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Qiwei Li, Ph.D.

Department of Mathematical Sciences, FO 35
The University of Texas at Dallas
800 W Campbell Rd
Richardson, TX 75080, United States

E-mail: qiwei.li@utdallas.edu
Phone: (972) 883-4689
Webpage: sites.google.com/site/liqiwei2000
GitHub: github.com/liqiwei2000

RESEARCH INTERESTS

Theory and Methodology

- Bayesian modeling, variable selection, spatial statistics, shape statistics, nonparametric Bayes

Applications

- Spatial transcriptomics, metagenomics, medical imaging, epidemiology, text analysis

WORKING EXPERIENCE

Assistant Professor of Statistics Aug 2019 –
The University of Texas at Dallas, Richardson, TX

Assistant Professor Sep 2018 – Jul 2019
The University of Texas Southwestern Medical Center, Dallas, TX

Postdoctoral Researcher Dec 2016 – Aug 2018
The University of Texas Southwestern Medical Center, Dallas, TX
Advisor: Dr. Guanghua Xiao

EDUCATION

Doctor of Philosophy and Master of Arts, Statistics Aug 2011 – Nov 2016
Rice University, Houston, TX
Advisor: Dr. Marina Vannucci
Thesis - Bayesian models for high-dimensional count data with feature selection

Master of Philosophy, Information Engineering Sep 2008 - Aug 2010
The Chinese University of Hong Kong, Hong Kong
Advisors: Dr. Xiaodan Fan and Dr. Shuo-Yen Robert Li
Thesis - Detecting short adjacent repeats in multiple sequences: A Bayesian approach

Bachelor of Science, Economics Sep 2007 - Jul 2008
Peking University, Beijing, China

Bachelor of Engineering, Electronic Engineering Aug 2004 - Jul 2008
Tsinghua University, Beijing, China

AWARDS

Paper and Poster Awards

- Student Paper Competition Award, ASA Section on Bayesian Statistical Science, JSM 2017
- Best Poster Award, Conference of Texas Statisticians 2017
- M. Clinton Miller III Outstanding Poster Award, SRCOS Summer Research Conference 2016
- Best Poster Award, Conference of Texas Statisticians 2016
- Best Poster Award, ACM-Hong Kong Bioinformatics Symposium 2010

Teaching Awards

- Rice Annual Outstanding Teaching Award Nominee, Rice University 2016

Travel Awards

- Travel Award, 21st Meeting of New Researchers in Statistics and Probability 2019
- Travel Award, The International Workshop on Objective Bayes Methodology 2017
- Travel Award, CBMS: Regional Conference on Spatial Statistics 2017
- Boyd Harshbarger Travel Award, SRCOS Summer Research Conference 2016

Fellowship and Scholarship

- Doctoral Student Fellowship, Rice University 2011 – 2012
- Hong Kong Postgraduate Studentship 2008 – 2010
- Peihua Outstanding Student Scholarship 2004 – 2008
- First-Prize Academic Scholarship, Tsinghua University 2006 – 2007
- Second-Prize Academic Scholarship, Tsinghua University 2005 – 2006
- Third-Prize Academic Scholarship, Tsinghua University 2004 – 2005

Other Awards

- Blackwell-Rosenbluth Award Nominee, the junior section of ISBA (j-ISBA) 2021
- Special Recognition Award, Chinese Institute of Engineering/USA Dallas-Fort Worth Chapter 2020

GRANTS

Awarded Projects

1. New Faculty Research Symposium Grant, UT Dallas Office of Research May 2020 - Apr 2021
Title: Defining the role of the microbiome in recurrent UTI: A Bayesian approach
Role: Principal Investigator Amount \$25,000
2. NIH 1R01DK131267-01 May 2021 - Apr 2026
Title: Defining the dynamics of urobiome structure and function in postmenopausal women and its role in recurrent UTI susceptibility
Role: Co-Investigator Effort: 0.5 person months
3. NIH 1R01GM141519-01 Aug 2021 - Jul 2025
Title: Developing novel algorithms for spatial molecular profiling technologies
Role: Site Principal Investigator Effort: 2.5 person months

Pending Proposals

4. 2022-25 National Science Foundation (NSF)
Source: Division of Mathematical Sciences (DMS) Statistics Program
Title: Developing modern spatial and shape analysis for new heterogeneous high-dimensional geospatial

- data
 Role: Principal Investigator Effort: 1.0 person months
5. 2022-24 NIH R21
 Title: Developing novel statistical models for shape analysis of tumor pathology images
 Role: Principal Investigator Effort: 2.5 person months
 6. 2022-24 NIH R21
 Title: Clinical testing of a quantitative tool for determining vaginal wall laxity and measuring age and disease associated changes
 Role: Site Principal Investigator Effort: 0.75 person months
 7. 2022-25 NIH U01
 Title: Inference of tumor-immune cell communications from spatial expression profiling data
 Role: Site Principal Investigator Effort: 1.0 person months
 8. 2022-24 NIH R15
 Title: Topology-based tumor analysis for medical images
 Role: Consultant Amount \$5,000

PUBLICATIONS

*Corresponding author/Co-corresponding author

⁺First/Co-first author

Submitted Manuscripts (First/corresponding-authored - Statistical Methodology)

1. X. Jiang, **Q. Li***, and G. Xiao, “A Bayesian modified Ising model for identifying spatially variable genes from spatial transcriptomics data,” *Statistics in Medicine*, in revision
2. E. Fernández Morales, S. Yang, S. H. Chiou, B. Yao, C. Moon, C. Zhang, G. Xiao, and **Q. Li***, “SAFARI: Shape analysis for AI-reconstructed images,” *BMC Medical Imaging*, in revision
3. **Q. Li⁺**, S. Jiang, G. Xiao, A. Y. Koh, M. L. Neugent, N. J. De Nisco, Y. Xie, and X. Zhan, “Bayesian modeling of metagenomic sequencing data for discovering microbial biomarkers in colorectal cancer,” *The Annals of Applied Statistics*, in revision
4. C. Zhang, **Q. Li***, C. Moon, G. Xiao, and M. Chen, “Bayesian landmark-based shape analysis of tumor pathology images,” *Journal of American Statistical Association*, in revision

Submitted Manuscripts (Co-authored - Collaborative Research)

5. S. Yang, S. Wang, Y. Wang, R. Rong, J. Kim, B. Li, A. Y. Koh, G. Xiao, D. Liu, **Q. Li**, and X. Zhan, “MB-SupCon: Microbiome-based predictive models via supervised contrastive learning”
6. M. L. Neugent, A. Kumar, N. V. Hulyalkar, K. C. Lutz, V. H. Nguyen, J. Fuentes, C. Zhang, A. Nguyen, B. M. Sharon, E. Fan, A. Kuprasertkul, A. P. Arute, **Q. Li**, C. Xing, V. Shulaev, P. E. Zimmern, K. L. Palmer, and N. J. De Nisco, “Recurrent urinary tract infection and estrogen shape the taxonomic ecology and functional potential of the postmenopausal urobiome”
7. C. Moon, **Q. Li**, and G. Xiao, “Predicting survival outcomes using topological features of tumor pathology images”
8. M. Zhang, S. Jiang, B. Yao, **Q. Li**, Y. Chen, D. Luo, D. M. Yang, T. Wang, Y. Xie, X. Zhan, and G. Xiao, “SpaCeV: A visualization tool for cell spatial organization”

Peer-reviewed Papers (First/corresponding-authored - Statistical Methodology)

9. **Q. Li^{+,*}**, M. Zhang, Y. Xie, and G. Xiao, “Bayesian modeling of spatial molecular profiling data via Gaussian process,” *Bioinformatics*, 2021, btab455

10. S. Jiang, Q. Zhou, X. Zhan, and **Q. Li***, "BayesSMILES: Bayesian segmentation modeling for longitudinal epidemiological studies," *Journal of Data Science*, 2021, Volume 19, Number 3, pp.365-389
11. **Q. Li⁺***, T. Bedi, C. U. Lehmann, G. Xiao, and Y. Xie, "Evaluating short-term forecast COVID-19 cases among different epidemiological models under a Bayesian framework," *GigaScience*, 2021, Volume 10, Issue 2, giab009
12. L. Zhang, R. Rong, **Q. Li⁺**, D. M. Yang, B. Yao, D. Luo, X. Zhang, X. Zhu, J. Luo, Y. Liu, X. Yang, X. Ji, Z. Liu, Y. Xie, Y. Sha, Z. Li, G. Xiao, "A deep learning-based model for screening and staging pneumoconiosis," *Scientific Report*, 2021, Volume 11, Number 1, 2201
13. S. Jiang, G. Xiao, A. Y. Koh, **Q. Li***, and X. Zhan, "A Bayesian zero-inflated negative binomial regression model for the integrative analysis of microbiome data," *Biostatistics*, 2021, Volume 22, Number 3, pp.522-540
14. S. Jiang, G. Xiao, A. Y. Koh, **Q. Li***, and X. Zhan, "HARMONIES: A hybrid approach for microbiome networks inference via exploiting sparsity," *Frontiers in Genetics*, 2020, Volume 11, 445
15. **Q. Li⁺**, X. Wang, F. Liang, and G. Xiao, "A Bayesian mark interaction model for analysis of tumor pathology images," *The Annals of Applied Statistics*, 2019, Volume 13, Number 3, pp.1708-1732
16. **Q. Li⁺**, A. Cassese, M. Guindani, and M. Vannucci, "Bayesian negative binomial mixture regression models for the analysis of sequence count and methylation data," *Biometrics*, 2019, Volume 75, Number 1, pp.183-192
17. **Q. Li⁺**, F. Yi, F. Liang, X. Wang, and G. Xiao, "A Bayesian hidden Potts mixture model for analyzing lung cancer pathology images," *Biostatistics*, 2019, Volume 20, Number 4, pp.565-581
18. M. Zhang, **Q. Li⁺**, and Y. Xie, "A Bayesian hierarchical model for analyzing methylated RNA immunoprecipitation sequence data," *Quantitative Biology*, 2018, Volume 6, Number 3, pp.275-286
19. **Q. Li⁺**, M. Guindani, B. J. Reich, H. D. Bondell, and M. Vannucci, "A Bayesian mixture model for clustering and selection of feature occurrence rates under mean constraints," *Statistical Analysis and Data Mining*, 2017, Volume 10, Number 6, pp.393-409
20. **Q. Li⁺***, D. B. Dahl, M. Vannucci, H. Joo, and J. Tsai, "KScons: A Bayesian approach for protein residue contact prediction using the knob-socket model of protein tertiary structure," *Bioinformatics*, 2016, Volume 32, Number 24, pp.3774-3781
21. **Q. Li⁺**, D. B. Dahl, M. Vannucci, H. Joo, and J. Tsai, "Bayesian modeling of protein primary sequence for secondary structure prediction," *PLOS One*, 2014, Volume 9, Number 10, pp.e109832
22. D. B. Dahl, **Q. Li⁺**, M. Vannucci, H. Joo, and J. W. Tsai, "A Bayesian model for protein secondary structure prediction," The 59th World Statistics Congress (**WSC 2013**)
23. **Q. Li⁺**, X. Fan, T. Liang, and S. -Y. R. Li, "An Markov chain Monte Carlo algorithm for detecting short adjacent repeats shared by multiple sequences," *Bioinformatics*, 2011, Volume 27, Number 13, pp.1772-1779
24. **Q. Li⁺**, T. Liang, X. Fan, C. Xu, W. Yu, and S. -Y. R. Li, "An automatic procedure to search highly repetitive sequences in genome as fluorescence in situ hybridization probes and its application on brachypodium distachyon," 2010 IEEE International Conference on Bioinformatics & Biomedicine (**BIBM 2010**), pp. 563-568
25. **Q. Li⁺**, T. Liang, S. -Y. R. Li, and X. Fan, "Bayesian approach for identifying short adjacent repeats in multiple DNA sequences," 2010 International Conference on Bioinformatics & Computational Biology (**BIOCOMP'10**), Volume 1, pp. 255-261

Peer-reviewed Papers (Co-authored - Collaborative Research)

26. A. S. Chao, J. Yang, Z. Liu, and **Q. Li**, "Network of words: A co-occurrence analysis of nation-building terms in the writings of Liang Qichao and Chen Duxiu," *Journal of Historical Network Research*, 2021, accepted

27. A. Czyst, B. L. Mason, **Q. Li**, C. Chin-Fatt, A. Minhajuddin, T. Carmody, and M. H. Trivedi, "Comparison of inflammatory markers as moderators of depression outcomes: A COMED study," *Journal of Affective Disorders*, 2021, Volume 295, pp.1066-1071
28. T. Ebrahimzadeh, A. Kuprasertkul, M. Neugent, K. Lutz, J. Fuentes, J. Gadhvi, F. Khan, C. Zhang, B. Sharon, K. Orth, **Q. Li**, P. Zimmern, and N. De Nisco, "Urinary prostaglandin E2 is a biomarker for recurrent urinary tract infection in postmenopausal women," *Life Science Alliance*, 2021, Volume 4, Number 7, e202000948
29. F. Zhou, K. He, **Q. Li**, R. Chapkin, and Y. Ni, "Bayesian biclustering for metagenomic sequencing data via multinomial matrix factorization," *Biostatistics*, 2021, kxab002
30. J. Kim, S. Jiang, G. Xiao, Y. Xie, D. Liu, **Q. Li**, A. Y. Koh, and X. Zhan, "MetaPrism: A toolkit for joint taxa/gene analysis of metagenomic sequencing data," *G3: Genes, Genomes, Genetics*, 2021, Volume 11, Issue 4, jkab046
31. R. Rong, S. Jiang, L. Xu, G. Xiao, Y. Xie, D. Liu, **Q. Li**, and X. Zhan, "MB-GAN: Microbiome simulation via generative adversarial network," *GigaScience*, 2021, Volume 10, Issue 2, giab005
32. M. Zhang, T. Sheffield, X. Zhan, **Q. Li**, D. M. Yang, Y. Wang, S. Wang, Y. Xie, T. Wang, and G. Xiao, "Spatial molecular profiling: Platforms, applications and analysis tools," *Briefings in Bioinformatics*, 2021, Volume 22, Number 3, bbab145
33. B. L. Mason, **Q. Li**, A. Minhajuddin, A. H. Czyst, L. A. Coughlin, S. Hussain, A. Y. Koh, and M. H. Trivedi, "Reduced anti-inflammatory gut microbiota are associated with depression and anhedonia," *Journal of Affective Disorders*, 2020, Volume 266, Number 1, pp.394-401
34. G. Jia, X. Wang, **Q. Li**, W. Lu, X. Tang, I. Wistuba, and Y. Xie, "RCRnorm: An integrated system of random-coefficient hierarchical regression models for normalizing NanoString nCounter data," *The Annals of Applied Statistics*, Volume 13, Number 3, pp.1617-1647
35. M. Zhang, **Q. Li**, D. Yu, B. Yao, W. Guo, Y. Xie, and G. Xiao, "GeNeck: A web-based tool for gene network construction and visualization," *BMC Bioinformatics*, 2019, Volume 13, Number 3, pp.1617-1647
36. A. S. Chao, **Q. Li**, and Z. Liu, "Integrating latent Dirichlet allocation and Poisson graphical model: A deep dive into the writings of Chen Duxiu, co-founder of the Chinese Communist Party," 2018 Digital Humanities (DH 2018)
37. L. Cai, **Q. Li**, Y. Du, J. Yun, Y. Xie, R. J. DeBerardinis, and G. Xiao, "Genomic regression analysis of coordinated expression," *Nature Communications*, 2017, Vol. 8, Number 2187
38. A. S. Chao and **Q. Li**, "A new and improved method to text-mining in Chinese: Closer language segmentation in detecting the shifting meaning of patriotism," 2017 Digital Humanities (DH 2017)
39. J. Xu, **Q. Li**, X. Fan, V. O. K. Li, and S. -Y. R. Li, "Improved short adjacent repeat identification using three evolutionary Monte Carlo schemes," *International Journal on Data Mining and Bioinformatics*, 2013, Vol.8, Number 4, pp.462-479
40. T. Liang, X. Fan, **Q. Li**, and S. -Y. R. Li, "Detection of short dispersed tandem repeats by reversible jump Markov chain Monte Carlo," *Nucleic Acids Research*, 2012, Vol.40, Number 19, pp.e147
41. Y. Li, M. Chen, **Q. Li**, and W. Zhang, "Enabling multi-level trust in privacy preserving data mining," *IEEE Transaction on Knowledge and Data Engineering*, 2012, Vol.24, Number 9, pp.1598-1612
42. J. Xu, A. Y. S. Lam, V. O. K. Li, **Q. Li**, and X. Fan, "Short adjacent repeat identification based on chemical reaction optimization," 2012 IEEE World Congress on Computational Intelligence (WCCI 2012), pp. 1-8
43. J. Xu, **Q. Li**, X. Fan, V. O. K. Li, and S. -Y. R. Li, "An evolutionary Monte Carlo algorithm for identifying short adjacent repeats in multiple sequences," 2010 IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010), pp. 643-648

SOFTWARE

Web Apps

1. SMP Gym: Spatial Molecular Profiling Gym (with Xiaowei Zhan and Gunaghua Xiao)
<https://lce.biohpc.swmed.edu/smp-gym/>
2. SAFARI: Shape Analysis For AI-Reconstructed Images (with Esteban Fernández Morales)
<https://lce.biohpc.swmed.edu/safari/>
3. Predicting US COVID-19 Cases by Statistical Models
qiwei.shinyapps.io/PredictCOVID19/
4. Predicting Global COVID-19 Cases (with Esteban Fernández Morales)
qiwei.shinyapps.io/PredictGlobalCOVID19/
5. Detecting Change Points for US COVID-19 Time-series data (with Shuang Jiang and Xiaowei Zhan)
zhanxw.github.io/BayesSMILES/

Open-source R/C++ Code

6. SAFARI: Shape Analysis For AI-Reconstructed Images (with Esteban Fernández Morales)
https://github.com/estfernandez/Slide_Image_Segmentation_and_Extraction
7. BayesLASA: Bayesian LAndmark-based Shape Analysis (with Cong Zhang)
<https://github.com/bougetsu/BayesLASA>
8. BOOST-GP: Bayesian mOdeling Of Sptial Transcriptomics data via Gaussian Process
<https://github.com/Minzhe/BOOST-GP>
9. BOOST-Ising: Bayesian mOdeling Of Sptial Transcriptomics data via Ising model (with Xi Jiang)
github.com/Xijiang1997/BOOST-Potts
10. BayesSMILES: Bayesian Segmentation ModelIng for Longitudinal Epidemiological Studies (with Shuang Jiang)
github.com/shuangj00/BayesSMILES
11. BayesEpiModels: A Bayesian framework for stochastic epidemic models
github.com/liqiwei2000/BayesEpiModels
12. HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity (with Shuang Jiang)
github.com/shuangj00/HARMONIES
13. MicrobiomeBayesDiff: A Bayesian framework for microbial differential abundance analysis
github.com/shuangj00/MicrobiomeBayesDiff
14. IntegrativeBayes: A Bayesian model for microbial integrative analysis (with Shuang Jiang)
github.com/shuangj00/IntegrativeBayes
15. BayesMarkIntercationModel: A Bayesian mark interaction model for analysis of multi-type point pattern data
github.com/liqiwei2000/BayesMarkInteractionModel
16. BayesHiddenPottsMixture: A Bayesian hidden Potts mixture model for analysis of multi-type point pattern data
github.com/liqiwei2000/BayesHiddenPottsMixture
17. BaySeqPeak: A Bayesian zero-inflated negative binomial regression model with spatial variable selection for analysis of sequencing data
github.com/liqiwei2000/BaySepMPeak
18. BayesNBMixReg: A Bayesian zero-inflated negative binomial mixture regression model with variable selection for integrative analysis of sequencing data
github.com/liqiwei2000/BayesNBMixReg

19. CoPoM: A Constrained Poisson Mixture model for clustering high-dimensional count data
github.com/liqiwei2000/CoPoM

R Packages

20. KScons: A Bayesian model for protein residue contact prediction
cran.r-project.org/src/contrib/Archive/kscons/
21. SAFARI: Shape Analysis For AI-Reconstructed Images
cran.r-project.org/web/packages/SAFARI/index.html

TALKS

Invited Talks

1. “A Bayesian variable selection framework for differential abundance analysis of microbiome count data,” East Asia Chapter - International Society for Bayesian Analysis 2021 Conference (**EAC-ISBA 2021**), online
2. “Bayesian modeling of spatial molecular profiling data,” The 34-th New England Statistics Symposium (**NESS 2021**), online
3. “Bayesian modeling of spatial molecular profiling data,” International Chinese Statistical Association 2021 Applied Statistics Symposium (**ICSA 2021**), online
4. “Bayesian modeling of metagenomic sequencing data for differential abundance analysis,” 2021 Joint Statistical Meetings (**JSM 2021**), online
5. “Recent advances in Bayesian methods for the analysis of tumor pathology images,” International Chinese Statistical Association 2020 Applied Statistics Symposium (**ICSA 2020**), online
6. “Bayesian modeling of metagenomic sequencing data,” Department of Statistics, **Northwestern University**, online, 2020
7. “A brief introduction to COVID-19 forecasting,” The Coronavirus Visualization Team (**CVT**), Scholars at Harvard, online
8. “A brief introduction to COVID-19 forecasting,” 2020 Chinese Institute of Engineering/USA Dallas-Fort Worth Chapter Annual Convention (**2020 CIE/USA-DFW**), online
9. “Spatial modeling of spatial molecular profiling data,” Center for Systems Biology, **The University of Texas at Dallas**, Richardson, TX, 2020
10. “Bayesian modeling of metagenomic sequencing data,” Center for Systems Biology, **The University of Texas at Dallas**, Richardson, TX, 2020
11. “Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images,” Statistical Methods in Imaging (**SMI 2019**), Irvine, CA
12. “Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images,” Department of Epidemiology and Biostatistics, **Texas A&M University**, College Station, TX, 2019
13. “Bayesian modeling of high-dimensional count data and its application on the analysis of microbiome data,” Department of Biostatistics, **The University of Texas at Dallas MD Anderson Cancer Center**, Houston, TX, 2019
14. “Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images,” Department of Biostatistics, **The University of Texas at Dallas MD Anderson Cancer Center**, Houston, TX, 2019
15. “Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images,” Department of Mathematical Sciences, **The University of Texas at Dallas**, Richardson, TX, 2019

16. "Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images," Cecil H. and Ida Green Comprehensive Center for Molecular, Computational, and Systems Biology, **The University of Texas Southwestern Medical Center**, Dallas, TX, 2018
17. "Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images," Department of Statistics, **Southern Methodist University**, Dallas, TX, 2018
18. "Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images," J. Mack Robinson College of Business, **Georgia State University**, Atlanta, GA, 2018
19. "A Bayesian hidden Potts mixture model for analyzing lung cancer pathological images," Eastern North American Region 2018 Spring Meetings (**ENAR 2018**), Atlanta, GA
20. "Bayesian models of high-dimensional count data," Eastern North American Region 2016 Spring Meetings (**ENAR 2016**), Austin, TX

Contributed Oral Presentations

21. "Bayesian modeling of spatial transcriptomics data," International Society for Bayesian Analysis 2021 World Meeting (**ISBA 2020**), online
22. "Bayesian modeling of metagenomics sequencing data for discovering microbial biomarkers in colorectal cancer," The 30th International Biometric Conference (**IBC 2020**), online
23. "Bayesian modeling of microbiome count data for network analysis," Eastern North American Region 2020 Spring Meetings (**ENAR 2020**), Nashville, TN
24. "A Bayesian hierarchical model for analyzing methylated RNA immunoprecipitation sequencing data," 2018 Joint Statistical Meetings (**JSM 2018**), Vancouver, BC
25. "A Bayesian mixture model for clustering and selection of feature occurrence rates under mean constraints," 2017 Joint Statistical Meetings (**JSM 2017**), Baltimore, MD
26. "A Poisson mixture model for clustering and feature selection of high-dimensional count data," 2015 Joint Statistical Meetings (**JSM 2015**), Seattle, WA
27. "Bayesian approach for predicting protein secondary structure," Eastern North American Region 2014 Spring Meetings (**ENAR 2014**), Baltimore, MD
28. "Poisson mixture models for next-generation RNA sequencing data," 2013 Joint Statistical Meetings (**JSM 2013**), Montreal, QC
29. "A Bayesian approach for tandem repeats detection," The 2nd Institute of Mathematical Statistics Asia Pacific Rim Meeting (**IMS-APRM 2012**), Tsukuba, Japan
30. "Bayesian approach for identifying short adjacent repeats in multiple DNA sequences," 2010 International Conference on Bioinformatics & Computational Biology (**BIOCOMP'10**), Las Vegas, NV

Contributed Poster Presentations

31. "Bayesian modeling of spatial point patterns and its application on the analysis of tumor pathology images," 21st Meeting of New Researchers in Statistics and Probability (**IMS NRG 2019**), Denver, CO
32. "Bayesian mark interaction functions and its applications," 2017 International Workshop on Objective Bayes Methodology (**O'Bayes 2017**), Austin, TX
33. "Bayesian hidden Potts models for pathological image analysis," 2017 Postdoctoral Research Symposium, **The University of Texas Southwestern Medical Center**, Dallas, TX
34. "Bayesian hidden Potts models for pathological image analysis," 2017 Conference of Texas Statisticians (**COTS 2017**), Dallas, TX
35. "Bayesian statistical models for complex data," 2016 Data Science Meet-up, **Rice University**, Houston, TX

36. "Bayesian models for predicting protein higher-order structures," Southern Regional Council on Statistics 2016 Summer Research Conference (**SRCOS 2016**), Bentonville, AR
37. "A Bayesian nonparametric model for clustering and feature selection of high-dimensional count data," 2016 Conference of Texas Statisticians (**COTS 2016**), San Antonio, TX
38. "Detection of tandem repeats in multiple DNA sequences via probabilistic approach," 2010 ACM-Hong Kong Bioinformatics Symposium, **Hong Kong University of Science and Technology**, Hong Kong

MENTORSHIP EXPERIENCE

Graduated Students

1. Cong Zhang (with Dr. Min Chen) Fall 2019 – Fall 2020
 Ph.D. in Statistics program, The University of Texas at Dallas
 Thesis - Tracking dissemination of plasmids in the murine gut using Hi-C sequencing & Bayesian landmark-based shape analysis of tumor pathology images
 Currently Senior Biostatistician at Novartis Institutes for BioMedical Research, Shanghai, China
2. Shuang Jiang (with Dr. Xiaowei Zhan) Summer 2018 – Spring 2021
 Ph.D. in Biostatistics program, The University of Texas Southwestern Medical Center/Southern Methodist University
 Thesis - Bayesian statistical modeling of metagenomic sequencing data
 Currently Data Scientist at Waste Management, Houston, TX
3. Esteban Fernández Morales Spring 2020 – Summer 2021
 Undergraduate in mathematics/computer science program, The University of Texas at Dallas
 Thesis - Extracting clinically meaningful features for the analysis of tumor pathology images
 Currently Ph.D. student in the Biostatistics program at Brown University, Providence, RI

Graduate students

4. Kevin Charles Lutz Spring 2020 – Now
 Ph.D. in Statistics program, The University of Texas at Dallas
5. Tejasv Bedi Summer 2020 – Now
 Ph.D. in Statistics program, The University of Texas at Dallas
6. Xi Jiang, (with Dr. Guanghua Xiao) Summer 2020 – Now
 Ph.D. in Biostatistics program, The University of Texas Southwestern Medical Center/Southern Methodist University
7. Jie Yang Spring 2021 -Now
 Ph.D. in Statistics program, The University of Texas at Dallas

Undergraduate students

8. Suhana Bedi Spring 2021 – Now
 Undergraduate in data science/biology programs, The University of Texas at Dallas
9. Yeyun Xu Fall 2021 – Now
 Undergraduate in data science program, The University of Texas at Dallas
10. Frank Gao Fall 2021 – Now
 Undergraduate in software engineering program, The University of Texas at Dallas

High-school students

11. Jerry Wang Spring 2021
 Highland Park High School, University Park, Texas

Ph.D. students that I served as a thesis committee member

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| 12. Yu Zhang
Ph.D. in Statistics program, The University of Texas at Dallas | Spring 2021 |
| 13. Jiaju Wu
Ph.D. in Statistics program, The University of Texas at Dallas | Summer 2021 |
| 14. Thao Nguyen Bach
Ph.D. in Biology program, The University of Texas at Dallas | |
| 15. Thanthirige Lakshika Maduwanthi Ruberu
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 16. Zhiwei Zhen
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 17. Xiufeng Xu
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 18. Tingfang Wang
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 19. Nisansala Wickramasinghe
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 20. Ibrahim Sajal
Ph.D. in Statistics program, The University of Texas at Dallas | |
| 21. Xinyu Chen
Ph.D. in Biology program, The University of Texas at Dallas | |

TEACHING EXPERIENCE

Instructor

The University of Texas at Dallas, Richardson, TX

- | | |
|--|-------------|
| • STAT 6390 Topics in Statistics: Bayesian Statistical Methods
Overall evaluation score - 4.91/5.00 | Spring 2021 |
| • STAT 3355 Data Analysis for Statisticians and Actuaries
Overall evaluation score - 4.68/5.00 | Spring 2021 |
| • STAT 3355 Data Analysis for Statisticians and Actuaries
Overall evaluation score - 4.58/5.00 | Fall 2020 |
| • STAT 3355 Data Analysis for Statisticians and Actuaries
Overall evaluation score - 4.36/5.00 | Spring 2020 |
| • STAT 3355 Data Analysis for Statisticians and Actuaries
Overall evaluation score - 3.20/5.00 | Fall 2019 |

Co-instructor

The University of Texas Southwestern Medical Center, Dallas, TX

- | | |
|--|-------------|
| • MB 5108 Advanced Data Analysis and Statistical Learning with Dr. Yang Xie | Spring 2019 |
| • BSCI 5106 Introduction to Biostatistics and Bioinformatics with Dr. Lindsay Cowell | Spring 2019 |

Southern Methodist University, Dallas, TX

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|---|-----------|
| • STAT 6390 Bayesian Data Analysis with Dr. Xinlei Wang | Fall 2018 |
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Rice University, Houston, TX

- | | |
|--|-------------------------|
| • STAT 422/622 Bayesian Data Analysis with Dr. Marina Vannucci | Spring 2016 – Fall 2016 |
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Teaching Assistant

2008 – 2015

Rice University, Houston, TX

- STAT 422/622 Bayesian Data Analysis with Dr. Marina Vannucci
- STAT 421/621 Applied Time Series and Forecasting with Dr. Katherine B. Ensor
- STAT 431 Overview of Mathematical Statistics with Dr. John A. Dohelman
- STAT 410 Regression Analysis with Dr. Rudy Guerra
- STAT 310 Probability and Statistics with Dr. David W. Scott
- STAT 305 Introduction to Statistics for the Biosciences with Dr. E. Neely Atkinson
- STAT 280 Elementary Applied Statistics with Dr. E. Neely Atkinson

The Chinese University of Hong Kong, Hong Kong

- BMEG5790 Bioinformatics with Dr. Xiaodan Fan
- ERG2040B Probability Models and Applications with Felix Hartanto
- IEG1810C Electronic Circuit Design Laboratory
- ERG2040D Probability Models and Applications with Dr. Soung-Chang Liew
- ERG2013C Advanced Engineering Mathematics with Dr. Wei-Keh Wei

PROFESSIONAL ACTIVITIES

Ad hoc Reviewer for Journals

- *The Annals of Applied Statistics*
- *Bioinformatics*
- *Biometrics*
- *Biostatistics*
- *BMC Bioinformatics*
- *Chinese Journal of Industrial Hygiene and Occupational Disease*
- *Computational and Mathematical Methods in Medicine*
- *Computational and Structural Biotechnology Journal*
- *Computational Statistics*
- *Computational Statistics and Data Analysis*
- *Computing*
- *Evolutionary Bioinformatics*
- *Frontiers in Cell and Developmental Biology*
- *Frontiers in Genetics*
- *Frontiers in Medicine*
- *Frontiers in Neurology*
- *Hacetatepe Journal of Mathematics and Statistics*
- *IEEE Transactions on Pattern Analysis and Machine Intelligence*
- *IEEE Transactions on Signal Processing*
- *Journal of Computational and Graphical Statistics*
- *Journal of the Korean Statistical Society*
- *Occupational Health and Emergency Rescue*
- *PLoS Computational Biology*

- *PLoS One*
- *Psychometrika*
- *Scientific Reports*
- *Statistical Applications in Genetics and Molecular Biology*
- *Statistics in Medicine*

Guest Editor for Journals

- *Cells*

Ad hoc Reviewer for Grant Proposals

- NSF Human-Environment and Geographical Sciences (HEGS) Program
- 2021-22 New Faculty Research Symposium Grant, UT Dallas Office of Research

Conference Program Committee Member

- 2019 International Conference on Intelligent Biology and Medicine (ICIBM 2019)
- 2018 International Conference on Intelligent Biology and Medicine (ICIBM 2018)
- 2016 International Conference on Intelligent Biology and Medicine (ICIBM 2016)

Conference Invited Session Organizer/Chair

- “Recent advances in statistical methods for the analysis of pathology images,” 2021 World Statistics Congress (**WSC 2021**), online
- “Statistical advances on microbiome data analysis II,” 2020 Computational and Methodological Statistics (**CMStatistics 2020**), online
- “Statistical advances on microbiome data analysis I,” 2020 Computational and Methodological Statistics (**CMStatistics 2020**), online
- “Recent advances in Bayesian methods for the analysis of microbiome count data,” 2020 Joint Statistical Meetings (**JSM 2020**), Philadelphia, PA

Conference Contributed Session Chair

- “Multivariate and high-dimensional data analysis,” Eastern North American Region 2020 Spring Meetings (**ENAR 2020**), Nashville, TN

Membership

- American Statistical Association (ASA)
- International Biometric Society (IBS)
- International Chinese Statistical Association (ICSA)
- Institute of Mathematical Statistics (IMS)
- International Society for Bayesian Analysis (ISBA)

Service to the Department, School, and University

- Faculty advisor of the student organization MEDiCS: Medicine in Computer Science Fall 2021 - Now
- Organizer of the Departmental Statistics Seminar Fall 2021 - Now
- Committee member of the Departmental Colloquium Fall 2019 - Now