



GUANXUN LI

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Academic Positions

Beijing Normal University at Zhuhai

Assistant Professor, Department of Statistics

Sep. 2024 – Present

Texas A&M University

Postdoctoral Research Associate, Department of Statistics

Sep. 2022 – Aug. 2024

Advisor: Xianyang Zhang

Education

Texas A&M University

Ph.D., Department of Statistics

– Dissertation: New Variational and Sampling Algorithms for Large-scale Bayesian Model Selection Problems.

Sep. 2018 – Aug. 2022

Advisor: Quan Zhou

Texas A&M University

M.S., Department of Mathematics

Sep. 2017 – May. 2018

Beihang University

B.S., Department of Mathematics

Sep. 2013 – Jun. 2017

Research Interests

Large-scale inference

Markov chain Monte Carlo sampling

Bayesian variable selection

Watermarking in large language models

Single-cell RNA sequencing data analysis

Microbiome sequencing data analysis

Publications

Notations: [AO] - Alphabetical ordering of authors, [CF] - Co-first author.

Preprints

Li, G. and Zhang, X., 2023. On E-values, Multiple Testing and Beyond. (arXiv)

Li, G., Smith, A., and Zhou, Q., 2023. Importance is Important: Generalized Markov Chain Importance Sampling Methods. Under review at *Biometrika*. (arXiv)

Li, G., Lin, G., Zhang, Z. and Zhou, Q., 2023. Fast Replica Exchange Stochastic Gradient Langevin Dynamics. Under review at *neurocomputing*. (arXiv)[AO]

Journal Publications

- Li, G.** and Zhang, X., 2024. A Note on E-values and Multiple Testing, *Biometrika*.
- Li, G.** and Zhou, Q., 2024. Bayesian Multi-Task Variable Selection with an Application to Differential DAG Analysis. *Journal of Computational and Graphical Statistics*, 33(1), pp.35-46.
- Li, G.**, Lu, Y., Chen, J. and Zhang, X., 2023. Robust Differential Abundance Analysis of Microbiome Sequencing Data. *Genes*, 14(11), p.2000.
- 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.bbada342.
- 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.
- 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.

Conference Publications

- Li, X., **Li, G.** ([CF]) and Zhang, X., 2024. Segmenting Watermarked Texts From Language Models. *Conference on Neural Information Processing Systems (NeurIPS) 2024*.

Teaching Experience

Instructor

- Introduction to Statistical Methods B*, Beijing Normal University at Zhuhai, Fall 2024.
- Introduction to Statistical Methods*, Texas A&M University, Summer 2020.

Teaching Assistant

Statistical Methodology II – Bayesian Modeling and Inference, Spring 2022.

Design and Analysis of Experiments, Fall 2019, 2020, 2021.

Applied Multivariate Analysis and Statistical Learning, Fall 2018, 2019.

Oral Presentations

Conference Presentations

EAC ISBA Conference, August 2023.

Joint Statistical Meetings (JSM), August 2024.

Invited Presentations

International Seminar on Selective Inference, March 2024.

Academic Service

Journal Reviews

Statistics and Computing, 2023.

BMC Bioinformatics, 2024.

ETRI Journal, 2024.

Conference Reviews

AISTATS, 2021, 2022, 2023, 2024.