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Education

Doctor of Philosophy	University of Iowa
Statistics	Iowa City, Iowa
	July, 1996
Master of Science	University of Iowa
Theoretical Statistics	Iowa City, Iowa
and Probability	May, 1993
Bachelor of Arts	Wartburg College
Mathematics with minor	Waverly, Iowa
in Computer Science	May, 1991

Dissertation

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

Work Experience

Laurence H. Baker Endowed Chair in Biological Statistics, Department of Statistics, Iowa State University, 2007 to present

Professor, Department of Statistics, Iowa State University, 2007 to present

Associate Professor, Department of Statistics, Iowa State University, 2002 to 2007

Assistant Professor, Department of Statistics, Iowa State University, 2000 to 2002

Assistant Professor, Department of Mathematics and Statistics, University of Nebraska-Lincoln, 1996 to 2000

Professional Interests

Statistical Methods for the Analysis of Data from Biological Experiments, Statistical Design and Analysis of Microarray and Next Generation Sequencing Experiments, Multiple Testing, Order Restricted Inference, Statistical Consulting

Refereed Journal Articles

Liang, K. and Nettleton, D. (2011). Adaptive and dynamic adaptive procedures for false discovery rate control and estimation. *Journal of the Royal Statistical Society, Series B.* Accepted.

Liebman, M., Graef, R., Nettleton, D., Cambardella, C. (2011). Use of legume green manures as nitrogen sources for corn production. *Renewable Agriculture and Food Systems*. Accepted.

Schneider, K.T., van de Mortel, M., Bancroft, T.J., Braun, E., Nettleton, D., Nelson, R.T., Frederick, R.D., Baum, T.J., Graham, M.A., Whitham, S.A. (2011). Biphasic gene expression changes elicited by Phakopsora pachyrhizi in soybean correlates with fungal penetration and haustoria formation. *Plant Physiology*. Accepted.

Liu, Z., Ramer-Tait, A., Henderson, A., Demirkale, C.Y., Nettleton, D., Wang, C., Hostetter, J., Jergens, A., Wannemuehler, M. (2011). Helicobacter bilis colonization enhances susceptibility to typhlocolitis following an inflammatory trigger. *Digestive Diseases and Sciences*. Accepted.

Uthe, J.J., Qu, L., Couture, O., Bearson, S.M.D., O'Connor, A.M., McKean, J.D., Rodriguez Torres, Y., Dekkers, J.C.M., Nettleton, D., Tuggle, C.K. (2011). Use of bioinformatic SNP predictions in differentially expressed genes to find SNPs associated with Salmonella colonization in swine. *Journal of Animal Breeding and Genetics*. Accepted.

Melnykov, V., Maitra, R., Nettleton, D. (2011). Accounting for spot matching uncertainty in the analysis of proteomics data from two-dimensional gel electrophoresis. *Sankhya Series B*. Accepted.

Moscou, M.J., Lauter, N., Caldo, R.A., Nettleton, D., Wise, R.P. (2011). Quantitative and temporal definition of the Mla transcriptional regulon during barley-powdery mildew interactions. *Molecular Plant-Microbe Interactions*. Accepted.

Kandoth, P.K., Ithal, N., Recknor, J., Maier, T., Nettleton, D., Baum, T.J., Mitchum, M.G. (2011). The soybean Rhg1 locus for resistance to the soybean cyst nematode Heterodera glycines regulates expression of a large number of stress- and defense-related genes in degenerating feeding cells. *Plant Physiology*. Accepted.

Uthe, J.J., Bearson, S.M.D., Dekkers, J.C.M., Qu, L., Nettleton, D., Rodriguez Torres, Y., O'Connor, A.M., McKean, J.D., Tuggle, C.K. (2011). Integrating comparative expression profiling data with association of SNPs to salmonella shedding for improved food safety and porcine disease resistance. *Animal Genetics*. Accepted.

Boddicker, N., Gabler, N.K., Spurlock, M.E., Nettleton, D., Dekkers, J.C.M. (2011). Effects of ad libitum and restricted feed intake on growth performance and body composition of Yorkshire pigs selected for reduced residual feed intake. *Journal of Animal Science.* **89** 40–51.

Sadler, L.J., Johnson, A.K., Lonergan, S.M., Nettleton, D., Dekkers, J.C.M. (2011). The effect of selection for residual feed intake on general behavioral activity and the occurrence of lesions in Yorkshire gilts. *Journal of Animal Science.* **89** 258 – 266**.**

Ciraci, C., Tuggle, C. K., Wannemuehler, M. J., Nettleton, D., Lamont, S. J. (2010). Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. *BMC Genomics.* **11** 545.

Qu, L., Nettleton , D., Dekkers, J.C.M., Bacciu, N. (2010). Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. *Statistics and Its Interface*. **3** 477–492.

Liang, K. and Nettleton, D. (2010). A hidden Markov model approach to testing multiple hypotheses on a tree-transformed gene ontology graph. *Journal of the American Statistical Association*. **105** 1444–1454.

Demirkale, C.Y., Nettleton, D., Maiti, T. (2010). Linear mixed model selection for false discovery rate control in microarray data analysis. *Biometrics*. **66** 621 – 629.

Lkhagvadorj, S., Qu, L., Cai, W., Couture, O.P., Barb, C.R., Hausman, G.J., Nettleton, D., Anderson, L.L., Dekkers, J.C.M., Tuggle, C.K. (2010). Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. *American Journal of Physiology – Regulatory, Integrative and Comparative Physiology.* **298** R494 – R507.

Xi, L., Moscou, M.J., Meng, Y., Xu, W., Caldo, R.A., Shaver, M., Nettleton, D., Wise, R.P. (2009). Transcript-based cloning of RRP46, a regulator of rRNA processing and R-gene-independent cell death in barley-powdery mildew interactions. *The Plant Cell*. **21** 3280 – 3295.

Nettleton, D. (2009). Testing for the supremacy of a multinomial cell probability. *Journal of the American Statistical Association*. **104** 1052–1059.

Schnable, P.S. et al. (2009). The B73 maize genome: complexity, diversity and dynamics. *Science*. **326** 1112 – 1115.

Swanson-Wagner, R.A., DeCook, R., Jia, Y., Bancroft, T., Ji, T., Zhao, X., Nettleton, D., Schnable, P.S. (2009). Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. *Science*. **326** 1118 – 1120.

Jia, Y., Lisch, D.R., Ohtsu, K., Scanlon, M.J., Nettleton, D., Schnable, P.S. (2009). Loss of RNA-dependent RNA Polymerase 2 (RDR2) function causes widespread and unexpected changes in the expression of transposons, genes and 24-nt small RNAs. *PLoS Genetics.* **5**(11): e1000737.

Springer, N.M., Ying, K., Fu, Y., Ji, T., Yeh. C.T., Jia, Y., Wu, W., Richmond, T., Kitzman, J., Rosenbaum, H., Iniguez, A.L., Barbazuk, W.B., Jeddeloh, J.A., Nettleton, D., Schnable, P.S. (2009). Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. *PLoS Genetics.* **5**(11):e1000734.

Liu, S., Yeh, C.T., Ji, T., Ying, K., Wu, H., Tang, H.M., Fu, Y., Nettleton, D., Schnable, P.S. (2009). Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic marks for open chromatin across the maize genome. *PLoS Genetics.* **5**(11): e1000733.

Lkhagvadorj, S., Qu, L., Cai, W., Couture, O.P., Barb, C.R., Hausman, G.J., Nettleton, D., Anderson, L.L., Dekkers, J.C.M., Tuggle, C.K. (2009). Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. *Physiological Genomics.* **38** 98 – 111.

Brooks, L., Strable, J., Zhang, X., Ohtsu, K., Zhou, R., Sarkar, A., Hargreaves, S., Eudy, D., Pawlowska, T., Ware, D., Janick-Buckner, D., Buckner, B., Timmermans, M.C.P., Schnable, P.S., Nettleton, D., Scanlon, M.J. (2009). Microdissection of shoot meristem functional domains. *PLoS Genetics*. **5**(5): e1000476.

Schwab, C.R., Baas, T.J., Stalder, K.J., Nettleton, D. (2009). Results from six generations of selection for intramuscular fat in Duroc swine using real time ultrasound. I. Direct and correlated phenotypic responses to selection. *Journal of Animal Science*. **87** 2774 – 2780.

Liu, Z., Henderson, A.L., Nettleton, D., Wilson-Welder, J.H., Hostetter, J.M., Ramer-Tait, A., Jergens, A.E., Wannemuehler, M.J. (2009). Mucosal gene expression profiles following the colonization of immunocompetent defined-flora C3H mice with Helicobacter bilis: a prelude to Typhlocolitis. *Microbes and Infection.* **11** 374 – 383.

Li, L. Foster, C., Gan, Q., Nettleton, D., James, M., Myers, A., Wurtele, E. (2009). Identification of the novel protein QQS as a component of the starch metabolic network in Arabidopsis leaves. *The Plant Journal*. **58** 485 – 498.

Li, X., Wei, Y., Nettleton, D., Brummer, E.C. (2009). Comparative gene expression profiles between heterotic and non-heterotic hybrids of tetraploid Medicago sativa. *BMC Plant Biology*. **9** article 107.

Uthe, J.J. Wang, Y., Qu. L., Nettleton, D., Tuggle, C.K., Bearson, S.M.D. (2009). Correlating blood immune parameters and a CCT7 genetic variant with the shedding of Salmonella enterica serovar Typhimurium in swine. *Veterinary Microbiology*. **135** 384 – 388.

Elling, A.A., Mitreva, M., Gai, X., Martin, J., Recknor, J., Davis, E.L., Hussey, R.S., Nettleton, D., McCarter, J.P., Baum, T.J. (2009). Sequence mining and transcript profiling to explore cyst nematode parasitism. *BMC Genomics*. **10** article 58.

Strable, J., Borsuk, L., Nettleton, D., Schnable, P.S., Irish, E.E. (2008). Microarray analysis of vegetative phase change in maize. *The Plant Journal*. **56** 1045 – 1057.

Tuggle, C.K., Wang, Y.F., Couture, O.P., Qu, L., Uthe, J.J., Kuhar, D., Lunney, J.K., Nettleton, D., Dekkers, J.C.M., Bearson, S.M. (2008). Computational integration of structural and functional genomics data across species to develop information on the porcine inflammatory gene regulatory pathway. *Developments in Biologicals*. **132** 105 – 113.

Wang, Y., Couture, O.P., Qu, L., Uthe, J.J., Bearson, S.M.D., Kuhar, D., Lunney, J.K., Nettleton, D., Dekkers, J.C.M., Tuggle, C.K. (2008). Analysis of porcine transcriptional response to Salmonella enterica serovar Choleraesuis suggests novel targets of NFkappaB are activated in the mesenteric lymph node. *BMC Genomics*. **9** article 437.

Skibbe, D.S., Wang, X., Borsuk, L.A., Ashlock, D.A. Nettleton, D., Schnable, P.S. (2008). Floret-specific differences in gene expression and support for the hypothesis that tapetal degeneration occurs via programmed cell death. *Journal of Genetics and Genomics*. **35** 603 – 616.

Flagel, L.M., Udall, J.A., Nettleton, D., Wendel, J.F. (2008). Duplicate gene expression in allopolyploid Gossypium reveals two temporally distinct phases of expression evolution. *BMC Biology*. **6** article 16.

Wang, D., Nettleton, D. (2008). Combining classical trait and microarray data to dissect transcriptional regulation: a case study. *Theoretical and Applied Genetics*. **116** 683–690.

Guo, B., Wang, Y., Shi, F., Barton, Y.-W., Plummer, P., Reynolds, D., Nettleton, D., Grinnage-Pulley, T., Lin, J., Zhang, Q. (2008). CmeR functions as a pleiotropic regulator and is required for optimal colonization of Campylobacter jejuni in vivo. *Journal of Bacteriology*. **190** 1879 – 1890.

Nettleton, D., Recknor, J., Reecy, J.M. (2008). Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. *Bioinformatics*. **24** 192 – 201.

Elling, A.A., Mitreva, M., Recknor, J., Gai, X., Martin, J., Maier, T.R., McDermott, J.P., Hewezi, T., Bird, D.M., Davis, E.L., Hussey, R.S., Nettleton, D., McCarter, J.P., Baum, T.J. (2007). Divergent evolution of arrested development in the dauer stage of Caenorhabditis elegans and the infective stage of Heterodera glycines. *Genome Biology*. **8** R211.

Madsen, M.L., Oneal, M.J., Gardner, S.W., Strait, E.L., Nettleton, D., Thacker, E.L., Minion, F.C. (2007). Array-based genomic comparative hybridization analysis of field strains of Mycoplasma hyopneumoniae. *Journal of Bacteriology*. **22** 7977 – 7982.

Dembinsky, D., Woll, K., Saleem, M., Liu, Y., Fu, Y., Borsuk, L.A., Lamkemeyer, T., Fladerer, C., Madlung, J., Barbazuk, B., Nordheim, A., Nettleton, D., Schnable, P.S., Hochholdinger, F. (2007). Transcriptomic and proteomic analyses of pericycle cells of the maize (Zea mays L.) primary root. *Plant Physiology*. **145** 575 – 588.

Ohtsu, K., Smith, M.B., Emrich, S.J., Borsuk, L.A., Zhou, R., Chen, T., Zhang, X., Timmermans, M.C.P., Beck, J., Buckner, B., Janick-Buckner, D., Nettleton, D., Scanlon, M.J., Schnable, P.S. (2007). Global gene expression analysis of the shoot apical meristem of maize (Zea mays L.) *The Plant Journal*. **52** 391 – 404.

van de Mortel, M. Recknor, J.C., Graham, M.A., Nettleton, D., Dittman, J.D., Nelson, R.T., Godoy, C.V., Abdelnoor, R.V., Almeida, A.M.R., Baum, T.J., Whitham, S.A. (2007). Distinct biphasic mRNA changes in response to Asian soybean rust infection. *Molecular Plant-Microbe Interactions*. **20** 887 – 899.

Zhang, X., Madi, S., Borsuk, L., Nettleton, D., Elshire, R.J., Buckner, B., Janick-Buckner, D., Beck, J., Timmermans, M., Schnable, P.S., Scanlon, M.J. (2007). Laser microdissection analyses of narrow sheath mutant meristems reveal domain-specific patterns of gene expression. *PLoS Genetics*. **3** Issue 6 e101.

Wang, Y., Qu, L., Uthe, J.J., Bearson, S.M.D., Kuhar, D., Lunney, J.K., Couture, O.P., Nettleton, D., Dekkers, J.C.M., Tuggle, C.K. (2007). Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. *Genomics*. **90** 72 – 84.

Zhang, W., Carriquiry, A., Nettleton, D., Dekkers, J.C.M. (2007). Pooling mRNA in microarray experiments and its effect on power. *Bioinformatics*. **23** 1217 – 1224.

Udall, J.A., Flagel, L.M., Cheung, F., Woodward, A.W., Hovav, R., Rapp, R.A., Swanson, J.M. Lee, J.J., Gingle, A.R., Nettleton, D., Town, C.D., Chen, Z.J., Wendel, J.F. (2007). Spotted cotton oligonucleotide microarrays for gene expression analysis. *BMC Genomics*. **8** article 81.

Zhao, H., Nettleton, D., Dekkers, J.C.M. (2007). Evaluation of linkage disequilibrium measures between multi-allelic markers as predictors of linkage disequilibrium between single nucleotide polymorphisms. *Genetical Research*. **89** 1 – 6.

Ithal, N., Recknor, J., Nettleton, D., Maier, T., Baum, T.J., Mitchum, M.G. (2007). Developmental transcript profiling of cyst nematode feeding cells in soybean roots. *Molecular Plant-Microbe Interactions*. **20** 510 – 525.

Yang, C., Guo, R., Jie, F., Nettleton, D., Peng, J., Carr, T., Yeakley, J.M., Fan, J.-B., Whitham, S.A. (2007). Spatial and temporal analysis of Arabidopsis thaliana gene expression in

response to Turnip mosaic virus infection. *Molecular Plant-Microbe Interactions*. **20** 358 – 370.

Ithal, N., Recknor, J., Nettleton, D., Hearne, L., Maier, T., Baum, T.J., Mitchum, M.G. (2007). Parallel genome-wide expression profiling of host and pathogen during soybean cyst nematode infection of soybean. *Molecular Plant-Microbe Interactions*. **20** 293 – 305.

Ruppert, D., Nettleton, D., Hwang, J.T.G. (2007). Exploring the information in *p*-values for the analysis and planning of multiple-test experiments. *Biometrics.* **63** 483 – 495.

Jia, H., Nettleton, D., Peterson, J.M., Vazquez-Carrillo, G., Jannink, J.-L., Scott, M.P. (2007). Comparison of transcript profiles in wild-type and o2 maize endosperm in different genetic backgrounds. *The Plant Genome.* **47** S45 – S59.

Nettleton, D. (2006). A discussion of statistical methods for design and analysis of microarray experiments for plant scientists. Invited by *The Plant Cell*. **18** 2112 – 2121.

Nettleton, D., Hwang, J.T.G., Caldo, R.A., Wise, R.P. (2006). Estimating the number of true null hypotheses from a histogram of *p*-values. *Journal of Agricultural, Biological, and Environmental Statistics.* **11** 337 – 356.

Skibbe, D.S., Wang, X., Zhao, X., Borsuk, L.A., Nettleton, D., Schnable, P.S. (2006). Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. *Bioinformatics*. **22** 1863 – 1870.

Udall, J.A., Swanson, J.M., Nettleton, D., Percifield, R.J., Wendel, J.F. (2006). A novel approach for characterizing expression levels of genes duplicated by polyploidy. *Genetics*. **173** 1823 – 1827.

Che, P., Lall, S., Nettleton, D., and Howell, S.H. (2006). Gene expression programs during shoot, root, and callus development in Arabidopsis tissue culture. *Plant Physiology*. **141** 620 – 637.

Caldo, R.A., Nettleton, D., Peng, J., Wise, R.P. (2006). Stage-specific suppression of basal defense discriminates barley plants containing fast- and delayed-acting Mla powdery mildew resistance alleles. *Molecular Plant-Microbe Interactions*. **19** 939 – 947.

Nettleton, D., Wang, D. (2006). Selective transcriptional profiling for trait-based eQTL mapping. *Animal Genetics*. **37** 13 – 17.

Swanson-Wagner, R. Jia, Y., DeCook, R., Borsuk, L., Nettleton, D., Schnable, P.S. (2006). All possible modes of gene action are observed in a global comparison of gene expression in a maize F1 hybrid and its inbred parents. *Proceedings of the National Academy of Sciences*. **103** 6805 – 6810.

Wang, D., Nettleton, D. (2006). Identifying genes associated with a quantitative trait or quantitative trait locus via selective transcriptional profiling. *Biometrics*. **62** 504 – 514.

Zhao, S.-H., Kuhar, D., Lunney, J.K., Dawson, H., Guidry, C., Uthe, J.J., Bearson, S.M.D., Recknor, J., Nettleton, D., Tuggle, C.K. (2006). Gene expression profiling in Salmonella Choleraesuis infected porcine lung using a long oligonucleotide microarray. *Mammalian Genome*. **17** 777 – 789.

Madsen, M.L., Nettleton, D., Thacker, E.L., Minion, F.C. (2006). Transcriptional profiling of Mycoplasma hyopneumoniae during iron depletion using microarrays. *Microbiology*. **152** 937 – 944.

Steelman, C. A., Recknor, J. C., Nettleton, D., Reecy, J.M. (2006). Transcriptional profiling of myostatin-knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. *The FASEB Journal*. 10.1096/fj.05 – 5125fje.

DeCook, R., Lall, S., Nettleton, D., Howell, S.H. (2006). Genetic regulation of gene expression during shoot development in Arabidopsis. *Genetics*. **172** 1155 – 1164.

Cook, R.N., Xin, H., Nettleton, D. (2006). Effects of cage stocking density on feeding behaviors of group-housed laying hens. *Transactions of the ASAE.* **49** 187 – 192.

DeCook, R., Nettleton, D., Foster, C.M., Wurtele, E. (2006). Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. *Computational Statistics and Data Analysis*. **50** 518 – 532.

Madsen, M.L., Nettleton, D., Thacker, E.L., Edwards, R., Minion, F. C. (2006). Transcriptional profiling of Mycoplasma hyopneumoniae during heat shock using microarrays. *Infection and Immunity*. **74** 160 – 166.

Zhao, S.-H., Recknor, J., Lunney, J.K., Nettleton, D., Kuhar, D., Orley, S., Tuggle, C.K. (2005). Validation of a first generation long oligonucleotide microarray for transcriptional profiling in the pig. *Genomics*. **86** 618 – 625.

Woll, K., Borsuk, L., Stransky, H., Nettleton, D., Schnable, P.S., Hochholdinger, F. (2005). Isolation, characterization and pericycle specific transcriptome analyses of the novel maize (Zea mays L.) lateral and seminal root initiation mutant rum1. *Plant Physiology*. **139** 1255 – 1267.

Zhao, H., Nettleton, D., Soller, M., Dekkers, J.C.M. (2005). Evaluation of linkage disequilibrium measures between multi-allelic markers as predictors of linkage disequilibrium between markers and QTL. *Genetical Research*. **86** 77 – 87.

Shen, C., Nettleton, D., Jiang, M., Kim, S. K., Powell-Coffman, J. A. (2005). Roles of HIF-1 hypoxia-inducible factor during hypoxia response in Caenorhabditis elegans. *The Journal of Biological Chemistry*. **280** 20580 – 20588.

Shen, L., Gong, J., Caldo, R. A., Nettleton, D., Cook, D., Wise, R. P., Dickerson, J. A. (2005). BarleyBase—an expression profiling database for plant genomics. *Nucleic Acids Research*. **33** D614 – D618.

Cocciolone, S. M., Nettleton, D., Snook, M. E., Peterson, T. (2005). Transformation of maize with the p1 transcription factor directs production of silk maysin levels, a corn earworm resistance factor, in concordance with a hierarchy of floral organ pigmentation. *Plant Biotechnology Journal.* **3** 225 – 235.

Lee, S. H., Zhao, S.-H., Recknor, J. C., Nettleton, D., Orley, S., Kang, S.-K., Lee, B.-C., Hwang, W.-S., Tuggle, C. K. (2005). Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. *Molecular Reproduction and Development*. **71** 129 – 139.

Peterson-Burch, B. D., Nettleton, D., Voytas, D. F. (2004). Genomic neighborhoods for Arabidopsis retrotransposons: genome sequence analysis reveals a role for targeted integration in the distribution of the Metaviridae. *Genome Biology*. **5** R78.

Caldo, R. A., Nettleton, D., Wise, R. P. (2004). Interaction-dependent gene expression in *Mla*-specified response to barley powdery mildew. *The Plant Cell.* **16** 2514 – 2528.

Lall, S., Nettleton, D., DeCook, R., Che, P., and Howell, S. H. (2004). QTLs associated with adventitious shoot formation in tissue culture and the program of shoot development in Arabidopsis. *Genetics*. **167** 1883 – 1892.

Manly, K. F., Nettleton, D., and Hwang, J. T. G. (2004). Genomics, prior probability, and statistical tests of multiple hypotheses. *Genome Research.* **14** 997 – 1001.

Persyn, K. E., Xin, H., Nettleton, D., Ikeguchi, A., and Gates, R. S. (2004). Feeding behaviors of laying hens with or without beak trimming. *Transactions of the ASAE.* **47**(2) 591 – 596. (Winner of ASAE Superior Paper Award)

Steward, B. L., Tian, L. F., Nettleton, D., and Tang, L. (2004). Reduced-dimension clustering for vegetation segmentation. *Transactions of the ASAE.* **47**(2) 609 – 616.

Fernando, R. L., Nettleton, D., Southey, B. R., Dekkers, J. C. M., Rothschild, M. F., and Soller, M. (2004). Controlling the proportion of false positives (PFP) in multiple dependent tests. *Genetics*. **166** 611 – 619.

Zhao, S.-H., Nettleton, D., Liu, W., Fitzsimmons, C., Ernst, C. W., Raney, N. E., and Tuggle, C. K. (2003). Complementary DNA macroarray analyses of differential gene expression in porcine fetal and postnatal muscle. *Journal of Animal Science.* **81** 2179 – 2188.

Puthoff, D. P., Nettleton, D., Rodermel, S. R., Baum, T. J. (2003). Arabidopsis gene expression changes during cyst nematode parasitism revealed by statistical analyses of microarray expression profiles. *The Plant Journal.* **33** 911 – 921.

Hwang, J. T. G. and Nettleton, D. (2003). Principal components regression with data-chosen components and related methods. *Technometrics*. **45** 70 – 79.

Nettleton, D. (2002). Testing for ordered means in a variation of the normal mixture model. *Journal of Statistical Planning and Inference.* **107** 143 – 153.

Hwang, J. T. G. and Nettleton, D. (2002). Investigating the probability of sign inconsistency in the regression coefficients of markers flanking QTL. *Genetics.* **160** 1697 – 1705.

Frame, B. R., Shou, H., Chikwamba, R. K., Zhang, Z., Xiang, C., Fonger, T. M., Pegg, S. E. K., Li, B., Nettleton, D., Pei, D., and Wang, K. (2002). Agrobacterium tumefaciens-mediated transformation of maize embryos using a standard binary vector system. *Plant Physiology*. **129** 13 – 22.

Huang, W., Nettleton, D., Gu, X. (2002). Expression pattern of yeast sporulation: a case study for regulatory changes after yeast genome duplication. *Information Sciences*. **145** 261 – 269.

Carson, J. A., Nettleton, D., and Reecy, J. M. (2001). Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. *The FASEB Journal.* 10.1096/fj.01 – 0544fje.

Nettleton, D. and Banerjee, T. (2001). Testing the equality of distributions of random vectors with categorical components. *Computational Statistics and Data Analysis.* **37** 195 – 208.

Bilder, C. R., Loughin, T. M., and Nettleton, D. (2000). Multiple marginal independence testing for pick any/c variables. *Communications in Statistics − Computation and Simulation*. **29**(4) 1285 – 1316.

Nettleton, D. and Doerge, R. W. (2000). Accounting for variability in the use of permutation testing to detect quantitative trait loci. *Biometrics*. **56** 52 – 58.

Nettleton, D. (1999). Convergence properties of the EM algorithm for inequality constrained parameter spaces. *The Canadian Journal of Statistics*. **27** 639 – 648.

Nettleton, D. (1999). Order restricted hypothesis testing in a variation of the normal mixture model. *The Canadian Journal of Statistics*. **27** 383 – 394.

Nettleton, D. and Praestgaard, J. (1998). Interval mapping of quantitative trait loci through order restricted inference. *Biometrics*. **54** 74 – 87.

Nettleton, D. (1998). Investigating home court advantage. *Journal of Statistics Education*. **6** n 2.

Invited Book Chapters

Nettleton, D. (2011). Design of gene expression microarray experiments. *Design and Analysis of Experiments, Volume 3: Special Designs and Applications*. Hinkelmann, K. (Editor). Wiley. Accepted.

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

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

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

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. $3,000,000.

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. $2,500,000.

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. $1,000,000.

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. $990,000.

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. $749,000.

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. (Nettleton, D. funded collaborator). GEPR: Genomic analyses of shoot meristem function in maize. National Science Foundation, September 2008 to August 2012. $5,000,000.

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., Cross, 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. $2,500,000.

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., 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. $3,939,129.

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

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 Kendziorski, *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

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, ENAR, 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, ENAR, 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

Teaching

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

Instructor of Statistical Methods (linear models, linear mixed effects models, general linear models, nonlinear models, generalized linear models, nonparametric regression, bootstrap), spring 2010.

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

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

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 2000-2003

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 to 2000

Winner of University of Nebraska-Lincoln College of Arts and Sciences Distinguished Teaching Award, spring 1999

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, 1992-93 academic year

PhD Students

Co-Major Professor (with Dan Nordman) for Ruo Xu, Statistics

Co-Major Professor (with Peng Liu) for Megan Orr, Statistics

Major Professor for Nick Larson, Statistics and Bioinformatics and Computational Biology

Co-Major Professor (with Peng Liu) for Tieming Ji, Statistics and Bioinformatics and Computational Biology

Major Professor for Steve Lund, Statistics

Major Professor for Heng Wang, Statistics

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 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 Jie Li, Statistics, Detecting Differential Expression in Maize RNAseq Data, summer 2011.

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

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 Bionformatics 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

Department Committees

Promotion and Tenure Committee Chair 2011 – present

Promotion and Tenure Committee, 2009 – present

MS and PhD Exam Committee, 2008 – 2009, 2010 – 2011

Graduate Committee Chair, 2007 – 2008

Advisory Committee to the Department Chair, 2007 – present

Journal Rating Committee, 2007 – 2008

MS Exam Committee, 2006 – 2007

150th ISU Anniversary/75th Statistical Laboratory Anniversary Committee, 2006 – 2007

Snedecor Hall Renovation Committee, summer 2006

Faculty Search Committee Chair, spring 2006

Seminar Chair, spring 2006

External Review Committee, 2005 – 2006

Strategic Planning Committee, fall 2004 to fall 2005

Social Committee Chair, summer 2001 to spring 2005

PhD Preliminary Examination Committee, fall 2002 to summer 2004

Faculty Search Committee, 2002 – 2003

Department Chair Search Committee, 2001 – 2002

MS Examination Committee, summer 2000 to spring 2001

Social Committee, summer 2000 to spring 2001

Editorial Activities

Associate editor of the *Journal of the American Statistical Association*, summer 2009 to present

Associate editor of the *Journal of Agricultural, Biological, and Environmental Statistics*, spring 2003 to present

Associate editor of *Biometrics*, spring 2005 to fall 2010

Statistical reviewer for *The Plant Cell*, spring 2008 through fall 2010

Journal Refereeing

Animal Genetics
Annals of the Institute of Mathematical Statistics
Annals of Statistics
Australian Journal of Statistics
Bioinformatics
BMC Bioinformatics
BMC Genomics
Biometrical Journal
Biometrics
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 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
Proceedings of the National Academy of Science
Science
Statistics and Its Interface
Technometrics

Proposal Review

Ad hoc reviewer of 7 proposals for the Genomics, Computational Biology and Technology
    (GCAT) NIH study section meeting, fall 2009

Panelist and reviewer of 9 proposals for the Joint DMS(NSF)/NIGMS(NIH) Initiative to Support Research in the Area of Mathematical Biology, fall 2007

Special emphasis review panel member for NIH predoctoral training in biostatistics, spring 2007

Reviewer of proposal submitted to the National Science Foundation, spring 2006

Reviewer of proposal submitted to the NIH NIGMS Centers of Excellence in Complex Biomedical Systems Research Program, spring 2004.

Panelist and reviewer of 12 proposals for the Joint DMS(NSF)/NIGMS(NIH) Initiative to Support Research in the Area of Mathematical Biology, fall 2003

Reviewer of proposal submitted to the National Science Foundation Division of Mathematical Sciences, spring 2003

Reviewer of proposal submitted to the Natural Sciences and Engineering Research Council of Canada, spring 2003

Panelist and reviewer of 11 proposals for the Joint DMS(NSF)/NIGMS(NIH) Initiative to Support Research in the Area of Mathematical Biology, fall 2002

Reviewer of proposal submitted to the National Science Foundation, spring 2002

Reviewer of proposal submitted to the National Science Foundation, fall 2001

Reviewer of 2 proposals submitted to the United States Department of Agriculture, spring 1999

Other Professional Activities

Member of the International Program Committee for the 2010 International Biometrics Conference in Florianopolis, Brazil, summer 2008 – December 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, spring 2007 – spring 2008

Vice President of the Iowa Chapter of the American Statistical Association, fall 2005 to spring 2007

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

Leader of Iowa State University Department of Statistics VIGRE Bioinformatics Working Group, fall 2002 through fall 2003, fall 2005 to spring 2006

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

Faculty member in the Bioinformatics and Computational Biology program at Iowa State University, fall 2000 to present

Faculty member in the Center for Integrated Animal Genomics at Iowa State University, fall 2002 to present

Member of the Center for Integrated Animal Genomics Advisory Board, fall 2002 to summer 2005

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

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

Fellow of the American Statistical Association, 2008

Mid-Career Award for Excellence in Research, Iowa State University, College of Liberal Arts and Sciences, 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