematics, Beihang University |

Publications

Preprint

- 📖 **Li, G.** and Zhang, X., 2023. On E-values, Multiple Testing and Beyond. Preprint.
- 📖 **Li, G.**, Smith, A. and Zhou, Q., 2023. Importance is Important: A Guide to Informed Importance Tempering Methods. Submitted to Journal of the American Statistical Association. arXiv preprint arXiv:2304.06251.
- 📖 **Li, G.**, Lin, G., Zhang, Z. and Zhou, Q., 2023. Fast Replica Exchange Stochastic Gradient Langevin Dynamics. Submitted to Journal of Computational Physics. arXiv preprint arXiv:2301.01898.

Journal Publications

- 📖 **Li, G.**, Lu, Y., Chen, J. and Zhang, X., 2023. Robust Differential Abundance Analysis of Microbiome Sequencing Data. Accepted by Genes.
- 📖 **Li, G.** and Zhou, Q., 2023. Bayesian Multi-task Variable Selection with an Application to Differential DAG Analysis. Journal of Computational and Graphical Statistics, pp.1-12.
- 📖 Yang, Y., Lin, Y.T., **Li, G.**, Zhong, Y., Xu, Q. and Cai, J.J., 2023. Interpretable modeling of time-resolved single-cell gene-protein expression with CrossmodalNet. Briefings in Bioinformatics, 24(6), p.bbaf342.
- 📖 Yang, Y., **Li, G.**, Zhong, Y., Xu, Q., Chen, B.J., Lin, Y.T., Chapkin, R.S. and Cai, J.J., 2023. Gene knockout inference with variational graph autoencoder learning single-cell gene regulatory networks. Nucleic Acids Research, p.gkad450.
- 📖 Yang, Y., **Li, G.**, Zhong, Y., Xu, Q., Lin, Y.T., Roman-Vicharra, C., Chapkin, R.S. and Cai, J.J., 2023. scTenifoldXct: A semi-supervised method for predicting cell-cell interactions and mapping cellular communication graphs. Cell Systems, 14(4), pp.302-311.
- 📖 Osorio, D., Zhong, Y., **Li, G.**, Xu, Q., Yang, Y., Tian, Y., Chapkin, R.S., Huang, J.Z. and Cai, J.J., 2022. scTenifoldKnk: An efficient virtual knockout tool for gene function predictions via single-cell gene regulatory network perturbation. Patterns, 3(3), p.100434.

Publications (continued)

- Xu, Q., **Li, G.**, Osorio, D., Zhong, Y., Yang, Y., Lin, Y.T., Zhang, X. and Cai, J.J., 2022. scInTime: A Computational Method Leveraging Single-Cell Trajectory and Gene Regulatory Networks to Identify Master Regulators of Cellular Differentiation. *Genes*, 13(2), p.371.
- Osorio, D., Zhong, Y., **Li, G.**, Huang, J.Z. and Cai, J.J., 2020. scTenifoldNet: a machine learning workflow for constructing and comparing transcriptome-wide gene regulatory networks from single-cell data. *Patterns*, 1(9), p.100139.
- Osorio, D., Yu, X., Zhong, Y., **Li, G.**, Serpedin, E., Huang, J.Z. and Cai, J.J., 2019. Single-cell expression variability implies cell function. *Cells*, 9(1), p.14.

Teaching Experience

Teaching

- Statistical Methods, 2020 Summer.

Teaching Assistant

- Statistical Methodology II-Bayesian Modeling and Inference, 2022 Spring.
- Design and Analysis of Experiments, 2019 fall; 2020 fall; 2021 fall.
- Applied Multivariate Analysis and Statistical Learning, 2018 Fall; 2019 Fall.
- Statistics in Research I, 2019 Summer.

Oral presentations

Invited Conference Presentation

- EAC ISBA, 2023 Bayesian Multi-task Variable Selection with an Application to Differential DAG Analysis

Poster section

- **TRIPODS Annual Data Science conference, 2022** Fast Replica Exchange Stochastic Gradient Langevin Dynamics.

Academic service

Conference review

- AISTATS 2021, 2022

Skills

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| Languages | ■ Strong reading, writing and speaking competencies for English, Mandarin Chinese. |
| Coding | ■ Python, R, Cpp, Matlab, \LaTeX . |