

Curriculum Vitae

Jun Xie
Professor and Graduate Chair
Department of Statistics
Purdue University
West Lafayette, IN 47907
USA

Email: junxie@purdue.edu
Website: <http://www.stat.purdue.edu/~junxie>
Phone: (765) 494-6032

Education

- Ph.D., Statistics, University of California, Los Angeles, 6/2000
- M.S., Probability and Statistics, Peking University, China, 7/1997
- B.S., Probability and Statistics, Peking University, China, 7/1994

Positions and Employment

- Professor, Department of Statistics, Purdue University, 8/2014-present
- Associate Professor, Department of Statistics, Purdue University, 8/2007-7/2014
- Sabbatical Research Fellow, Biostatistics and Programming, Sanofi-Aventis, 12/2007-7/2008
- Assistant Professor, Department of Statistics, Purdue University, 8/2001-7/2007
- Statistician and Lecturer, Department of Psychology and Department of Statistics, UCLA, 9/2000-6/2001

Academic Administrative Services

Dr. Xie serves on several administrative committees of the Department, College, and University at Purdue. She has been the Chair of the Graduate Committee in the Statistics Department at Purdue University for 15 years. The department is one of the biggest Statistics departments in the US. The Chair of the Graduate Committee is one of the principal administrative positions in the department. Dr. Xie reviews the graduate programs, supervises graduate teaching assistants, and advises a large number of graduate students.

At the university level, Dr. Xie has served in the Graduate School Faculty Council for many years, acting as an Area Committee Chair.

- Graduate Admission Chair, Department of Statistics, Purdue University, 8/2016-present
- Department Head Search Committee Chair, 2019-2020
- Graduate Chair, Department of Statistics, Purdue University, since 2008
- Faculty hiring committee, Chair or member, every year since 2012
- College of Science Graduate Committee, since 2013
- Graduate School Faculty Council, Area Committee Chair, 2014-2018

Other Professional Experience

Dr. Xie was an organizer of several national conferences, a member of an academic program review committee for Georgia Institute of Technology, a member of a national institute grant review committee of Canada, and a member of the Data Safety Monitoring Board of several clinical trials in the US. In 2019, Dr. Xie participated in a leadership program, Faculty Insights Forum, in the Office of Provost at Purdue University.

- 2021 Natural Sciences and Engineering Research Council of Canada, national institute grants selection committee
- 2020 NIH grant review panel, Big Data Science to Elucidate the Neural Mechanisms of Addiction and Substance Use Disorder
- 2019-2020 Purdue leadership program, the Office of Provost
- 2019 Academic Program Review Committee, Georgia Institute of Technology
- 2018 Conference Organization Committee, the 9th International Purdue Symposium on Statistics
- 2016 Invited session organizer, Joint Statistical Meeting, Chicago, IL
- 2015- Biostatistician in several Data Safety Monitoring Boards of clinical trials
- 2015 NIH grant review panel, Big Data to Knowledge (BD2K) training program
- 2013-2014 Associate Director, Statistical Consulting Service, Purdue University
- 2013 Opening workshop participant, Statistical and Applied Mathematical Sciences Institute (SAMSI), Research Triangle Park, NC
- 2013 Conference Organization Committee, the 8th International Purdue Symposium on Statistics
- 2011 NSF grant review panel, Statistics Program
- 2010 Conference Organization Committee, the 19th Applied Statistics Symposium of the International Chinese Statistical Association, Indianapolis, IN
- 2007 Topic-contributed session organizer, Joint Statistical Meeting
- 2004-2005 Assistant Director, Statistical Consulting Service, Purdue University
- 2003-2004 NSF grant review panel, Integrative Graduate Education and Research Traineeship (IGERT)

Awards

- 2010, Graduate Student Mentoring Award, College of Science, Purdue
- 2012, Seed for Success Award, Purdue
- 2014, Seed for Success Award, Purdue
- 2015, Team Award, College of Science, Purdue
- 2016, Outstanding Service Award, College of Science, Purdue
- 2018, Leadership Award, College of Science, Purdue
- 2020, Graduate Student Mentoring Award, College of Science, Purdue
- 2021, Seed for Success Award, Purdue

Teaching Experiences

- Statistical Methods for Biology:
Introductory statistics course for both undergraduate and graduate students in the life sciences
- Statistical Methods:
Introductory statistics course for students in engineering and physical sciences
- Mathematical Statistics:
Core PhD level statistical theory course
- Statistical Methods for Computational Biology:
Graduate level bioinformatics course with emphasis on statistical methodology

Ph.D. Students and Postdoc

Dr. Xie has advised a dozen PhD students and two postdocs. She has also served as an advisory committee member for hundreds of MS and PhD students. She is the mentor of many graduate students and has extensive experience in graduate education.

1. Ph.D. Students

- 1) Nak-Kyeong Kim, Ph.D. 2005,
Assistant Professor in Biostatistics at Virginia Commonwealth University, Virginia.
- 2) Chuancai Wang, Ph.D. 2004 (Co-advised with Dr. Bruce Craig),
Assistant Professor in Biostatistics at Pennsylvania State University.
- 3) Lingmin Zeng, Ph.D. 2008,
Senior Principal Statistician in a pharmaceutical company Astrazeneca in Maryland.
- 4) Riyan Cheng, Ph.D. 2009 (Co-advised with Dr. Rebecca Doerge),
Postdoc in University of Chicago.
- 5) Jingyi Zhu, Ph.D. 2014,
Data Analyst
- 6) Yaowu Liu, Ph.D., 2017,
Faculty in Southwestern University of Finance and Economics, China
- 7) Donglai Chen, Ph.D., 2019
Data Analyst in Sam's Club.
- 8) Pengcheng Yang
- 9) Muye Liu
- 10) Haoze Li
- 11) Jinyong Lee

2. Postdoc

- 1) Won Chul Song,
Now an assistant professor at Milwaukee School of Engineering
- 2) Zhongyuan Chen

Publications

1. Chen Z and Xie J, 2023, “Estimating heterogeneous treatment effects versus building individualized treatment rules: Connection and disconnection”, *Statistica & Probability Letter*, preprint available online, [https://authors.elsevier.com/sd/article/S0167-7152\(23\)00078-0](https://authors.elsevier.com/sd/article/S0167-7152(23)00078-0)
2. Chen Z, Wang Z, Song Q, and Xie J, 2022, “Data-guided treatment recommendation with feature scores”, *Statistica Sinica*, 32, 2497-2519.
3. do Nascimento NC, Bailey TW, Santos AP, Duan C, Mohallem R, Franco J, Aryal UK, Xie J, Cox A, Sivasankar MP, “Proteomic analysis reveals that aging rabbit vocal folds are more vulnerable to changes caused by systemic dehydration”. *BMC Genomics*, 2022 Nov 21;23(1):762. doi: 10.1186/s12864-022-08975-x.
4. do Nascimento NC, Santos AP, Ferreirab RM, Aryal UK, Xie J, Cox A, Sivasankar MP, “Furosemide-induced systemic dehydration alters the proteome of rabbit vocal folds”, *Journal of Proteomics*, 252, 104431 (2022), <https://doi.org/10.1016/j.jprot.2021.104431>.
5. Bailey TW, Santos AP, do Nascimento NC, Sivasankar MP, Xie J, and Cox A, “Recurring exposure to low humidity induces transcriptional and protein level changes in the vocal folds of rabbits”, *Scientific Reports*, 11, 24180 (2021), <https://doi.org/10.1038/s41598-021-03489-0>.
6. Wei L, Fitzgerald M, Graham J, Hutson N, Zhang C, Huang Z, Hu Q, Zhan F, Xie J, Zhang J, Liu S, Remenyik E, Gellen E, Colegio OR, Christensen S, Lin H, Bax M, Xu J, Huss WJ, Foster BA, Paragh G, 2020, “Ultra-deep sequencing differentiates patterns of skin clonogenic mutations associated with sun-exposure status”, *Science Advances*, 7(1), doi: 10.1126/sciadv.abd7703.
7. Hutson N, Zhan F, Graham J, Murakami M, Zhang H, Ganaparti S, Hu Q, Yan L, Ma C, Liu S, Xie J, and Wei L, 2020, “An adaptive method of defining negative mutation status for multi-sample comparison using next-generation sequencing”, *BMC Medical Genomics*, <https://doi.org/10.1186/s12920-021-00880-8>.
8. Liu Y and Xie J, 2020, “Cauchy combination test: a powerful test with analytic p-value calculation under arbitrary dependency structures”, *Journal of the American Statistical Association*, 115(529), 393-402, doi: 10.1080/01621459.2018.1554485
9. Liu Y and Xie J, 2019, “Accurate and Efficient P-value Calculation via Gaussian Approximation: A Novel Monte-Carlo Method”, *Journal of the American Statistical Association*, 114(525), 384-392.
10. Song W and Xie J, 2019, “Group Feature Screening via the F Statistic”, *Communications in Statistics – Simulation and Computation*, doi: 10.1080/03610918.2019.1691223.
11. McBride Z, Chen D, Lee Y, Aryal U, Xie J, and Szymanski D, 2019, “A Label Free Mass Spectrometry Method to Predict Endogenous Protein Complex Composition”, *Molecular & Cellular Proteomics*, mcp.RA119.001400.
12. Liu Y and Xie J, 2018, “Powerful test based on conditional effects for genome-wide screening”, *the Annals of Applied Statistics*, 12(1), 567-585.
13. McBride Z, Chen D, Reick C, Xie J, Szymanski DB, 2017, “Global analysis of membrane-associated protein oligomerization using protein correlation profiling”, *Molecular & Cellular Proteomics*, doi: 10.1074/mcp.RA117.000276.
14. Aryal UK, McBride Z, Chen D, Xie J, Hall MC, Szymanski DB, 2017, “Analysis of protein complexes in Arabidopsis leaves using size exclusion chromatography and label-free protein correlation profiling”, *Journal of Proteomics*, doi: 10.1016/j.jprot.2017.06.004.

15. Chen D, Liu C and Xie J, 2016, “Multi-locus test and correction for confounding effects in genome-wide association studies”, *International Journal of Biostatistics*, doi: 10.1515/ijb-2015-0091.
16. Zhu J and Xie J, 2014, “Nonparametric variable selection for predictive models and subpopulations in clinical trials”, *Journal of Biopharmaceutical Statistics*, doi: 10.1080/10543406.2014.920861.
17. Aryal UK, Xiong Y, McBride Z, Kihara D, Xie J, Hall MC, Szymanski DB, 2014, “A proteomic strategy for global analysis of plant protein complexes”, *Plant Cell*, doi: tpc.114.127563.
18. Liang H, Studach L, Hullinger R, Xie J and Andrisani O, 2014, “Down-regulation of RE-1 Silencing Transcription Factor (REST) in advanced prostate cancer by hypoxia-induced miR-106b~25”, *Experimental Cell Research*, 320(2): 188-99, doi: 10.1016/j.yexcr.2013.09.020.
19. Liu C and Xie J, 2013, “Probabilistic Inference for Multiple Testing”, *International Journal of Approximate Reasoning*, doi: 10.1016/j.ijar.2013.09.017.
20. Liu C and Xie J, 2013, “Large Scale Two Sample Multinomial Inferences and Its Applications in Genome Wide Association Studies”, *International Journal of Approximate Reasoning*, doi: 10.1016/j.ijar.2013.04.010.
21. Zeng L and Xie J, 2012, “Group Variable Selection via SCAD-L2”, *Statistics: A Journal of Theoretical and Applied Statistics*, doi: 10.1080/02331888.2012.719513.
22. Qiu X, Sun W, McDonnell C, Li H, Steele LD, Wu J, Xie J, Muir W and Pittendrigh BR, 2012, “Genome-wide Analysis of Genes Associated with Moderate and High DDT Resistance in *Drosophila Melanogaster*”, *Pest Management Science*, doi: 10.1002/ps.3454.
23. Xie J, Quan H and Zhang J, 2012, “Blinded Assessment of Treatment Effect for Survival Endpoint in an Ongoing Trial”, *Pharmaceutical Statistics*, doi: 10.1002/pst.535.
24. Zeng L and Xie J, 2012, “Group Variable Selection for Data with Dependent Structures”, *Journal of Statistical Computation and Simulation*, 82(1), 95-106.
25. Sun L, Li H, Seufferheld MJ, Walters K, Margam V, Jannasch A, Diaz N, Riley CP, Sun W, Li YF, Muir WM, Xie J, Wu J, Zhang F, Chen JY, Barker EL, Adamec J, and Pittendrigh BR, 2011, “Systems-scale Analysis Reveals Pathways Involved in Cellular Response to Methamphetamine”, *PLoS ONE*, 6(4): e18215. doi: 10.1371/journal.pone.0018215.
26. Qiao B, Huang CH, Cong L, Xie J, Lo SH, and Zheng T, 2009, “Genome-wide Gene-based Analysis of Rheumatoid Arthritis-associated Interaction with PTPN22 and HLA-DRB1”, *BMC Proceedings*, 3(Suppl. 7):S132.
27. Huang CH, Cong L, Xie J, Qiao B, Lo SH, and Zheng T, 2009, “Rheumatoid Arthritis-associated Gene-gene Interaction Network for Rheumatoid Arthritis Candidate Genes”, *BMC Proceedings*, 3(Suppl. 7):S75.
28. Zeng L, Wu J, and Xie J, 2008, “Statistical Methods in Integrative Analysis for Gene Regulatory Modules”, *Statistical Applications in Genetics and Molecular Biology*, 7(1), Article 28.
29. Li H, Sun L, Mittapalli O, Muir WM, Xie J, Wu J, Schemerhorn B, Sun W, Murdock L, and Pittendrigh BR, 2008, “Transcriptional Signatures in Response to Wheat Germ Agglutinin and Starvation in *Drosophila melanogaster* Larval Midgut”, *Insect Molecular Biology*, doi: 10.1111/j.1365-2583.2008.00844.x.
30. Li H, Buczkowski G, Mittapalli O, Xie J, Wu J, Westerman R, Schemerhorn B, Murdock LL, and Pittendrigh BR, 2008, “Transcriptomic Profile of *Drosophila Melanogaster* Third-instar Larval Midgut and Responses to Oxidative Stress”, *Insect Mocular Biology*, 17(4), 325-339.

31. Li J, Abraham S, Cheng L, Witzmann FA, Koch M, Xie J, Rahman M, and Mohammed SI, 2008, "Proteomic-Based Approach for Biomarkers Discovery in Early Detection of Invasive Urothelial Carcinoma", *Proteomics – Clinical Applications*, 78-89.
32. Wu J and Xie J, 2008, "Computation-Based Discovery of Cis-Regulatory Modules by Hidden Markov Models", *Journal of Computational Biology*, 15(3), 279-290.
33. Antuofermo E, Miller MA, Pirino S, Xie J, Badve S, and Mohammed SI, 2007, "Spontaneous Mammary Intraepithelial Lesions in Dogs - A Model for Breast Cancer", *Cancer Epidemiology, Biomarkers & Prevention*, 16, 2247-2256.
34. Bae SH, Tang H, Wu J, Xie J, Kim S, 2007, "dPattern: Transcription Factor Binding Site (TFBS) Discovery in Human Genome Using a Discriminate Pattern Analysis", *Bioinformatics*, doi:10.1093/bioinformatics/btm288.
35. Liu C, Xie J, Zhang Y, 2007, "Weighted Nonparametric Maximum Likelihood Estimate of a Mixing Distribution in Nonrandomized Clinical Trials", *Statistics in Medicine*, doi:10.1002/sim.2914.
36. Liu C, Shen W, and Xie J, 2007, "Nonparametric Empirical Bayes Method for Comparison of Treatment Effects with Application to Stress Urinary Incontinence Data", *Pharmaceutical Statistics*, doi: 10.1002/pst.264.
37. Abad PC, Lewis J, Mian IS, Badve S, Xie J, and Lelièvre SA, 2006, "Influence of NuMA on Higher Order Chromatin Structure in Human Mammary Epithelium", *Molecular Biology of the Cell*, 18, 348-361.
38. Kim NK and Xie J, 2006, "Protein Multiple Alignment Incorporating Primary and Secondary Sequence Information", *Journal of Computational Biology*, 13(10), 1735-1748.
39. Zhang M, Gazo R, Cassens DL, and Xie J, 2006, "Moisture Distribution in a Dried Red Oak Lumber Package Stored in a High Humidity Environment", *Forest Products Journal*, 56(4), 75-80.
40. Wang C, Xie J, and Craig B, 2005, "Context Dependent Models for Discovery of Transcription Factor Binding Sites", *Statistical Methodology*, 3, 55-68.
41. Xie J and Kim NK, 2005, "Bayesian Models and Markov Chain Monte Carlo Methods for Protein Motifs with the Secondary Characteristics", *Journal of Computational Biology*, 12(7), 952-970.
42. Ameen A, Wang C, Kaakeh W, Bennett GW, King EJ, Karr LL, and Xie J, 2005, "Residual Activity and Population Effects of Noviflumuron for German Cockroach (Dictyoptera: Blattellidae) Control", *Journal of Economic Entomology*, 98(3), 899-905.
43. Xie J and Liu C, 2005, "Adjusted Kaplan-Meier Estimator and Log-rank Test with Inverse Probability of Treatment Weighting for Survival Data", *Statistics in Medicine*, 24(20), 3089-3110.
44. Xie J, Li KC, and Bina M, 2004, "A Bayesian Insertion/Deletion Algorithm for Distant Protein Motif Searching via Entropy Filtering", *Journal of the American Statistical Association*, 99(466), 409-420.
45. Xie J and Bentler PM, 2003, "Covariance Structure Models for Gene Expression Microarray Data", *Structural Equation Modeling*, 10(2), 566-582.
46. Gong G, Qian M, and Xie J, 2001, "Reversible Algorithm of Simulating Multivariate Densities with Multi-hump", *Science in China Series A*, 44(3), 357-364.
47. Bentler PM and Xie J, 2000, "Corrections to Test Statistics in Principal Hessian Directions", *Statistics & Probability Letters*, 47, 381-389.

48. Catoni O, Chen D, and Xie J, 2000, “The Reduction Method, the Loop Erased Exit Path, and the Meta-stability of the Biased Majority Vote Process”, *Stochastic Processes and Their Applications*, 86(2), 231-261.

Book Chapters

1. Liu C and Xie J, 2012, “Large Scale Multinomial Inferences and Its Applications in Genome Wide Association Studies”, *Advances in Intelligent and Soft Computing* 164, Eds. Denoeux and Masson, Belief Functions: Theory and Applications, 367-374.
2. Xie J and Zeng L, “Group Variable Selection Methods and Their Applications in Analysis of Genomic Data”, a chapter in *Frontiers in Computational and System Biology*, Springer, 2010.
3. Wu J and Xie J, “Hidden Markov Model and Its Applications in Motif Findings”, a chapter in *Statistical Methods in Molecular Biology*, Humana Press, 2009.

Some Invited Lectures in the recent five years

1. Seminar at Fred Hutchinson Cancer Center, Seattle, WA, October, 2023.
2. Lecture of distinguished women in Data Science and Statistics, UCLA, May 23, 2023
3. Mathematical Biology seminar at Georgia Institute of Technology, April 2020, postponed due to the pandemic.
4. “Large scale inference and applications in genetic variant association testing”, July 2019, Workshop at Fudan University, China.
5. “Powerful statistical tests for genetic variant sets with scalable algorithms”, December 2018, Fred Hutchinson Cancer Center, Seattle, WA.
6. “Powerful statistical tests for large-scale inference with applications in genome-wide association studies”, International Chinese Statistical Association Conference, July 2018, Qingdao, China.
7. “New Statistical Methods of Large-Scale Inference with Applications on Genomics Data”, Conference at University of Connecticut, May 2017.

Research Grants

1. National Institutes of Health (NIH), 2022-2027
“Estrogenic regulation of systemic vocal fold dehydration”
Role: Co-PI
2. National Institute of Food and Agriculture, 2022-2026
"Mechanism of Regulation of Postnatal Growth Efficiency in Piglets by Maternal Live Yeast Supplementation"
Role: Co-PI
3. National Science Foundation (NSF), 2020-2024
“Plant Genome Research: A systems biology approach to enable cotton fiber engineering”
Role: Co-PI
4. NIH Data Science Rotation for Advancing Discovery Trip (RoAD Trip) program, 2019
“Predict skin cancer risk by statistical analysis of UV-induced clonal mutations”
Role: senior data science mentor
5. National Institutes of Health (NIH), 2019-2021
“Mechanisms of Hepatocyte Transformation by the Hepatitis B Virus X Protein”, Renewal grant

- Role: Co-PI
6. National Institutes of Health (NIH), 2016-2018
“Overcoming Drug Resistance of Castration-Resistant Prostate Cancer”
Role: Co-PI
 7. National Institutes of Health (NIH), 2016-2018
“Enhancing Anti-Neoplastic Activity of Metformin in Prostate Cancer”
Role: Co-PI
 8. National Science Foundation (NSF), subcontract of Washington State University, 2015-2019
“Deciphering the role of RNA binding proteins in RNA transport, localization and post-transcriptional processes in plants”
Role: Co-PI
 9. Army Medical Research Acquisition Activities, 2014-2018
“Developing Novel Therapeutic Strategies for Castration-Resistant Prostate Cancer”
Role: Co-PI
 10. National Institutes of Health (NIH), 2014-2017
“Nonparametric Methods for Clinical Predictive Model in Pharmacogenomics Research”
Role: PI
 11. American Cancer Society, 2013-2016,
“Plk1 in UV-Induced Melanoma Formation”
Role: Co-PI.
 12. National Science Foundation (NSF), 2011-2016
“TRPGR: Novel Quantitative Proteomic Methods to Discover and Localize Endogenous Protein Complexes”
Role: Co-PI
 13. National Science Foundation (NSF), 2013-2018
“MCTP: Sophomore Transitions: Bridges into a Statistics Major and Big Data Research Experience via Learning Communities”
Role: Co-PI
 14. National Institutes of Health (NIH), 2011-2016
“Mechanism(s) of Hepatocyte Transformation by the Hepatitis B Virus X Protein”
Role: Co-PI
 15. National Science Foundation (NSF), Division of Mathematics, Statistics Program, 2010-2014
“Large Scale Multinomial Inferences and Its Applications in Genome Wide Association Studies”
Role: Co-PI
 16. National Science Foundation (NSF), Division of Mathematics, Statistics Program, 2006-2009
“Bayesian Models and Monte Carlo Strategies in Identifying Protein or DNA Motifs”
Role: PI
 17. National Institutes of Health (NIH), PHS-NIH-National Cancer Institute, 2006-2008
“LCM & 2D PAGE in Early Detection of Pancreatic Cancer”
Role: Co-PI.
 18. Collaboration in Life Sciences and Informatics Research Pilot Grant, Indiana University Bloomington and Purdue University, 2006
“Integrative Analysis of Gene Regulatory Elements and Gene Expression”
Role: PI