Haijun Gong, PhD

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Research Interests

Systems Biology/Bioinformatics	Statistics/Data Science
Machine Learning	Deep Learning
Quantum Computing	Model Checking/Formal Verification

Professional Appointment

2025 -	Professor of Statistics (Tenured)
2017 – 2025	Saint Louis University, USA Associate Professor of Statistics (Tenured) Department of Mathematics and Statistics Saint Louis University, USA
2018 - 2019	Associate Professor of Statistics (on sabbatical) Research School of Finance, Actuarial Studies and Statistics Australian National University, Australian
2012 - 2017	Assistant Professor of Statistics Department of Mathematics and Statistics Saint Louis University
2009 - 2012	Postdoctoral Fellow Computer Science Department Advisor: Edmund Clarke (Turing Awardee-2007) Carnegie Mellon University (CMU), Pittsburgh, PA

Education

08/2009	Ph.D., Department of Physics, Carnegie Mellon University, USA Advisor: Russell Schwartz (Head of Computational Biology Department)
05/2008	M.S., Department of Statistics, Carnegie Mellon University

Funded Projects

 NIH-NIGMS R15 09/2022-08/2025 Novel Systems Biology Methods for the Cell-type-specific Regulatory Networks Reconstruction from scRNA-seq Data. 1R15GM148915-01: \$454,500 3R15GM148915-01S1: \$90,096 Total Amount: \$544,596 Role: PI

Completed Projects

 President's Research Funds (PRF), Saint Louis University GAN-based deep learning methods for the scRNA-sequencing data analysis Amount: \$25,000 Role: PI

•	NIH-NIGMS R15 A Systems Biology Amount: \$454,500 Role: PI	Approach to Investigate the Structure Changes of B	09/2018-08/2022 iological Network
•	NIH R01 T New Bioanalytical I Role: co-Investigat	Tomasz Heyduk (PI) Methods Based on Next Generation Sequencing For	01/2015-06/2017
•	President's Research Computational Ana Amount: \$25,000 Role: PI	h Funds (PRF), Saint Louis University lysis of Signaling Pathways in the Cancer	03/2014-08/2015

Publication

Note: <u>underline</u> with * denotes SLU undergraduates, ** denotes SLU graduates under my direction

- A1. Yunge Wang**, Lingling Zhang, Tong Si, Sarah Roberts*, Yuqi Wang, **Haijun Gong**, Reconstructing Dynamic Gene Regulatory Networks Using f-Divergence From Time-Series scRNA-Seq Data. *Current Issues in Molecular Biology*, 47(6), (2025)
- A2. Wen-shan Liu^{**}, Tong Si, Aldas Kriauciunas^{*}, Snell M^{*}, **Haijun Gong**. Bidirectional f-Divergence-Based Deep Generative Method for Imputing Missing Values in Time-Series Data. *Stats*. 8(1) (2025)
- A3. Yunge Wang**, Lingling Zhang, Tong Si, Graham Bishop*, **Haijun Gong**. Anomaly Detection in High-Dimensional Time Series Data with Scaled Bregman Divergence. *Algorithms*. 18(2) (2025)
- A4. Tong Si**, Yunge Wang**, Lingling Zhang, Evan Richmond*, Tae-Hyuk Ahn, **Haijun Gong**. Multivariate Time Series Change- Point Detection with a Novel Pearson-like Scaled Bregman Divergence. *Stats*;7(2):462-480 (2024)
- A5. Tong Si**, Zackary Hopkins**, John Yanev*, Jie Hou, **Haijun Gong**, A novel f-divergence based generative adversarial imputation method for scRNA-seq data analysis. *PLoS One* 18(11): e0292792. (2023)
- A6. Helen Richards*, Yunge Wang**, Tong Si**, Hao Zhang*, **Haijun Gong**, Intelligent Learning and Verification of Biological Networks. *Advances in Artificial Intelligence, Computation, and Data Science* (2021)
- A7. W. Feng, Z. Yu, M. Kang, Haijun Gong, T.-H. Ahn, Practical Evaluation of Different Omics Data Integration Methods. Studies in Computational Intelligence, International Workshop on Health Intelligence (W3PHAI'19) In conjunction with the 33rd AAAI Conference on Artificial Intelligence (AAAI-19) (2019)
- A8. Zi Wang*, Yun Guo*, **Haijun Gong**, An Integrative Analysis of Time-varying Regulatory Networks from High-dimensional Data, *IEEE International Conference on Big Data*, Page 3798-3807 (2018)
- McCoy, M., Paul, A., Victor, M., Richner, M., Gabel, Haijun Gong, H., Yoo, A., Ahn, T. (2018), LONGO: an R package for interactive gene length dependent analysis for neuronal identity, *Bioinformatics*, V34, Issue 13: i422-i428.
- A10. Ma, Y.**, Feng, L.*, Guo, Y., **Haijun Gong** (2016). Statistical Analysis and Probabilistic Verification of Stress-induced Signaling Pathways, *International Journal of Data Mining and Bioinformatics*, Vol. 14, No. 2.
- A11. Ma, Y.**, Zhang, L, Geneus, C.**, **Haijun Gong** (2015). Weighted Gene Coexpression Network Analysis of Prostate Cancer, *IEEE International Conference on Computational Advances in Bio and Medical Sciences* (ICCABS).
- A12. Ma, Y.**, Damazyn, K.*, Klinger, J.*, **Haijun Gong** (2015), Inference and Verification of Probabilistic Graphical Models from High-dimensional Data, International Conference on Data Integration in the Life Sciences, *Lecture Notes in Bioinformatics* (LNBI), Vol. 9162.
- A13. Haijun Gong, Klinger, J.*, Damazyn, K.*, Li, X.**, Huang, S.* (2015). A novel procedure for statistical inference and verification of gene regulatory subnetwork, *BMC Bioinformatics*, V16, S7.
- A14. Haijun Gong, Feng, L.* (2014). Computational Analysis of the Roles of ER-Golgi Network in the

Cell Cycle. BMC Systems Biology, 8, S4.

- A15. **Haijun Gong**, Feng, L.* (2014). Probabilistic Verification of ER Stress-induced Signaling Pathways. Proceedings of *IEEE International Conference on Bioinformatics and Biomedicine* (BIBM, UK).
- A16. **Haijun Gong**, Wu, T.T., Clarke, E.M. (2014). Pathway-Gene Identification for Pancreatic Cancer Survival via Doubly Regularized Cox Regression. *BMC Systems Biology*, 8, S1:S3.
- A17. **Haijun Gong**, Tong Tong Wu, Edmund M. Clarke (2014). Statistical Analysis of High-Dimensional Data for Pancreatic Cancer", Molecular Diagnostics and Treatment of Pancreatic Cancer: Systems and Network Biology Approaches (Chapter 6). Elsevier Academic Press.
- A18. **Haijun Gong** (2013). Analysis of Intercellular Signal Transduction in the Tumor Microenvironment. *BMC Systems Biology*, 7, S3.
- A19. Haijun Gong, Zuliani, P., Clarke, E.M. (2013) Model checking of a synchronous diabetes-cancer logical network. *Current Bioinformatics*, Volume 8: 9-15.
- A20. **Haijun Gong**, Zuliani, P., A. Komuravell, Faeder, J., Clarke, E.M. (2012). Computational modeling and verification of signaling pathways in cancer. Algebraic and Numeric Biology, *Lecture Notes in Computer Science* (LNCS), Vol. 6479.
- A21. Wu, T.T., **Haijun Gong**, Clarke, E.M. (2011). A Transcriptome analysis by Lasso penalized Cox regression for pancreatic cancer survival. *Journal of Bioinformatics and Computational Biology*, V 9.
- A22. **Haijun Gong**, Zuliani, P., Wang, Q., Clarke, E.M. (2011). Formal analysis for logical models of pancreatic cancer. Proceedings of 50th *IEEE Conference on Decision & Control and European Control Conference*.
- A23. Haijun Gong, Wang, Q., Zuliani, P., Faeder, J., M. Lotze, Clarke, E.M. (2011). Symbolic model checking of signaling pathways in pancreatic cancer. Proceedings of 3rd *International Conference on Bioinformatics and Computational Biology* (BICoB).
- A24. **Haijun Gong**, P. Zuliani, E. Clarke, "Model Checking of a Diabetes-Cancer Model", International symposium on computational models for life sciences, AIP Conf. Proc. 1371 (2011)
- A25. **Haijun Gong**, Zuliani, P., Komuravell, A., Faeder, J., Clarke, E.M. (2010). Analysis and verification of the HMGB1 signaling pathway. *BMC Bioinformatics*, 11 (S7).
- A26. Ayorkor Korsah, G., Mostow, J., MB Dias, TM Sweet, S. Belousov, MF Dias, Haijun Gong (2010), "Improving Child Literacy in Africa: Experiments with an Automated Reading Tutor", Information Technologies & International Development.
- A27. Ayorkor Mills-Tettey, G., J. Mostow, MB Dias, TM Sweet, S. Belousov, MF Dias, **Haijun Gong** (2009), "Improving Child Literacy in Africa: Experiments with an Automated Reading Tutor", International Conference on Information and Communication Technologies & Development.
- A28. **Haijun Gong**, Guo, Y., Linstedt, A., Schwartz, R. (2010). Discrete, continuous and stochastic models of protein sorting in the Golgi. *Physical Review E*, 81.
- A29. Haijun Gong, Sengupta, D., Linstedt, A., Schwartz, R. (2008). Simulated de novo assembly of Golgi compartments by selective cargo capture during vesicle budding and targeted vesicle fusion. Biophysical Journal, Volume 95.
- A30. **Haijun Gong**, Sun, J., Du, D. (2002), "Analysis of Ds → Ф Л Beyond Naïve Factorization", High Energy Physics and Nuclear Physics, Volume 26.
- A31. Du, D., **Haijun Gong**, Sun, J., Yang, D., Zhu, G. (2002), "Phenomenological Analysis of Charmless Decays B → PV with QCD Factorization", Physical Review D 65, 094025.
- A32. Du, D., **Haijun Gong**, Sun, J., Yang, D., Zhu, G. (2002), "Phenomenological Analysis of B → PP Decays with QCD Factorization", Physical Review D 65, 074001.

Professional Activities

- NSF Proposal Review Panelist: 2015 Present
- NIH Proposal Review Panelist: 2019
- Associate Editor Heliyon Journal: 2023 Present
- Alzheimer's Association International Research Program Grant Reviewer (2013)

- Program co-Chair, International Conference on Bioinformatics and Biomedical Technology (2021-2023)
- Local organizing committee: International Meeting on Information and Statistics in Nuclear Experiment and Theory (ISNET-9), Washington University St. Louis, May 22-26, 2023
- Computers in Biology and Medicine, Editorial Board Member 2013 April 2015
- Member of American Association for Cancer Research (AACR): Member
- International Society for Computational Biology (ISCB): Member
- Review papers for the following journals:
- Nature Genetics; BMC Systems Biology; BMC Developmental Biology; Biometrics; PLOS Computational Biology; IEEE/ACM Transactions on Computational Biology and Bioinformatics; International Journal of Machine Learning and Cybernetics; Computers in Biology and Medicine; Journal of Theoretical Biology; Journal of Chemical Physics; Biophysical Journal; Mathematical Biosciences; Journal of Molecular Modeling; Applied Physics Letters; Journal of Applied Physics; European Physical Journal; PLoS Computational Biology; International Journal of Biomathematics; Computational & Mathematical Methods in Medicine; Bioinformatics and Biology Insights ...
- SLU Master's Program in Bioinformatics and Computational Biology
- SLU Science and Engineering Research Council (SERC) Representative 2020 -
- SLU CAS Academic Affairs Committee: 2014 2015
- Grant Reviewer for President's Research Funds (PRF)
- Judge of Annual Graduate Research Symposium
- SLU Statistics Committee
- SLU New Statistics Faculty Searching Committee

Awards

2010	Best Paper Award, International Conference on Bioinformatics (InCoB'10)
2009	"Honorable Mention" Student Paper Award, ICICTD conference

Teachings

- 1. Probability Theory: 2012 Fall, 2013 Fall, 2015 Spring, 2019 Fall, 2021 Fall
- 2. Mathematical Statistics: 2013 Spring, 2015 Fall, 2016 Spring, 2020 Spring
- 3. Applied Regression Analysis: 2014 Spring, 2016 Spring, 2018 Spring, 2023 Spring, 2024 Spring, 2025
- 4. Time Series Data Analysis: 2016 Fall, 2017 Fall, 2022/2023 Spring
- 5. Bayesian Data Analysis and Statistical Computing: 2017 Spring, 2022/2023 Fall
- 6. Statistical Models: 2024 Spring
- 7. Data Science Capstone: 2022 Fall, 2023 Spring/Fall
- 8. Elementary Statistics with Computers: 2014 Spring
- 9. Calculus I: 2014 Fall
- 10. Probability & Statistics for Engineers: 2012 Fall, 2013 (Spring & Fall), 2014 Spring, 2015 (Spring, Fall)
- 11. Foundations of Statistical Analysis: 2016 Fall, 2017 (Spring & Fall), 2018 Spring, 2019-2022

Teaching at Australian National University

Applied Statistics: 2019 Winter

Students Mentoring at SLU

I have supervised 2 PhD students, over 10 Master students, over 20 undergraduate students on statistics and bioinformatics research since 2012.