

Dan Nettleton

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Work Address

2115 Snedecor Hall
Department of Statistics
Iowa State University
Ames, Iowa 50011-1090

Web Address

<https://dnett.github.io>

Telephone

515-294-7754

Education

Doctor of Philosophy
Statistics

University of Iowa
Iowa City, Iowa
July, 1996

Master of Science
Statistics

University of Iowa
Iowa City, Iowa
May, 1993

Bachelor of Arts
Mathematics (major)
Computer Science (minor)

Wartburg College
Waverly, Iowa
May, 1991

Dissertation

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

Work Experience

Director, Laurence H. Baker Center for Bioinformatics and Biological Statistics, 2016 –
Distinguished Professor, Department of Statistics, Iowa State University, 2015 –
Laurence H. Baker Endowed Chair in Biological Statistics, Department of Statistics, Iowa State University, 2007 –
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

Professional Interests

Statistical Methods for the Analysis of Data from Biological Experiments, Statistical Design and Analysis of Transcriptomic Profiling Experiments, Multiple Testing, Order Restricted Inference, Statistical Consulting, Sports Analytics, Statistical Learning

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

- Qiu, Y., Chen, S. X., Nettleton, D. (2017). Detecting rare and faint signals via thresholding maximum likelihood estimators. *Annals of Statistics*. Accepted.
- Xu, Y., Li, Y., and Nettleton, D. (2017). Nested hierarchical functional data modeling and inference for the analysis of functional plant phenotypes. *Journal of the American Statistical Association*. Accepted.
- Lin, H.-Y., Liu, Q., Li, X., Yang, J., Huang, Y., Scanlon, M. J., Nettleton, D., Schnable, P. (2017). eRD-GWAS reveals substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation. *Genome Biology*. Accepted.
- Surana, P., Xu, R., Fuerst, G., Chapman, A. V. E., Nettleton, D., Wise, R. P. (2017). Inter-chromosomal transfer of immune regulation during infection of barley with the powdery mildew pathogen. *G3: Genes, Genomes, Genetics*. Accepted. DOI: 10.1534/g3.117.300125
- Kusmec, A., Srinivasan, S., Nettleton, D., Schnable, P. S. (2017). Distinct genetic architectures for phenotype means and plasticities in *Zea mays*. *Nature Plants*. **3** 715–723. DOI: 10.1038/s41477-017-0007-7
- Cullen, J. N., *Lithio, A., Seetharam, A. S., Zheng, Y., Li, G., Nettleton, D., O'Connor, A. M. (2017). Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. *Veterinary Microbiology*. Accepted. DOI: 10.1016/j.vetmic.2017.07.003
- Hey, S., Baldauf, J., Opitz, N., *Lithio, A., Pasha, A., Provart, N., Nettleton, D., Hochholdinger, F. (2017). Complexity and specificity of the maize (*Zea mays* L.) root hair transcriptome. *Journal of Experimental Botany*. **68** 2175–2185.
- Guan, X., Okazaki, Y., *Lithio, A., Li, L., Zhao, X., Jin, H., Nettleton, D., Saito, K., Nikolau, B. (2017). The 3-hydroxyacyl-ACP dehydratase component of the plant mitochondrial fatty acid synthase system. *Plant Physiology*. **173** 2010–2028. DOI: 10.1104/pp.16.01732
- Marcon, C., Paschold, A., Malik, W. A., *Lithio, A., Baldauf, J., Altrogge, L., Opitz, N., Lanz, C., Schoof, H., Nettleton, D., Piepho, H.-P., Hochholdinger, F. (2016). Stability of single parent gene expression complementation in maize hybrids upon water deficit stress. *Plant Physiology*. DOI:10.1104/pp.16.01045
- Tai, H., Opitz, N., *Lithio, A., Lu, X., Nettleton, D., Hochholdinger, F. (2016). Nonsyntenic genes drive RTCS-dependent regulation of the maize (*Zea mays* L.) embryo transcriptome during seminal root primordia formation. *Journal of Experimental Botany*. erw422. DOI: 10.1093/jxb/erw422
- Swanson, R., *Xu, R., Nettleton, D., Glatz, C. (2016). Accounting for host cell protein behavior in anion–exchange chromatography. *Biotechnology Progress*. **32** 1453–1463. DOI 10.1002/btpr.2342
- Boddicker, R. L., Koltes, J. E., Fritz-Waters, E. R., Koesterke, L., Weeks, N., Yin, T., Mani, V., Nettleton, D., Reecy, J. M., Baumgard, L. H., Spencer, J. D., Gabler, N. K., Ross, J. W. (2016). Genome-wide methylation profile following prenatal and postnatal dietary omega-3 fatty acid supplementation in pigs. *Animal Genetics*. **47**(6) 658–671. DOI:10.1111/age.12468
- Zuo, T., Zhang, J., *Lithio, A., Dash, S., Weber, D. F., Wise, R. P., Nettleton, D., Peterson, T. (2016). Genes and small RNA transcripts exhibit dosage-dependent expression pattern in

- maize copy-number alterations. *Genetics*. **203** 1133–1147.
DOI:10.1534/genetics.116.188235
- Jones, D. C., Zheng, W., Huang, S., Du, C., Zhao, X., Yennamalli, R. M., Sen, T. Z., Nettleton, D., Wurtele, E. S., Li, L. (2016). A clade-specific Arabidopsis gene connects primary metabolism and senescence. *Frontiers in Plant Science*. **7** 983. 18 pages. DOI: 10.3389/fpls.2016.00983
- *Xu, R., Nettleton, D., Nordman, D. J. (2016). Case-specific random forests. *Journal of Computational and Graphical Statistics*. **25** 49–65. DOI: 10.1080/10618600.2014.983641
- Yu, P., Baldauf, J., *Lithio, A., Marcon, C., Nettleton, D., Li, C., Hochholdinger, F. (2016). Root type specific reprogramming of maize pericycle transcriptomes by local high nitrate results in disparate lateral root branching patterns. *Plant Physiology*. **170** 1783–98. DOI: 10.1104/pp.15.01885
- Liu, H., Nguyen, Y. T., Nettleton, D., Dekkers, J. C. M., Tuggle, C. K. (2016). Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. *BMC Genomics*. **17** 73. 18 pages. DOI: 10.1186/s12864-016-2395-x.
- Sadler, L. J., Johnson, A. K., Nettleton, D., Lewis, C. R. G., Young, J. M., Lonergan, S. M., Dekkers, J. C. M. (2016). The effect of selection for residual feed intake on scale activity and exit score in Yorkshire gilts. *Animal Production Science*. **56**(11) 1875–1881.
<http://dx.doi.org/10.1071/AN14849>.
- Tai, H., Lu, X., Opitz, N., Marcon, C., Paschold, A., *Lithio, A., Nettleton, D., Hochholdinger, F. (2015). Transcriptomic and anatomic complexity of primary, seminal and crown roots highlight root type-specific functional diversity in maize. *Journal of Experimental Botany*. **67** (4) 1123–1135. DOI:10.1093/jxb/erv513
- Li, L., Zheng, W., Zhu, Y., Ye, H., Tang, B., Arendsee, Z., Jones, D., Li, R., Ortiz, D., Zhao, X., *Du, C., Nettleton, D., Scott, P., Salas-Fernandez, M., Yin, Y., Wurtele, E. S. (2015). The QQS orphan gene regulates carbon and nitrogen partitioning across species via NF-Y interactions. *Proceedings of the National Academy of Sciences of the USA*. **112** 14734–14739.
- *Lithio, A., Nettleton, D. (2015). Hierarchical modeling and differential expression analysis for RNA-seq experiments with inbred and hybrid genotypes. *Journal of Agricultural, Biological, and Environmental Statistics*. **20** 598–613.
- *Nguyen, Y., Nettleton, D., Liu, H., Tuggle, C. K. (2015). Detecting differentially expressed genes with RNA-seq data using backward selection to account for the effects of relevant covariates. *Journal of Agricultural, Biological, and Environmental Statistics*. **20** 577–597.
- Niemi, J., Mittman, E., Landau, W., Nettleton, D. (2015). Empirical Bayes analysis of RNA-seq data for detection of gene expression heterosis. *Journal of Agricultural, Biological, and Environmental Statistics*. **20** 614–628. DOI: 10.1007/s13253-015-0230-5
- Opitz, N., Marcon, C., Paschold, A., Malik, W. A., *Lithio, A., Brandt, R., Piepho, H.-P., Nettleton, D., Hochholdinger, F. (2015). Exceptional tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. *Journal of Experimental Botany*. **67** (4) 1095–1107. DOI:10.1093/jxb/erv453
- Yang, J., Jiang, H., Yeh, C.-T., Yu, J., Jeddelloh, J., Nettleton, D., Schnable, P. (2015). Extreme Phenotype-Genome-Wide Association Study (XP-GWAS): a method for identifying trait-

- associated variants by sequencing pools of individuals selected from a diversity panel. *The Plant Journal*. **84** 587–596.
- Jiang, F., An, C., Bao, Y., Zhao, X., Jernigan, R., *Lithio, A., Nettleton, D., Li, L., Wurtele, E., Nolan, L., Lu, C., Li, G. (2015). ArcA Controls Metabolism, Chemotaxis and Motility Contributing to the Pathogenicity of Avian Pathogenic *E. coli*. *Infection and Immunity*. **83** 3545–3554.
- Whigham, E., Qi, S., Mistry, D., Surana, P., *Xu, R., Fuerst, G., Pliego, C., Bindschedler, L. V., Spanu, P. D., Dickerson, J. A., Innes, R. W., Nettleton, D., Bogdanove, A. J., Wise, R. P. (2015). Broadly conserved fungal effector BEC1019 suppresses host cell death and enhances pathogen virulence in powdery mildew of barley. *Molecular Plant-Microbe Interactions*. **28** 968–983.
- Xu, W., Meng, Y., Surana, P., Fuerst, G., Nettleton, D., Wise, R. P. (2015). The knottin-like Blufensin family regulates genes involved in nuclear import and the secretory pathway in barley-powdery mildew interactions. *Frontiers in Plant Science*. **6** 409. DOI: 10.3389/fpls.2015.00409
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- Li, L., Hill-Skinner, S., Liu, S., Beuchle, D., Tang, H. M., Yeh, C.-T., Nettleton, D., Schnable, P. S. (2015). The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase (FPGS). *The Plant Journal*. **81** 493–504.
- Li, L., Hur, M., Lee, J.-Y., Zhou, W., Song, Z., Ransom, N., *Demirkale, C. Y., Nettleton, D., Westgate, M., Arendsee, Z., Iyer, V., Shanks, J., Nikolau, B., Wurtele, E. S. (2015). A systems biology approach toward understanding seed composition in soybean. *BMC Genomics*. **16** S9, pages 1–19.
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- Wise, R., Surana, P., Fuerst, G., *Xu, R., Mistry, D., Dickerson, J., Nettleton, D. (2014). Flor revisited (again): eQTL and mutational analysis of NB-LRR mediated immunity to powdery mildew in barley. *Journal of Integrative Agriculture*. **13** 237–243. DOI: 10.1016/S2095-3119(13)60651-6.
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- *Orr, M., Liu, P., Nettleton, D. (2014). An improved method for computing q-values when the distribution of effect sizes is asymmetric. *Bioinformatics*. **30** 3044–3053.
- Yu, X., *Lund, S. P., Greenwald, J. W., Records, A. H., Scott, R., Nettleton, D., Lindow, S. E., Gross, D. C., Beattie, G. A. (2014). Transcriptional analysis of the global regulatory

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- Gu, T., Zhu, M.-J., Schroyen, M., Qu, L., Nettleton, D., Kuhar, D., Lunney, J. K., Ross, J. W., Zhao, S. H., Tuggle, C. K. (2014). Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. *BMC Genomics*. **15** 156. DOI:10.1186/1471-2164-15-156
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- *Lock, D., Nettleton, D. (2014). Using random forests to estimate win probability before each play of an NFL game. *Journal of Quantitative Analysis in Sports*. **10** 192–205.
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- *Xu, R., Nettleton, D., Nordman, D. J. (2014). Predictor augmentation in random forests. *Statistics and Its Interface*. **7** 177–186.
- Tang, H. M., Liu, S., Hill-Skinner, S., Wu, W., Reed, D., Yeh, C.-T., Nettleton, D., Schnable, P. S. (2014). The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. *The Plant Journal*. **77** 380–392.
- *Bancroft, T., *Du, C., Nettleton, D. (2013). Estimation of false discovery rate using sequential permutation p-values. *Biometrics*. **69** 1–7.
- Froelich, A., Nettleton, D. (2013). Does my baby really look like me? Using tests for resemblance between parent and child to teach topics in categorical data analysis. *Journal of Statistics Education*. **21** 19 pages.
- Plego, C., Nowara, D., Bonciani, G., Gheorghe, D. M., *Xu, R., Surana, P., Whigham, E., Nettleton, D., Bogdanove, A. J., Wise, R. P., Schweizer, P., Bindschedler, L.V., Spanu, P. D. (2013). Host-induced gene silencing in barley powdery mildew reveals a class of RNase-like effectors. *Molecular Plant-Microbe Interactions*. **26** 633–642.
- Yu, X., *Lund, S. P., Scott, R. A., Greenwald, J. W., Records, A. H., Nettleton, D., Lindow, S. E., Gross, D. C., Beattie, G. A. (2013). Transcriptional responses of *Pseudomonas syringae*

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- *Orr, M., Liu, P., Nettleton, D. (2012). Estimating the number of genes that are differentially expressed in both of two independent experiments. *Journal of Agricultural, Biological, and Environmental Statistics*. **17** 583–600.
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- 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 *Listeria 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., and 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., and 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.

Invited Presentations

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

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

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

Graduate Commencement Speaker, Iowa State University, May 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 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

Case-Specific Random Forests, Department of Biostatistics, 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

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

Identifying Genes that are Differentially Expressed in Both of Two Independent Experiments, *JABES* 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

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

Accounting for Nuisance Covariates when Using RNA-Seq Data to Identify Differentially Expressed Genes, ENAR, Baltimore, March 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

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

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

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, ENAR, New Orleans, March 2010.

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

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, 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

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

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

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, WNAR Meeting, University of California, Davis, June 2008

A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Directed Acyclic Graph, IMS-China International Conference on Statistics and Probability, Hangzhou, China, June 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 Seminar, University of Missouri-Columbia, October 2007

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

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

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

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

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

One-Day Short Course on Introduction to Statistical Design and Analysis of Microarray Experiments, ENAR Meeting, Tampa, Florida, March 2006

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

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 Kendzierski, *JASA Applications and Case Studies Invited Paper Award Winner*, Joint Statistical Meetings, Minneapolis, August 2005

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

Using observed p -values to estimate the number of true null hypotheses when conducting many tests, University of Alabama Birmingham, May 2005

Mixed linear model analysis of two-color microarray data, University of Arizona International Long-Oligonucleotide Microarray Workshop, May 2005

Using observed p -values to estimate the number of true null hypotheses when conducting many tests, Arizona State University, May 2005

Statistical design and analysis of microarray experiments, International Symposium on Heterosis in Plants, University of Hohenheim, Stuttgart, Germany, January 2005

Mixed linear model analysis of two-color microarray data, University of Arizona Long-Oligonucleotide Microarray Workshop, December 2004

Using observed p -values to estimate the number of true null hypotheses when conducting many tests, Cornell University, December 2004

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

Using statistical design and analysis to detect differentially expressed genes in microarray experiments, University of Colorado Health Science Center, March 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

Methods for controlling false positive rates when identifying differentially expressed genes, The Jackson Laboratory, Statistics Colloquium, May 2002

Statistical methods for identifying differentially expressed genes with microarray data, Joint Iowa/Iowa State Bioinformatics Workshop, April 2002

A comparison of methods for managing type I errors when testing for changes in gene expression, University of Georgia, Department of Statistics Colloquium, February 2002

A comparison of methods for managing type I errors when testing for changes in gene expression, Purdue University, Bioinformatics Seminar, October 2001

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

Mapping quantitative trait loci through principal components regression, Iowa State University, Department of Statistics Colloquium, January 2000

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

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

Testing for association between categorical variables with multiple-response data, Cornell University, Statistics Colloquium, February 1999

Developments in the use of permutation testing to detect quantitative trait loci, 6th Purdue International Symposium on Statistics, June 1998

Thoughts on permutation testing in the mapping of quantitative trait loci, Purdue University, Biostatistics/Statistical Genetics Seminar, February 1998

Interval mapping of quantitative trait loci through order restricted inference, Kansas State University, Department of Statistics Colloquium, October 1997

Interval mapping of quantitative trait loci through order restricted inference, University of Missouri-Rolla, Mathematics and Statistics Colloquium, spring 1996

Interval mapping of quantitative trait loci through order restricted inference, Purdue University, Department of Statistics Colloquium, spring 1996

Interval mapping of quantitative trait loci through order restricted inference, Harvard University, Department of Statistics Colloquium, spring 1996

Interval mapping of quantitative trait loci through order restricted inference, University of Nebraska, Department of Mathematics and Statistics Colloquium, spring 1996

Contributed Presentations

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

Using Quasi-Likelihood Analysis of RNA-Seq Data to Identify Differentially Expressed Genes, North Central Coordinating Committee 170, Puerto Rico, 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.

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

Identification of Differentially Expressed Gene Categories in Microarray Studies Using Nonparametric Multivariate Analysis, 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, NCCC-170 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, 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, IMS Conference for New Researchers in Probability and Statistics, July 1997

Courses Taught

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

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

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 and developer of a one-day short course on Statistical Design and Analysis of Microarray Experiments, ENAR, Tampa, spring 2006

Instructor and developer of a two-day short course on Statistical Design and Analysis of Microarray Experiments, Iowa State University, summer 2005

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)

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

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

4.71 instructor rating on a 5-point scale based on 628 Iowa State student responses

4.71 instructor rating on a 5-point scale based on 235 Nebraska student responses

PhD Students

Major Professor for Hyeongseon Jeon, Statistics

Major Professor for Yet Nguyen, Statistics

Major Professor for Meiling Liu, Co-Major in Statistics and Bioinformatics and Computational Biology

Co-Major Professor (with Ulrike Genschel) for Andrew Sage, Statistics

Co-Major Professor (with Yehua Li) for Haozhe Zhang, Statistics

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. Currently Research Scientist at Eli Lilly and Company.

Major Professor for Dennis Lock, Statistical methods in sports with a focus on win probability and performance evaluation, PhD in Statistics, fall 2016. Currently Director of Analytics for the Miami Dolphins of the National Football League.

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. Currently Assistant Professor in Psychology at the University of Nevada-Reno.

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

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. Currently Assistant Professor in the Department of Statistics at North Dakota State University.

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. Currently Assistant Professor in the Department of Statistics at the University of Missouri-Columbia.

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. Currently Assistant Professor in the Department of Statistics and Probability at Michigan State University.

Major Professor for Steve Lund, Statistical methods for identifying differentially expressed genes using hierarchical models, PhD in Statistics, spring 2012. Currently Mathematical Statistician at the National Institute of Standards and Technology.

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. Currently Assistant Professor of Biostatistics, Mayo Clinic, Division of Biomedical Statistics and Informatics.

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. Currently working in China.

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. Currently Assistant Professor in the Department of Statistics and Actuarial Science at the University of Waterloo.

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. Currently Senior Analyst, Health Economics and Outcomes Research, OptumInsight.

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. Currently at SRA International, Inc.

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. Currently Statistician at W. L. Gore and Associates, Inc.

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. Currently Lecturer and Statistical Consultant at the University of Iowa.

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. Formerly Tenured Associate Professor at the University of Nebraska, Lincoln; Statistics and Mathematics Leader at Dow AgroSciences. Currently Mathematical Statistician at Food and Drug Administration National Center for Toxicological Research.

MS Students

Major Professor for Ryan Morgan, Statistics.

Major Professor for Jason Westra, Statistics.

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 –

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 109 completed PhD committees
Served on 72 completed MS committees
Currently serve on more than 30 MS and PhD committees

Departmental Service

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, 2015 – 2016
 J. L. Lush Endowed Chair in Animal Breeding and Genetics Search Committee, 2006, 2016

University Service

Member of the Faculty Review Board Pool, 2017 –
 Committee on Lectures, 2013 –
 Vice President for Research Grand Challenges Faculty Advisory Committee, 2017
 Speaker, Office of the Provost Workshop on Mentoring Graduate Students, October 2017

Editorial Activities

Associate editor for *The American Statistician*, 2014 –
 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; 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; Mathematical Biosciences; Metrika; 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

NIH Biostatistical Methods and Research Design Review Panel, June 2017
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
NSF Review Panelist, Division of Mathematical Sciences Statistics Program, January 2012
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, fall 2007
NIH Special Emphasis Review Panelist, Predoctoral Training in Biostatistics, March 2007
NSF proposal review, spring 2006
NIH NIGMS Centers of Excellence in Complex Biomedical Systems Research Program, proposal review, spring 2004.
NSF-NIH Panelist for the Joint DMS-NIGMS Initiative to Support Research in the Area of Mathematical Biology, fall 2003
NSF Division of Mathematical Sciences Statistics Program proposal review, spring 2003
Natural Sciences and Engineering Research Council of Canada, proposal review, spring 2003
NSF-NIH Panelist for the Joint DMS-NIGMS Initiative to Support Research in the Area of Mathematical Biology, fall 2002
NSF, proposal review, spring 2002
NSF, proposal review, fall 2001
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, American Statistical Association Section on Statistics in Genomics and Genetics, 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

Co-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

Co-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

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 –

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