# Dan Nettleton

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**Education**

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| Doctor of Philosophy<br>Statistics | University of Iowa<br>Iowa City, Iowa<br>July, 1996 |
| Master of Science<br>Statistics | University of Iowa<br>Iowa City, Iowa<br>May, 1993 |
| Bachelor of Arts<br>Mathematics (major)<br>Computer Science (minor) | Wartburg College<br>Waverly, Iowa<br>May, 1991 |

**Dissertation**
Interval Mapping of Quantitative Trait Loci through Order Restricted Inference
Advisors: Tim Robertson and Jens Praestgaard

**Work Experience**
Chair, Department of Statistics, 2019–
Distinguished Professor, Department of Statistics, Iowa State University, 2015–
Laurence H. Baker Endowed Chair in Biological Statistics, Department of Statistics, Iowa State University, 2007–
Director, Laurence H. Baker Center for Bioinformatics and Biological Statistics, 2016–2022
Professor, Department of Statistics, Iowa State University, 2007–2015
Associate Professor, Department of Statistics, Iowa State University, 2002–2007
Assistant Professor, Department of Statistics, Iowa State University, 2000–2002
Assistant Professor, Department of Mathematics and Statistics, University of Nebraska-Lincoln, 1996–2000

**Research Interests**
Statistical Methods for the Design and Analysis of High-throughput Biological Experiments, Multiple Testing, Statistical Learning, Predictive Inference, Sports Analytics, Data Science, Order Restricted Inference

**Refereed Journal Articles** (* Indicates Nettleton student and/or research assistant coauthor)

[194] Hatfield, B. M., LaSarre, B., *Liu, M., Dong, H., Nettleton, D., Beattie, G. A. (2023). Light cues induce protective anticipation of environmental water loss in terrestrial bacteria. *Proceedings of the National Academy of Sciences*. Accepted.

[193] *Jeon, H., Lim, K.-S., Nguyen, Y., Nettleton, D. (2023). Adjusting for gene-specific covariates to improve RNA-seq analysis. *Bioinformatics*. Accepted.

[192] *Guo, X., Qiu, Y., Nettleton, D., Schnable, P. S. (2023). High-throughput field plant phenotyping: a self-supervised sequential CNN method to segment overlapping plants. *Plant Phenomics*, 5.

[191] Ananya, A., Holden, K. G., *Gu, Z., Nettleton, D., Mallapragada, S. K., Wannemuehler, M. J., Kohut, M. L., Narasimhan. B. (2023). "Just right" combinations of adjuvants with nanoscale carriers activate aged dendritic cells without overt inflammation. *Immunity & Ageing*. 20, 10.

[190] *Yu, S., Kusmec, A. M., Wang, L., Nettleton, D. (2023). Fusion learning of functional linear regression with application to genotype-by-environment interaction studies. *Journal of Agricultural, Biological, and Environmental Statistics*. Accepted.

[189] Ding, G., Mugume, Y., Dueñas, M. E., Lee, Y. J., *Liu, M., Nettleton, D., Zhao, X., Li, L., Bassham, D. C., Nikolau, B. J. (2023). Biological insights from multi-omics analysis strategies: complex pleotropic effects associated with autophagy. *Frontiers in Plant Science*. 14. DOI: 10.3389/fpls.2023.1093358

[188] Baldauf, J. A., *Liu, M., Vedder, L., Yu, P., Piepho, H.-P., Schoof, H., Nettleton, D., Hochholdinger, F. (2022). Single parent expression complementation contributes to phenotypic heterosis in maize hybrids. *Plant Physiology*. 189, 1625–1638. DOI: 10.1093/plphys/kiac180

[187] *Peng, L., *Qu, L., Nettleton, D. (2021). Variable importance assessments and backward variable selection for multi-sample problems. *Journal of Multivariate Analysis*. 186, 104807. DOI: 10.1016/j.jmva.2021.104807

[186] *Guo, X., Qiu, Y., Nettleton, D., Yeh, C.-T., Zheng, Z., Hey, S., Schnable, P. S. (2021). KAT4IA: K-means assisted training for image analysis of field-grown plant phenotypes. *Plant Phenomics*. Article ID 9805489, DOI: 10.34133/2021/9805489

[185] *Sage, A. J., Genschel, U., Nettleton, D. (2021). A residual-based approach for robust random forest regression. *Statistics and Its Interface*. 14(4), 389–402.

[184] Silva, F. A., Chatt, E. C., Mahalim, S. N., Guirgis, A., *Guo, X., Nettleton, D., Nikolau, B. J., Thornburg, R. W. (2020). Metabolomic profiling of *Nicotiana* spp. nectars indicates that pollinator feeding preference is a stronger determinant than plant phylogenetics in shaping nectar diversity. *Metabolites*. 10(5), 214. DOI: 10.3390/metabo10050214

[183] *Nguyen, Y., Nettleton, D. (2020). rmRNAseq: RNA-seq analysis for repeated-measures data. *Bioinformatics*. 36(16), 4432–4439. DOI: 10.1093/bioinformatics/btaa525

[182] *Mao, X., Dutta, S., Wong, R. K. W., Nettleton, D. (2020). Adjusting for spatial effects in genomic prediction. *Journal of Agricultural, Biological, and Environmental Statistics*. 25, 699–718. DOI: 10.1007/s13253-020-00396-1.

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## Books Edited

Datta, S., Nettleton, D. (2014). Co-Editors of *Statistical Analysis of Next Generation Sequencing Data.* Springer.

## Book Chapters

O'Conner, S., Neudorf, A., Zheng, W., Qi, M., Zhao, X., Du, C., Nettleton, D., Li L. (2018) From Arabidopsis to crops: the Arabidopsis QQS orphan gene modulates nitrogen allocation across species. In: *Engineering Nitrogen Utilization in Crop Plants* (Shrawat, A., Zayed, A., Lightfoot, D. A., eds), pp. 95-117. Springer.

Nettleton, D. (2014). Design of RNA sequencing experiments. In: *Statistical Analysis of Next Generation Sequencing Data.* Datta, S. and Nettleton, D. (Co-Editors). Springer. Chapter 5, 93–113.

Nettleton, D. (2012). Design of gene expression microarray experiments. In: *Design and Analysis of Experiments, Volume 3: Special Designs and Applications.* Hinkelmann, K. (Editor). Wiley. Chapter 2, 73–108.

## Invited Discussions of Refereed Journal Articles

Nettleton, D. (2006). Invited discussion of "Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions" by Ming Yuan and Christina Kendziorski. *Journal of the American Statistical Association.* 101, 1334–1338.

## Refereed Conference Proceedings Articles

Koesterke, L. Stanzione, D., Vaughn, M., Welch, S. M., Kusnierczyk, W., Yang, J., Yeh, C.-T., Nettleton, D., Schnable, P. S. (2011). An efficient and scalable implementation of SNP-pair interaction testing for genetic association studies. *IEEE International Parallel and Distributed Processing Symposium.* 523–530.

Ding, J., Berleant, D., Nettleton, D., and Wurtele, E. (2002). Mining Medline: Abstracts, sentences, or phrases? *Pacific Symposium on Biocomputing.* 7, 326–337.

Nettleton, D. (1999). A computationally efficient method for determining significance in interval mapping of quantitative trait loci. *Proceedings of the Kansas State University Conference on Applied Statistics in Agriculture*. 130–144.

**Non-refereed Conference Proceedings Articles**

*Zhang, H., Nettleton, D., Zhu, Z. (2017). Regression-enhanced random forests. In *JSM Proceedings,* Section on Statistical Learning and Data Science. Alexandria, VA: American Statistical Association. 636–647.

*Zimmerman, J., Nettleton, D. (2015). Case-specific random forests for big data prediction. In *JSM Proceedings,* General Methodology. Alexandria, VA: American Statistical Association. 2537–2543.

Nettleton, D. (1999). Testing for association between categorical variables with multiple-response data. *The Proceedings of the American Statistical Association Section on Survey Research Methods*. 492–496.

**Research Funding** (PI is listed first. Dollar figures are approximate total award amounts.)

Tavanapong, W., Mallapragada, S. K., Nettleton, D., Weber, E., Rajan, H. Dependable Data-Driven Discovery. National Science Foundation Research Traineeship Program. July 2022 to June 2027. $2,998,973.

Ganapathysubramanian, B., Kantor, G. A., Lawrence-Dill, C. J., Merchant, N., Sarkar, S., Schnable, P. S., Segovia, M. S., Singh, A., Singh, A. K., (Nettleton, D. funded collaborator among 26 others). AI Institute for Resilient Agriculture. National Science Foundation and United States Department of Agriculture National Institute of Food and Agriculture. September 2021 to December 2026. $20,000,000.

Kohut, M., Narasimhan, B., Mallapragada, S., Wannemuehler, M., Verhoeven, D., Nettleton, D., Bronikowski, A. Combination Nanovaccine-Mediated Protection Against Influenza Virus in the Aged, National Institutes of Health. February 16, 2021 to February 15, 2026. $3,518,508.

King, A., Niederdeppe, J., Margolin, D., Chunara, R. (funded collaborator: Nettleton, D.) Using Natural Language Processing and Crowdsourcing to Monitor and Evaluate Public Information and Communication Disparities About Colon Cancer, National Institutes of Health. February 16, 2021 to February 15, 2025. $1,548,266.

Rajan, H., Nettleton, D., Weber, E., Aduri, P., Hegde, C. HDR TRIPODS: Dependable Data-Driven Discovery Institute, National Science Foundation. October 1, 2019 to September 30, 2022. $1,499,995.

Beattie, G., Nettleton, D., Nikolau, B. Mechanistic Drivers Shaping Root Microbiomes and Microbiome Drivers of Fitness Benefits in Drought-Stressed Plants, National Institute of Food and Agriculture. May 1, 2019 to April 30, 2022. $749,591.

Scanlon, M. J., Owens, T., Janick-Buckner, D., Buckner, B., Muehlbauer, G., Schnable, P., Timmermans, M., Yu, J., Zhang, X. (funded collaborators: Lawrence, C., Nettleton, D.) Genetic networks regulating structure and function of the maize shoot apical meristem, National Science Foundation, February 1, 2013 to August 31, 2020. $7,579,252.

Nettleton, D. Conference on Predictive Inference and Its Applications, National Science Foundation, May 1, 2018 to April 30, 2019. $10,000.

Wise, R. P., Altpeter, F., Innes, R. W., Bogdanove, A. J., Nettleton, D. Host Targets of Fungal Effectors as Keys to Durable Disease Resistance, National Science Foundation, April 1, 2014 to March 31, 2019. $2,500,000.

Nettleton, D., Liu, P., Niemi, J., Schnable, P. Hierarchical Modeling and Parallelized Bayesian Inference for the Analysis of RNAseq Data, National Institutes of Health, September 1, 2013 to May 31, 2018. $1,088,156.

Nettleton, D. (funded collaborator: Long Qu). Distance-Based Variable Selection for High-Dimensional Biological Data, National Science Foundation, September 15, 2013 to September 14, 2016. $150,000.

Patience, J. F., Anderson, L., Campbell, R., Dekkers, J., DeRouchey, J., Gabler, N., Gilbert, H. Huff-Lonergan, E., Johnson, A., Kerr, B., Liu, P., Lonergan, S., Mabry, J., Nettleton, D., Rothschild, M., Rowland, R. R., Tokach, M., Tuggle, C., van Kessel, A., Weber, T. Enhancing sustainability and competitiveness of the U.S. pork industry by improving nutrient utilization and feed efficiency through innovative scientific and extension approaches, United States Department of Agriculture, March 1, 2011 to February 29, 2016. $4,799,158.

Schnable, P. S., Buckner, B., Lawrence, C. J., Nettleton, D. Functional Structural Diversity among Maize Haplotypes. National Science Foundation, March 15, 2011 to February 28, 2013. $2,763,095.

Wise, R. P., Leshem-Ackerman, A., Bogdanove, A. J., Nettleton, D., Dickerson, J. A. The Functional Interactome of Cereals with the Fungal Biotroph, Blumeria graminis. National Science Foundation, March 15, 2010 to February 28, 2014. $2,298,540.

Peterson, T., Nettleton, D., Weber, D. F., Zhang, J. Mechanism and Genetic Impacts of Transposon-Induced Duplications in Maize. National Science Foundation, September 1, 2009 to August 31, 2012. $999,751.

Garrick, D.J., Dekkers, J. C. M., Fernando, R.L., Nettleton, D. Bioinformatics to Implement Genomic Selection. United States Department of Agriculture, January 2009 to December 2012. $909,439.

Tuggle, C., Honovar, V., Wannemuehler, M., Nettleton, D., Bearson, S., Lunney, J. Developing Predictive Models for Identifying Pigs with Superior Immune Response and Improved Food Safety. United States Department of Agriculture, January 2009 to December 2012. $749,345.

White, F., Bogdanove, A.J., Yang, B., Nettleton, D. GEPR: Transcription profiling and functional analyses of bacterial disease susceptibility pathways of rice. National Science Foundation, September 2008 to August 2012. $3,300,000.

Scanlon, M. J., Janick-Buckner, D., Muehlbauer, G.J., Timmermans, M., Yu, J. (funded collaborator: Nettleton, D.). GEPR: Genomic analyses of shoot meristem function in maize. National Science Foundation, September 2008 to August 2012. $5,310,987.

Aluru, S., Aluru, M., Nettleton, D. CPA-ACR: Parallel Algorithms and Software for Large Scale Microarray Data Analysis and Gene Network Inference. National Science Foundation, July 2008 to June 2011. $375,000.

Beattie, G., Gross, D., Lindow, S., Nettleton, D. Functional Genomics of the Pathogenic and Epiphytic Lifestyle of the Bacterial Plant Pathogen Pseudomonas syringae. United States Department of Agriculture, January 2008 to December 2011. $900,000.

Baum, T.J., Davis, E.L., Mitchum, M.G., Nettleton, D.  Functional Genomics of Soybean Cyst Nematode Parasitism of Plants.  United States Department of Agriculture, April 2008 to March 2011.  $749,624.

Nettleton, D., Chen, S., Dekkers, J., Liu, P., Tuggle, C.  Development of High-Dimensional Data Analysis Methods for the Identification of Differentially Expressed Gene Sets.  National Science Foundation, August 2007 to August 2011.  $552,927.

Kohut, M., Buss, J., Cunnick, J., Nettleton, D., Wannemuehler, M., Yoon, K.-J.  Exercise-Induced Immunomodulation in the Aged: Mechanisms.  National Institutes of Health, March 2007 to February 2012.  $2,415,855.

Dekkers, J., Fernando, R., Nettleton, D., Rothschild, M.  Training in the Development and Application of Quantitative Methods and Tools for Animal Genomics.  United States Department of Agriculture, November 2006 to November 2009.  $252,000.

Minion, C. Nettleton, D.  Molecular Basis for the Development of Sanitizer Tolerance in Lysteria Monocytogenes.  United States Department of Agriculture (sub-contract from University of Georgia), September 2005 to August 2007.  $81,772.

Wise, R. Dickerson, J., Nettleton, D., Whitham, S.  ISGA: Functional genomics of plant disease defense pathways.  National Science Foundation, June 2005 to May 2009.  $2,093,192.

Dekkers, J., Rekaya, R., Hausman, G., Barb, R., Tuggle, C., Anderson, L. Honovar, V., Nettleton, D.   Integration of functional genomics and quantitative genetics to improve feed efficiency in pigs.  United States Department of Agriculture, March 2005 to February 2008.  $876,000.

Baum, T. J., Davis, E. L., Mitchum, M. G., Nettleton, D. Functional genomics of soybean response to cyst nematode parasitism proteins.  United States Department of Agriculture, March 2005 to February 2008.  $900,000.

Meeker, W., Cook, D., Carriquiry, A., Opsomer, J., Nettleton, D.  Computing Equipment to Support Research in Statistics.  National Science Foundation, September 2004 to August 2006.  $72,565.

Tuggle, C., Geisert, R., Lunney, J., Nettleton, D., Reecy, J. Identifying Molecular Genetic Mechanisms Controlling Pig Litter Size: Expression Profiling of Peri-implantation Conceptus and Endometrium. United States Department of Agriculture, September 2003 to August 2006.  $300,000.

Scanlon, M. J., Buckner, B., Nettleton, D., Janick-Buckner, D., Timmermans, M., Schnable, P. S. Functional analyses of genes involved in meristem organization and leaf initiation. National Science Foundation, Plant Genome Program. September 2003 to August 2007.  $1,979,543.

Howell, S., Nettleton, D. Regulation of shoot development in Arabidopsis. National Science Foundation, Integrative Plant Biology. June 2003 to May 2006. $399,964.

Dickerson, J., Brendel, V., Wise, R., Nettleton, D., Cook, D.  BarleyBase, a prototype online database for cereal microarrays with integrated tools for data visualization and statistical analysis.  United States Department of Agriculture, Plant Genome Program.  August 2002 to August 2005. $500,000.

Baenziger, P. S., Gill, K., Nettleton, D., Eskridge, K.  The Genetic Basis of Agronomic Traits Controlled by Chromosome 3A in Wheat.  United States Department of Agriculture, Plant Genome Program.  August 2000 to August 2003.  $250,000.

Nettleton, D. Improved Statistical Methods for Detecting QTL and Estimating Their Effects. United States Department of Agriculture, Animal Genetic Mechanisms and Gene Mapping. November 1998 to June 2002. $75,000.

**Seminar Presentations at Colleges, Universities, or Research Organizations**

Resource-Constrained Machine Learning Guided by Out-of-Bag Error Prediction, National Science Foundation TRIPODS PI Meeting, presented by Zoom, September 2021

Generating Predictive Distributions from Random Forest Prediction Errors, Department of Mathematics and Statistics, Air Force Institute of Technology, presented by Zoom, April 2021

Generating Predictive Distributions from Prediction Errors, Department of Statistics, Kansas State University, presented by Zoom, April 2021

Generating Predictive Distributions from Prediction Errors, Department of Statistics, University of Virginia, presented by Zoom, March 2021

Random Forest Prediction Intervals, Department of Mathematics and Statistics, Old Dominion University, October 2019

Random Forest Prediction Intervals, Department of Mathematics, Statistics, and Computer Science, University of Illinois at Chicago, September 2019

Statistical Modeling and Inference for Temporally Dependent RNA-seq Data, Department of Mathematics and Statistics, Washington University in St. Louis, October 2018

Random Forest Prediction Intervals, Department of Statistics, Brigham Young University, March 2018

Accounting for Within-gene Correlation Structure in RNA-seq Differential Expression Analysis, Peking University Center for Bioinformatics, Beijing, China, May 2017

Accounting for Within-gene Correlation Structure in RNA-seq Differential Expression Analysis, Department of Biostatistics, University at Buffalo, May 2017

Random Forest Prediction Intervals, Department of Biomedical Informatics, The Ohio State University, February 2017

Random Forest Confidence and Prediction Intervals, Department of Economics and Statistics, University of Delaware, November 2016

Case-specific Random Forests for Big Data Prediction, Department of Statistics, Northwestern University, June 2016

Case-specific Random Forests for Big Data Prediction, Department of Statistics, Kansas State University, November 2015

A New Look at Predicting Plant Phenotype from Genotype and Environment, Biotechnology / Life Sciences Seminar Series, University of Nebraska Lincoln, October 2015

Case-specific Random Forests for Big Data Prediction, Department of Statistics, Temple University, October 2015

Case-specific Random Forests, Department of Biostatistics, University of Iowa, Iowa City, Iowa, April 2015

Case-specific Random Forests, National Institute of Environmental Health Sciences, Biostatistics and Computational Biology Branch, Research Triangle Park, North Carolina, April 2015

Case-specific Random Forests, Department of Statistics, Catholic University of Chile, Santiago, Chile, March 2015

Case-specific Random Forests, Department of Statistics and Actuarial Science, University of Waterloo, Canada, November 2014

Using Quasi-likelihood Analysis of RNA-seq Data to Identify Differentially Expressed Genes, Department of Statistics and Probability, Michigan State University, September 2014

Statistical Design and Analysis of RNA-seq Experiments, Jeffrey L. Houpt Lecture in Genome Sciences, University of North Carolina, Chapel Hill, April 2014

Augmented and Case-specific Random Forests, Department of Statistics, Colorado State University, September 2013

Using Quasi-likelihood Analysis of RNA-seq Data to Identify Differentially Expressed Genes, Department of Statistics, University of Alabama Birmingham, April 2013

Using Quasi-likelihood Analysis of RNA-seq Data to Identify Differentially Expressed Genes, Department of Statistics, Oklahoma State University, April 2013

Testing Union-of-cones Hypotheses for the Identification of Traits that Exhibit Heterosis, Department of Statistics, Yale University, October 2012

Using RNAseq Technology to Detect Differentially Expressed Genes, Department of Mathematics and Statistics, University of Calgary, September 2012

Identifying Differentially Expressed Gene Sets and the Important Genes within Such Sets, St. Jude Children's Research Hospital, November 2010

Testing for the Supremacy of a Multinomial Cell Probability, Department of Statistics, Iowa State University, August 2009

Testing for the Supremacy of a Multinomial Cell Probability, Department of Statistics, University of South Carolina, August 2009

Testing for Differentially Expressed Gene Categories on the Gene Ontology Directed Acyclic Graph, Department of Biostatistics, University of California Los Angeles, May 2009

Identifying Differentially Expressed Gene Categories via a Hidden Markov Model Approach for Testing Nodes on a Directed Acyclic Graph, Department of Statistics, University of California Irvine, May 2009

Identifying Differentially Expressed Gene Categories via a Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, Department of Statistics, North Carolina State University, December 2008

Identifying Differentially Expressed Gene Categories via a Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, Science at the Edge Seminar, Quantitative Biology Initiative, Michigan State University, October 2008

Identifying Differentially Expressed Gene Categories via a Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, Department of Statistics, University of Iowa, September 2008

Identification of Differentially Expressed Gene Categories in Microarray Studies Using Multivariate Nonparametric Analysis, Bioinformatics Seminar, University of Northern Iowa, December 2007

Exploring the Information in $p$-values for the Analysis and Planning of Multiple-Test Experiments, Department of Statistics, University of Missouri-Columbia, October 2007

Exploring the Information in $p$-values for the Analysis and Planning of Multiple-Test Experiments, Department of Biostatistics, University of Minnesota, October 2007

Statistical Challenges in the Analysis of Microarray Experiments, Wartburg College, November 2006

Introduction to Statistical Design and Analysis of Microarray Experiments, Plant Breeding Lecture Series on Data Analysis Innovations Contributing to Crop Improvement, Iowa State University, May 2006

Using *p*-values for the Planning and Analysis of Microarray Experiments, Department of Biostatistics and Medical Informatics, University of Wisconsin, November 2005

Using Observed *p*-values to Estimate the Number of True Null Hypotheses When Conducting Many Tests, Section on Statistical Genetics, University of Alabama Birmingham, May 2005

Using Observed *p*-values to Estimate the Number of True Null Hypotheses When Conducting Many Tests, Arizona State University, May 2005

Using Observed *p*-values to Estimate the Number of True Null Hypotheses When Conducting Many Tests, Department of Statistics, Cornell University, December 2004

Using Statistical Design and Analysis to Detect Differentially Expressed Genes in Microarray Experiments, University of Colorado Health Science Center, March 2004

Methods for Controlling False Positive Rates When Identifying Differentially Expressed Genes, The Jackson Laboratory, May 2002

A Comparison of Methods for Managing Type I Errors When Testing for Changes in Gene Expression, Department of Statistics, University of Georgia, February 2002

A Comparison of Methods for Managing Type I Errors When Testing for Changes in Gene Expression, Bioinformatics Seminar, Purdue University, October 2001

Mapping Quantitative Trait Loci through Principal Components Regression, Department of Statistics, Iowa State University, January 2000

Mapping Quantitative Trait Loci through Principal Components Regression, Cornell University, Statistics Colloquium, October 1999

Mapping Quantitative Trait Loci through Principal Components Regression, Department of Statistics, University of Iowa, October 1999

Testing for Association Between Categorical Variables with Multiple-response Data, Statistics Seminar, Cornell University, February 1999

Thoughts on Permutation Testing in the Mapping of Quantitative Trait Loci, Biostatistics/Statistical Genetics Seminar, Purdue University, February 1998

Interval Mapping of Quantitative Trait Loci Through Order Restricted Inference, Department of Statistics, Kansas State University, October 1997

Interval Mapping of Quantitative Trait Loci Through Order Restricted Inference, Department of Mathematics and Statistics, University of Missouri-Rolla, spring 1996

Interval Mapping of Quantitative Trait Loci Through Order Restricted Inference, Department of Statistics, Purdue University, spring 1996

Interval Mapping of Quantitative Trait Loci Through Order Restricted Inference, Department of Statistics, Harvard University, spring 1996

Interval Mapping of Quantitative Trait Loci Through Order Restricted Inference, Department of Mathematics and Statistics, University of Nebraska, spring 1996

**Invited Conference Presentations**

Who Is Winning?  Determining Whether a Candidate Leads in a Ranked-Choice Election, 50th Hogg and Craig Lectures Keynote Address, University of Iowa, April 2023

My Adventures in Sports Statistics, Beginning with Bob Hogg, 50th Hogg and Craig Lectures Keynote Address, University of Iowa, April 2023

The Dependable Data-Driven Discovery Institute, 13th International Conference of the ERCIM WG on Computational and Methodological Statistics (CMStatistics 2020), King's College London, UK, presented by Zoom, December 2020

Estimating Plant Growth Curves and Derivatives by Modeling Crowdsourced Imaged-based Data, International Chinese Statistical Association Applied Statistics Symposium, Raleigh, June 2019

Random Forest Prediction Intervals, 11th International Conference of the European Research Consortium for Informatics and Mathematics Working Group on Computational and Methodological Statistics, Pisa, Italy, December 2018

Statistical Methods for Prediction and Discovery, Clemson Integrated Plant Sciences Symposium, Clemson University, April 2018

Statistical Analysis of Complex Phenotypes Derived from Sequential Images, 2018 NIFA FACT Workshop on High-Throughput, Field-Based Phenotyping Technologies for the Genomes to Fields (G2F) Initiative, Iowa State University, January 2018

Accounting for Within-gene Correlation Structure in RNA-seq Differential Expression Analysis, International Chinese Statistical Association Applied Statistics Symposium, Chicago, June 2017

Statistical Challenges in Analysis of Complex Phenotypes Derived from Sequential Images, The Graybill Conference, Colorado State University, June 2017

Statistical Challenges in Analysis of Complex Phenotypes Derived from Sequential Images, The Second Conference on High-Dimensional Statistics in the Age of Big Data, Peking University, Beijing, China, May 2017

Differential Expression Analysis for RNA-seq Data with Repeated Measures, Statistical Inference on Biomedical Big Data Workshop, Department of Biostatistics, University of Florida, April 2017

Case-specific Random Forests for Big Data Prediction, Joint Statistical Meetings, Seattle, August 2015

My Iowa Experience from 1991–1996, Semi-Centennial Symposium, Department of Statistics and Actuarial Science, University of Iowa, Iowa City, Iowa, April 2015

An Introduction to Random Forest Methods for Outcome Prediction, Keynote Address, Mathematics on the Northern Plains Conference, Dordt College, April 2015

Identifying Genes that are Differentially Expressed in Both of Two Independent Experiments, *Journal of Agricultural, Biological, and Environmental Statistics* Showcase Session, Joint Statistical Meetings, Boston, August 2014

Case-specific Random Forests, Joint Applied Statistics Symposium of the International Chinese Statistical Association and the Korean International Statistical Society, Portland, June 2014

Accounting for Nuisance Covariates when Using RNA-seq Data to Identify Differentially Expressed Genes, Meeting of the Eastern North American Region of the International Biometrics Society, Baltimore, March 2014

Relative Variable Importance and Backward Variable Selection for High-Dimensional Response Data, Conference on Large Scale Statistical Inference and Learning, University of Minnesota, April 2012.

Testing for or Against a Union-of-Cones Hypothesis with Applications to Genomic Data Analysis, Joint Statistical Meetings, Miami, August 2011

Estimating Gene Expression Heterosis, Gordon Research Conference, Galveston, Texas, February 2011

Multiple Testing Using Sequential Permutation $p$-values, Army Conference on Applied Statistics Plenary Lecture, Cary, North Carolina, October 2010

Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis, *Biometrics* Showcase Session, Joint Statistical Meetings, Vancouver, British Columbia, August 2010

Testing for Heterosis in Gene Expression, International Chinese Statistical Association Symposium, Indianapolis, June 2010

Challenges Associated with Testing Multiple Hypotheses in Genomic Studies, Symposium on Methodological and Statistical Challenges in Obesity and Health Research, Iowa State University, May 2010

Borrowing Information Across Genes and Across Experiments for Improved Residual Variance Estimation in Microarray Data Analysis, Meeting of the Eastern North American Region of the International Biometrics Society, New Orleans, March 2010.

The Role of Permutation and Randomization Tests in High-Dimensional Studies, Joint Statistical Meetings, Washington, D.C., August 2009

Testing for Heterosis in Gene Expression, Conference Celebrating 75 Years of Statistics at Iowa State, Iowa State University, June 2009

Testing for Differentially Expressed Gene Categories on the Gene Ontology Directed Acyclic Graph, Statistical Genetics of Livestock for the Post-Genomic Era Symposium, University of Wisconsin, Madison, May 2009

Exploring the Information in $p$-values for the Analysis and Planning of Multiple-Test Experiments, Joint Statistical Meetings, Denver, Colorado, August 2008

A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, Meeting of the Western North American Region of the International Biometrics Society, University of California, Davis, June 2008

A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, Institute of Mathematical Statistics-China International Conference on Statistics and Probability, Hangzhou, China, June 2008

A Discussion of False Discovery Rate and the Identification of Differentially Expressed Gene Categories in Microarray Studies, Use R! Conference, Iowa State University, August 2007

Modeling Massive Data Sets: The Netflix Challenge from a Statistical Perspective, (Joint Talk with Heike Hofmann), Spring Research Conference, Iowa State University, May 2007

Identifying Genes Associated with a Quantitative Trait or Quantitative Trait Locus via Selective Transcriptional Profiling, Symposium on the Integration of Structural and Functional Genomics, Iowa State University, September 2005

Identifying Genes Associated with a Quantitative Trait or Quantitative Trait Locus via Selective Transcriptional Profiling, First European Farm Animal Functional Genomics Workshop, Edinburgh, Scotland, September 2005

Discussion of "Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions" by Ming Yuan and Christina Kendziorski, *Journal of the American Statistical Association* Applications and Case Studies Invited Paper Award Winner, Joint Statistical Meetings, Minneapolis, August 2005

Statistical Design and Analysis of Microarray Experiments, International Symposium on Heterosis in Plants, University of Hohenheim, Stuttgart, Germany, January 2005

Some Example Microarray Experimental Designs and Analyses, NCR170: North-Central Regional Research Project and USSES: University Statisticians of Southern Experiment Stations, University of Florida, July 2004.

The Relationships Among Scan Intensity, Expression Level, and the Power to Detect Differential Expression Using cDNA Microarrays, International Conference on the Analysis of Genomic Data, Harvard Medical School, May 2004

Analysis of a Large-scale Split-split-plot Experiment Using the Affymetrix Barley1 GeneChip, Workshop on Statistical Methods in Microarray Analysis, Institute for Mathematical Sciences, National University of Singapore, January 2004

Identifying Differentially Expressed Genes in Unreplicated Multiple-treatment Microarray Experiments, The Graybill Conference at Colorado State University, June 2003

Estimating the Number of Differentially Expressed Genes in a Microarray Experiment, Joint Iowa/Iowa State Bioinformatics Workshop, April 2003

Statistical Methods for Identifying Differentially Expressed Genes with Microarray Data, Joint Iowa/Iowa State Bioinformatics Workshop, April 2002

Mapping Quantitative Trait Loci through Principal Components Regression, International Indian Statistical Association, International Conference on Recent Developments in Statistics and Probability and Their Applications, December 2000

Testing the Equality of Distributions of Vectors with Categorical Components, 4th International Triennial Calcutta Symposium on Probability and Statistics, December 2000

Developments in the Use of Permutation Testing to Detect Quantitative Trait Loci, 6th Purdue International Symposium on Statistics, June 1998

## Contributed Conference Presentations

Expression-Level-Dependent Correlation Structure Estimation for Repeated-Measures RNA-seq Data, Topic Contributed Session, Joint Statistical Meetings, Denver, July 2019.

An Alternative to the Ratings Percentage Index for Ranking Iowa High School Football Teams, Midwest Sports Analytics Conference, Central College, Pella, Iowa, November 2018

Statistical Challenges in Analysis of Complex Phenotypes Derived from Sequential Images, Topic Contributed Session, Joint Statistical Meetings, Baltimore, August 2017.

Using Random Forests to Estimate Win Probability Before Each Play of an NFL Game, Midwest Sports Analytics Conference, Central College, Pella, Iowa, November 2016

To Go or Not to Go: Fourth Down Analysis in the NFL, Joint Statistical Meetings, Chicago, July 2016

A Glimpse Inside the Random Forest Black Box, Meeting of the North-Central Coordinating Committee 170 on Research Advances in Agricultural Statistics, Puerto Rico, June 2015

Using Quasi-likelihood Analysis of RNA-seq Data to Identify Differentially Expressed Genes, Meeting of the North-Central Coordinating Committee 170 on Research Advances in Agricultural Statistics, Lincoln, July 2014

Design of RNA Sequencing Experiments, Kansas State Conference on Applied Statistics in Agriculture, Manhattan, Kansas, April 2014

Multiple Testing for Differential Expression Using RNA-seq Data, Topic Contributed Session, Joint Statistical Meetings, Montreal, Canada, August 2013.

Statistical Methods for Identifying Gene Expression Heterosis, (Joint Talk with Jarad Niemi), Kansas State Conference on Applied Statistics in Agriculture, Manhattan, Kansas, April 2013

Relative Variable Importance and Backward Variable Selection for High-Dimensional Response Data, Topic Contributed Session, Joint Statistical Meetings, San Diego, July 2012.

Identification of Differentially Expressed Gene Categories in Microarray Studies Using Nonparametric Multivariate Analysis, Meeting of the Eastern North American Region of the International Biometrics Society, Atlanta, March 2007

Identification of Differentially Expressed Functional Categories in Microarray Studies Using Nonparametric Multivariate Analyses, Meeting of the North-Central Coordinating Committee 170 on Research Advances in Agricultural Statistics, University of Wisconsin Madison, July 2006

Probe-level Analysis of a Large-scale Split-split-plot Experiment Using the Affymetrix Barley1 GeneChip, Affymetrix GeneChip Microarray Low-level Workshop, University of California-Berkeley, August 2003

Estimating the Number of False Null Hypotheses in a Multiple Test Situation, Meeting of the Eastern North American Region of the International Biometrics Society, Tampa, Florida, April 2003

A Comparison of Methods for Managing Type I Errors When Testing for Gene Expression Changes, Joint Statistical Meetings, New York, August 2002

Using Graph-theoretic Measures of Association to Detect Differences among Distributions with Sparse Multivariate Categorical Data, Joint Statistical Meetings, Atlanta, August 2001

Statistical Analysis of Gene Expression Data from Hypertrophying and Normal Muscle Tissue, Kansas State Conference on Applied Statistics in Agriculture, spring 2001

Testing for Association Between Categorical Variables with Multiple-response Data, Joint Statistical Meetings, Baltimore, August 1999

Accounting for Variability in the Use of Permutation Testing to Detect Quantitative Trait Loci, Kansas State Conference on Applied Statistics in Agriculture, spring 1999

Order Restricted Hypothesis Testing in a Variation of the Normal Mixture Model, Institute of Mathematical Statistics Conference for New Researchers in Probability and Statistics, July 1997

**Invited Short Courses and Invited Workshop Presentations**

Instructor of introductory modules on probability and design and analysis of microarray experiments, NIH-NSF Summer Institute in Bioinformatics and Computational Biology, summer 2003–2006, 2008

Cluster Analysis for Microarray Data, 7th International Long-oligonucleotide Microarray Workshop, Tucson, Arizona, January 2007

Cluster Analysis for Microarray Data, Plant Microarray Short Course on Design and Analysis of Microarray Experimentation, Boston, August 2006

One-day short course on Introduction to Statistical Design and Analysis of Microarray Experiments, Meeting of the Eastern North American Region of the International Biometrics Society, Tampa, Florida, March 2006

Two-day short course on Introduction to Statistical Design and Analysis of Microarray Experiments, Iowa State University, July 2005

Clustering and Classification Analysis of Microarray Data, Plant Microarray Short Course on Design and Analysis of Microarray Experimentation, University of Wisconsin, Madison, June 2005

Mixed Linear Model Analysis of Two-color Microarray Data, University of Arizona International Long-oligonucleotide Microarray Workshop, May 2005

Mixed Linear Model Analysis of Two-color Microarray Data, University of Arizona Long-oligonucleotide Microarray Workshop, December 2004

**Selected Internal Invited Presentations**

Experiences of a New Chair, College of Liberal Arts and Sciences New Chair Orientation, August 2021

Chair Panel on Advancing from Associate to Full Professor, ISU ADVANCE Workshop, Iowa State University, October 2020

Panelist for Developing and Sharing Mentoring Philosophies, Office of the Provost Workshop on Reflection, Retooling, and Renewal, Iowa State University, September 2019

Introduction to Statistics, Midwest Big Data Summer School, Iowa State University, May 2019

Advising Graduate Students: Ten Tips for Major Professors, Center for Excellence in Learning and Teaching, Iowa State University, October 2018

Mentoring Graduate Students, Office of the Provost Workshop on Mentoring Graduate Students, October 2017

Predictive Phenomics in Plants (P3), Statistics Boot Camp, Iowa State University, August 2017

Predictive Phenomics in Plants (P3), Statistics Boot Camp, Iowa State University, August 2016

Graduate Commencement Speaker, Iowa State University, May 2016

**Courses Taught**

Instructor of Statistical Methods (linear models, linear mixed models, generalized linear models, generalized linear mixed models), spring 2015, 2017, 2019, 2020

Instructor and developer of an independent study course: Introduction to Sports Data Science, fall 2019

Instructor of Statistical Methods (linear models, linear mixed models, generalized linear models, generalized linear mixed models), on campus and distance sections, spring 2014, 2016, 2018

Instructor of Statistical Methods (linear models, linear mixed effects models, general linear models, nonlinear models, generalized linear models, nonparametric regression, bootstrap), on campus and distance sections, spring 2010, 2012

Instructor of Theory and Applications of Linear Models, fall 2005, 2007, 2011, 2012

Instructor of Statistical Design and Analysis of Gene Expression Experiments, spring 2011

Instructor and developer of Statistical Design and Analysis of Microarray Experiments, spring 2005, 2006, 2007, 2009

Instructor of Statistical Design and the Analysis of Experiments, spring 2001, 2002, 2004

Instructor of Statistical Methods for Research Workers, fall 2000, 2001, 2002, 2003 (on campus and distance sections in 2003)

Coordinator and instructor for Elements of Statistics, University of Nebraska-Lincoln's introductory statistics course, 1996–2000

Developer and instructor for an honors course on introductory statistics, fall 1998, 1999

Instructor of Applied Nonparametric Statistics, spring 1998

Instructor of Applied Regression and Analysis of Variance, fall 1996, 1997

Instructor for Applied Multivariate Statistical Analysis, spring 1997

Instructor for Biostatistics, University of Iowa, spring 1996

Instructor for Elementary Statistics and Inference, University of Iowa, fall 1995

Teaching Assistant for Statistics and Society, University of Iowa, 1992–1993

## Student Evaluations of Teaching

4.72 average instructor rating on a 5-point scale based on all Iowa State student responses

4.71 average instructor rating on a 5-point scale based on all Nebraska student responses

## PhD Students

Co-Major Professor for Zhiling Gu (with Lily Wang), Statistics

Co-Major Professor for Yan Wang (with Huaiqing Wu), Active learning with random forests, PhD in Statistics, summer 2023.

Major Professor for Hyeongseon Jeon, Advances in random forest tuning and improvements in false discovery rate controlling procedures via test-specific covariate adjustments, PhD in Statistics, summer 2022.

Co-Major Professor for Xingche Guo (with Somak Dutta and Yehua Li), Statistical methods for multi-environment field trials, high-dimensional functional data, and image-based high-throughput phenotyping, PhD in Statistics, summer 2021.

Major Professor for Chancellor Johnstone, Shape-restricted random forests and semiparametric prediction intervals, PhD in Statistics, fall 2020.

Co-Major Professor for Shan Yu (with Lily Wang), Model estimation, identification and inference for next-generation functional data and spatial data, PhD in Statistics, summer 2020.

Major Professor for Meiling Liu, Assessing and accounting for correlation in RNA-seq data analysis, PhD in Statistics and Bioinformatics and Computational Biology, fall 2019.

Co-Major Professor (with Yehua Li) for Haozhe Zhang, Topics in functional data analysis and machine learning predictive inference, PhD in Statistics, summer 2019.

Co-Major Professor (with Song Xi Chen and Raymond Wong) for Xiaojun Mao, Topics in matrix completion and genomic prediction, PhD in Statistics, summer 2018.

Co-Major Professor (with Ulrike Genschel) for Andrew Sage, Random forest robustness, variable importance, and tree aggregation, PhD in Statistics, spring 2018.

Major Professor for Yet Nguyen, Multiple hypothesis testing and RNA-seq differential expression analysis accounting for dependence and relevant covariates, PhD in Statistics, spring 2018.

Co-Major Professor (with Song Chen) for Liuhua Peng, Topics in statistical inference for massive data and high-dimensional data, PhD in Statistics, summer 2017.

Co-Major Professor (with Ranjan Maitra) for Andrew Lithio, Statistical methods for estimation, testing, and clustering with gene expression data, PhD in Statistics, summer 2017.

Major Professor for Dennis Lock, Statistical methods in sports with a focus on win probability and performance evaluation, PhD in Statistics, fall 2016.

Co-Major Professor for Yueran Yang (with Stephanie Madon), To deny or confess: An interrogation decision-making model, PhD in Psychology and Statistics, summer 2016.

Co-Major Professor (with Dan Nordman) for Ruo Xu, Improvements to random forest methodology, PhD in Statistics, spring 2013.

Co-Major Professor (with Peng Liu) for Megan Orr, Assessing differential expression when the distribution of effect sizes is asymmetric and evaluating concordance of differential expression across multiple gene expression experiments, PhD in Statistics, summer 2012.

Co-Major Professor (with Peng Liu and Pat Schnable) for Tieming Ji, Statistics and Bioinformatics and Computational Biology, Borrowing information across genes and experiments for improved error variance estimation in microarray data analysis and statistical inferences for gene expression heterosis, PhD in Statistics, summer 2012.

Major Professor for Heng Wang, Application of order restricted statistical inference and hidden Markov modeling to problems in biology and genomics, PhD in Statistics, summer 2012.

Major Professor for Steve Lund, Statistical methods for identifying differentially expressed genes using hierarchical models, PhD in Statistics, spring 2012.

Co-Major Professor for Nick Larson (with Jack Dekkers), Investigation and development of statistical methods for gene expression data analysis, PhD in Statistics and Bioinformatics and Computational Biology, fall 2011.

Co-Major Professor (with Jack Dekkers) for Long Qu, Improving statistical inference for gene expression profiling data by borrowing information, PhD in Statistics and Bioinformatics and Computational Biology, summer 2010.

Major Professor for Kun Liang, Hidden Markov models for simultaneous testing of multiple gene sets and adaptive and dynamic adaptive procedures for false discovery rate control and estimation, PhD in Statistics, summer 2010.

Major Professor for Tim Bancroft, Estimating the number of true null hypotheses and false discovery rate from multiple discrete non-uniform permutation p-value, PhD in Statistics, fall 2009.

Co-Major Professor (with Taps Maiti) for Cumhur Yusuf Demirkale, Classical and Bayesian Mixed Model Analysis of Microarray Data for Detecting Gene Expression and DNA Differences, PhD in Statistics, summer 2009.

Major Professor for Justin Recknor, New methods for designing and analyzing microarray experiments for the detection of differential expression, PhD in Statistics and Bioinformatics and Computational Biology, fall 2006.

Major Professor for Rhonda DeCook, New statistical methods in bioinformatics for the analysis of quantitative trait loci (QTL), microarrays, and eQTL, PhD in Statistics, summer 2006.

Co-Major Professor (with Song Xi Chen) for Dong Wang, New aspects of statistical methods for missing data problems with applications in bioinformatics and genetics, PhD in Statistics, spring 2006.


**MS Students**

Major Professor for Marie Hardt, Statistics, New Approaches to Modeling Golf Hole Scores with Hardy Distributions, fall 2022

Major Professor for Scott Thatcher, Statistics, Nonlinear Variability in Human Movement Analysis, summer 2021

Major Professor for Lin Quan, Statistics, Piecewise Linear Regression for Leaf Appearance Rate Data, spring 2021

Major Professor for Saeed Khaki, Statistics, Conformal Prediction Intervals for Neural Networks Using Cross Validation, spring 2020

Major Professor for Zihao Chen, Statistics, Exhaustive Search Algorithms to Find Alpha(0,1) Designs with High Harmonic Mean Canonical Efficiency Factors, fall 2019

Major Professor for Jason Westra, Statistics, Analyzing Metabolomics Data for Association with Genotypes using Two-component Gaussian Mixture Distributions, spring 2018

Major Professor for Ryan Morgan, Statistics, Estimating Win Probabilities for College Football Teams Ranked in the AP Poll, spring 2018

Major Professor for Yifan Wang, Statistics, Predicting Crop Yields Using Matrix Completion and Improving Tests for Sparse Covariance Matrices, summer 2017

Major Professor for Hyeongseon Jeon, Statistics, Statistical Inference for Proteomics Data with Missing Peptide Concentrations, spring 2017

Major Professor for Joshua Zimmerman, Statistics, Random Forests for Big Data Prediction and Interval Estimation, MS in Statistics, spring 2016

Major Professor for Andrew Sage, Predicting Student Retention in STEM: A Random Forest Based Approach, MS in Statistics, spring 2015

Major Professor for Samuel Benidt, SimSeq: A Nonparametric Approach to Simulation of RNA-sequence Datasets, MS in Statistics, summer 2014

Major Professor for Nathan Zimmerman, Estimation of On-Base Probability in Major League Baseball via Hierarchical Modeling of Plate Appearance Data, MS in Statistics, fall 2013

Major Professor for Andrew Lithio, Analysis of Binomial Response Data with Generalized Linear Mixed Effects Models, MS in Statistics, summer 2013

Major Professor for Yet Nguyen, Estimating False Discovery Proportion under Arbitrary Dependence with Application to the Analysis of Gene Expression Data, MS in Statistics, summer 2013

Major Professor for Shuang Song, Zero-Inflated Regression with Sequence-Error Accounting to Detect Presence/Absence Variation in Maize Genotypes, MS in Statistics, spring 2013

Co-Major Professor (with Jarad Niemi) for Casey Oliver, Modeling NFL Field Goal Attempt Outcomes in a Bayesian Framework Using Informative Missingness, MS in Statistics, spring 2012

Major Professor for Jie Li, Detecting Differential Expression in Maize RNAseq Data, MS in Statistics, summer 2011

Major Professor for Ruo Xu, Tree Ensemble Classification under Generalized Error Loss with Applications to Ordinal Response Data, MS in Statistics, spring 2010

Major Professor for Nick Larson, Exploring histogram-based estimators of differentially expressed gene proportions in microarray data analysis, MS in Statistics, summer 2008

Major Professor for Tim Bancroft, Detecting group differences with right-censored counts from serial dilution assays, MS in Statistics, spring 2007

Major Professor for Fang Qiu, Gene expression profiling during soybean seed development, MS in Statistics, summer 2005

Major Professor for Stuart Gardner, Evaluation of a pooling method for gene-specific variance estimation in the analysis of microarray data, MS in Statistics, spring 2005

Major Professor for Rong Guo, Probe nucleotide affinity modeling and mixed linear model analysis of Arabidopsis ATH1 GeneChip data for differential gene expression upon viral infection, MS in Statistics, spring 2005

Major Professor for Fei Jie, Mixed model analyses of fiber optic array experiments for Arabidopsis differential gene expression in response to viral infections, MS in Statistics, fall 2004

Major Professor for Honghua Zhao, Evaluation of linkage disequilibrium measures between markers as predictors of linkage disequilibrium between markers and QTL, MS in Statistics, summer 2004

Major Professor for Cumhur Yusuf Demirkale, A comparison of nonparametric methods for testing for group differences and identifying multiple clumping with multivariate data, MS in Statistics, summer 2004

Major Professor for Hongwu Jia, A comparison of statistical methods for analyzing cDNA microarray data from Maize B45 opaque2 mutant, MS in Statistics, fall 2003

Major Professor for Rhonda DeCook, Affymetrix GeneChip Data Analysis in a Two-Way ANOVA without Replication, MS in Statistics, fall 2002

Major Professor for Jianying Gu, Investigating Primate Tissue-Specific Expression Pattern through Affymetrix Data Analysis, MS in Statistics, fall 2002

Major Professor for Wei Huang, Statistical analysis of differentially expressed genes in cDNA microarray experiments, MS in Statistics, spring 2002

Major Professor for Wei Liu, Mixed model analyses of cDNA macroarray data for differential gene expression in porcine fetal and postnatal skeletal muscles, MS in Statistics, spring 2002

Major Professor for Chunfa Jie, Some statistical methods for microarray data analysis, MS in Statistics, summer 2001

Major Professor for Deqing Pei, Statistical methods for analyzing proportion data collected from a maize callus induction experiment, MS in Statistics, summer 2001

Major Professor for Hui-Rong Qian, ANOVA analysis of cDNA microarray data to identify differentially expressed genes, MS in Statistics, spring 2001

## Other Advising

Undergraduate Sports Analytics Club Faculty Advisor, 2015–2021

Internship mentor for Johnny Pippins, a member of an underrepresented group who completed an MS degree in statistics while incarcerated at Anamosa State Penitentiary, 2019–2020

Advisor for Freshman Honors Project by Cameron Stocker, Association between top scorer performance metrics and winning percentage in the NBA, spring 2017

Preparing Future Faculty Advisor for Andee Kaplan, 2016–2017

Preparing Future Faculty Advisor for Ignacio Alvarez, 2015–2016

Preparing Future Faculty Advisor for Yueran Yang, 2014–2015

Co-Mentor (with Peng Liu) for Alliance students Jared Mills and Katrina Williams, summer 2010

Mentor for NSF-NIH Computational and Systems Biology Summer Institute student Eric Tiede, summer 2008

Mentor for NSF-NIH Summer Institute in Bioinformatics and Computational Biology student Kelly Robbins, summer 2004

Mentor for NSF-VIGRE undergraduate Yuan Ji, summer 2003

McNair Summer Research Program Mentor for statistics undergraduate Jeff Garza, summer 1997

## Other Student Committees (member, non-major professor)

Served on 131 completed PhD committees

Served on 56 completed MS committees

Currently serve on 8 PhD committees

Currently serve on 2 MS committees

## Departmental Service

2018–2019:  Data Science Faculty Search Committee (chair), Distinguished Lectures Committee (chair), PhD and MS Exam Committee, Social Committee

2017–2018:  Faculty Search Committee, Department Enhancement Project Committee, Distinguished Lectures Committee, Governance Document Review and Update Committee, Social Committee

2016–2017: Advisory Committee on Promotion and Tenure (chair), Advisory Committee to the Department Chair, Distinguished Lectures Committee, Governance Document Review and Update Committee

2015–2016: Advisory Committee on Promotion and Tenure, Honors and Awards Committee (chair), MS and PhD Exam Committee

2014–2015: Advisory Committee on Promotion and Tenure, Honors and Awards Committee

2013–2014: Advisory Committee to the Department Chair, Honors and Awards Committee, MS and PhD Exam Committee, Faculty Search Committees (chair of one, member of two others), Department Chair Search Committee

2012–2013: Department Chair Search Committee, Memorial Lectures Committee (chair)

2011–2012: Advisory Committee on Promotion and Tenure (chair), Memorial Lectures Committee (chair), Social Committee (chair)

2010–2011: Advisory Committee on Promotion and Tenure, Advisory Committee to the Department Chair, MS and PhD Exam Committee

2009–2010: Advisory Committee on Promotion and Tenure, Advisory Committee to the Department Chair

2008–2009: Advisory Committee to the Department Chair, MS and PhD Exam Committee

2007–2008: Advisory Committee to the Department Chair, Graduate Committee Chair, Journal Rating Committee

2006–2007: MS Exam Committee, 150th ISU Anniversary/75th Statistical Laboratory Anniversary Committee, Snedecor Hall Renovation Committee (summer 2006)

2005–2006: Faculty Search Committee (chair), Seminar Chair (spring), External Review Committee

2004–2005: Social Committee (chair), Strategic Planning Committee

2003–2004: PhD Preliminary Examination Committee, Social Committee (chair)

2002–2003: PhD Preliminary Examination Committee, Social Committee (chair), Faculty Search Committee

2001–2002: Social Committee (chair), Department Chair Search Committee

2000–2001: MS Exam Committee, Social Committee

**Interdepartmental Service**

Bioinformatics and Computational Biology Admissions Committee Chair, 2017–2018

Bioinformatics and Computational Biology Admissions Committee, 2015–2017

Predictive Phenomics in Plants (P3) Instructor for a three-hour introduction to statistical reasoning for plant phenomics, August 2016, 2017

Predictive Phenomics in Plants (P3) Admissions Committee, 2016–2018

J. L. Lush Endowed Chair in Animal Breeding and Genetics Search Committee, 2006, 2016

**College Service**

College of Liberal Arts and Senior Manager Budget and Finance Search Committee, 2022

College of Liberal Arts and Sciences Budget Advisory Council, 2020–

Chair of the Department of Mathematics Chair Search Committee, 2020–2022

College of Agriculture and Life Sciences Fiscal Officer Search Committee, 2020

College of Agriculture and Life Sciences Master's Degree Task Force, 2019–2020

College of Agriculture and Life Sciences Student Innovation Center Space Utilization Task Force, fall 2019

College of Agriculture and Life Sciences Dean Search Committee, 2018

## University Service

At Large Representative to the Department Chairs Cabinet, 2020–

Winter Session Executive Planning Committee, fall 2020, 2021

Committee on Lectures, 2013–2021

Member of the Faculty Review Board Pool, 2017–

Vice President for Research Grand Challenges Faculty Advisory Committee, 2017

## Editorial Activities

Associate editor for *The American Statistician*, 2014–2020

Associate editor for the *Journal of Agricultural, Biological, and Environmental Statistics*, 2003–2015

Associate editor for the *Journal of the American Statistical Association*, 2009–2012

Associate editor for *Biometrics*, 2005–2010

Statistical reviewer for *The Plant Cell*, 2008–2010

## Journal Refereeing

*The American Statistician; Animal Genetics; Animals; Annals of the Institute of Mathematical Statistics; Annals of Statistics; Australian Journal of Statistics; Bioinformatics; BMC Bioinformatics; BMC Genetics; BMC Genomics; Biometrical Journal; Biometrics; Briefings in Bioinformatics; Computational Statistics and Data Analysis; Conservation Biology; Crop Science; Electronic Journal of Statistics; Genetical Research; Genetics; Geosphere; International Journal of Plant Genomics; Journal of Agricultural, Biological, and Environmental Statistics; Journal of the American Statistical Association; Journal of Computational and Graphical Statistics; Journal of Quantitative Analysis of Sports; Journal of the Royal Statistical Society – Series B; Journal of Statistical Planning and Inference; Journal of Statistics Education; Knowledge and Information Systems; Mathematical Biosciences; Metrika; Nature Communications; Physiological Genomics; The Plant Cell; Plant Physiology; PLOS Computational Biology; PLOS ONE; Proceedings of the National Academy of Science; Science; Statistica Sinica; Statistical Applications in Genetics and Molecular Biology; Statistics and Its Interface; Statistics and Probability Letters; Technometrics; Test*

## Proposal Review

NSF 2001–2003, 2006, 2012, 2023

NSF Division of Mathematical Sciences, Reverse Site Visit Team Member for Evaluation of Mathematical Sciences Research Institutes, September 2019

NIH Biostatistical Methods and Research Design Review Panel, June 2017, February 2019

NIH Special Emphasis Review Panelist, Predoctoral Training in Biomedical Big Data Science, October 2016

NIH Special Emphasis Review Panelist, BRAIN Initiative Review: Transformative Approaches for Cell-Type Classification in the Brain, summer 2014

NIH Ad Hoc Reviewer, Genomics, Computational Biology and Technology Study Section, fall 2009

NSF-NIH Panelist for the Joint DMS-NIGMS Initiative to Support Research in the Area of Mathematical Biology, 2002, 2003, 2007

NIH Special Emphasis Review Panelist, Predoctoral Training in Biostatistics, March 2007

NIH NIGMS Centers of Excellence in Complex Biomedical Systems Research Program, proposal review, spring 2004.

Natural Sciences and Engineering Research Council of Canada, proposal review, spring 2003

US Civilian Research and Development Foundation, proposal review, July 2001

USDA, proposal review, spring 1999

## Program Reviews

Biostatistics and Computational Biology Branch of the National Institute of Environmental Health Sciences, November 2016

## Other Professional Activities

Chair Elect, Chair, Past Chair American Statistical Association Caucus of Academic Representatives, 2022–2025

American Statistical Association Working Group on Engagement with the National Science Foundation Division of Mathematical Sciences, 2022–2023

*The American Statistician* Editor Search Committee Member, 2023

Secretary, American Association for the Advancement of Science Section U (Statistics), 2020–2023

American Statistical Association Strategic Planning Working Group, focusing on membership retention, membership recruitment, and public awareness, 2021–2022

Lead organizer of the Dependable Data-Driven Discovery Institute Conference on Data Science, October 2021

Chair Elect, Chair, Past Chair, American Statistical Association Section on Statistics in Genomics and Genetics, 2018–2020

Invited Participant in National Science Foundation Workshop "Statistics at a Crossroads: Challenges and Opportunities in the Data Science Era", October 2018

Lead organizer of the Conference on Predictive Inference and Its Applications, Iowa State University, May 2018

External Thesis Evaluator, Department of Mathematics and Statistics, University of Calgary, January 2018

Member of the Organizing Committee for the 2017 Graybill Conference on Statistical Genomics, Colorado State University, 2016–2017

Co-leader of the Statistical and Applied Mathematical Sciences Institute Working Group on Analysis of High-Dimensional Discrete Data, 2014

Lead organizer of the Conference on New Statistical Methods for Next-Generation Sequencing Data Analysis, Iowa State University, May 2012

Member of the International Program Committee for the 2010 International Biometrics Conference in Florianopolis, Brazil, 2008–2010

Lead organizer of the Fall Conference on Statistics in Biology, Iowa State University, October 2008

Organizer of an invited session on methodological advances in testing and estimation of gene expression differences for the Joint Statistical Meetings in Denver, August 2008

President of the Iowa Chapter of the American Statistical Association, 2007–2008

Vice President of the Iowa Chapter of the American Statistical Association, 2005–2007

Advisory committee member for the NSF-sponsored Maize Oligonucleotide Array Project led by Vicki Chandler at the University of Arizona, 2003–2006

Leader of Iowa State University Department of Statistics VIGRE Bioinformatics Working Group, 2002–2003, 2005–2006

Faculty member in the Baker Center for Bioinformatics and Biological Statistics at Iowa State University, 2000–

Faculty member in the Bioinformatics and Computational Biology program at Iowa State University, 2000–

Faculty member in the Center for Integrated Animal Genomics at Iowa State University, 2002–2013

Member of the Center for Integrated Animal Genomics Advisory Board, 2002–2005

Organizer of a microarray working group for the Baker Center for Bioinformatics and Biological Statistics, 2002–2003

Organizer of a topic contributed session on microarray analyses at the Joint Statistical Meetings in New York, August 2002

Participant in a workshop on the analysis of gene expression data at the National Institute of Statistical Sciences, July 2000

Vice President of the Nebraska Chapter of the American Statistical Association, 1999-2000

American Statistical Association National Project Competition Judge, May 1997, 1998, 1999

Participant in North Carolina State Statistical Genetics Institute, June 1997

## Awards and Honors

50th Hogg and Craig Lecturer, University of Iowa, 2023

College of Liberal Arts and Sciences Award for Early Achievement in Departmental Leadership, 2021

Iowa State University Margaret Ellen White Graduate Faculty Award for excellent guidance and encouragement of graduate students, 2017

Iowa State University Plant Sciences Institute Scholar, 2015–2022

College of Liberal Arts and Sciences Outstanding Career Achievement in Research Award, 2015

Best Associate Editor Award for the *Journal of Agricultural, Biological, and Environmental Statistics*, 2013

Iowa State University Award for Mid-Career Achievement in Research, 2012

Fellow of the American Statistical Association, 2008

College of Liberal Arts and Sciences Mid-Career Award for Excellence in Research, 2007

Plant Sciences Institute Outstanding Collaborator Award, 2006

University of Nebraska College of Arts and Sciences Distinguished Teaching Award, 1999

Gallup Professorship recipient, 1998–1999

University of Nebraska Faculty Summer Research Fellowship recipient, 1998

Allen T. Craig Award presented for outstanding service as a teaching assistant, 1996

Henry L. Rietz Award presented to the outstanding newly qualified PhD student, 1994

University of Iowa Fellowship recipient, 1991–1995

NCAA Postgraduate Scholarship recipient, 1991

Wartburg College Senior Honor Award presented to the most outstanding senior student, 1991

Wartburg College Senior Mathematics Award presented to the top math major, 1991

GTE Academic All-America Player of the Year for NCAA Division III Basketball, 1991

GTE First Team Academic All-America, NCAA Division III Basketball, 1990 and 1991

Wartburg College Regents Scholar, 1987–1991