

# Guanxun Li

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## EDUCATION

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

## PUBLICATIONS

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- Preprint
  - **Li, G.**, Smith, A. and Zhou, Q., 2023. Importance is Important: A Guide to Informed Importance Tempering Methods. arXiv preprint arXiv:2304.06251.
  - 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 using CrossmodalNet. bioRxiv, pp.2023-05.
  - **Li, G.**, Lin, G., Zhang, Z. and Zhou, Q., 2023. Fast Replica Exchange Stochastic Gradient Langevin Dynamics. arXiv preprint arXiv:2301.01898.
- Journal Publications
  - **Li, G.** and Zhou, Q., 2022. Bayesian Multi-task Variable Selection with an Application to Differential DAG Analysis. Accepted by Journal of Computational and Graphical Statistics.
  - 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

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

## ORAL PRESENTATIONS

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- 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

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- **Conference reviewing**: AISTATS 2021, 2022.

## SKILLS SUMMARY

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- **Software & Tools** R, Python, Matlab