Guanxun Li

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Academic positions

Sep. 2022 - Now *Postdoctoral Research Associate, Department of Statistics, Texas A&M University*

- Advisor: Xianyang Zhang

Education

Sep. 2018 - Aug. 2022 *Ph.D., Department of Statistics, Texas A&M University*

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

Sep. 2017 - May. 2018 *M.S., Department of Mathematics, Texas A&M University*

Sep. 2013 - Jun. 2017 *B.S., Department of Mathematics, Beihang University*

Research interests

Large-scale inference, Markov chain Monte Carlo sampling, Bayesian variable selection, graphical models, single-cell RNA sequencing data analysis, microbiome sequencing data analysis.

Publications

[AO]: alphabetical ordering of authors

Preprint

- **Li, G.** and Zhang, X., 2023. On E-values, Multiple Testing and Beyond. Reject and resubmit at *Biometrika*. (arXiv)

- **Li, G.**, Smith, A. and Zhou, Q., 2023. Importance is Important: A Guide to Informed Importance Tempering Methods. Under review at *Biometrika*. (arXiv)

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

Journal publications

- **Li, G.**, Lu, Y., Chen, J. and Zhang, X., 2023. Robust Differential Abundance Analysis of Microbiome Sequencing Data. *Genes*, 14(11), p.2000.

- **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.bbad342.

- 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.

Teaching experience

Teaching - Instructor

- Introduction to 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

08/2023 EAC ISBA Conference

Invited presentation

03/2024 International Seminar on Selective Inference

Poster presentation

09/2022 TRIPODS Annual Data Science conference

Academic service

Journal review

Statistics and Computing 2023

Conference review

AISTATS 2021, 2022, 2023