Curriculum vitae: Rebecca W. Doerge

Address

Department of Statistics
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Personal

Born Stamford, NY, United States
United States citizen
Website: `http://www.stat.purdue.edu/~doerge`
Google Scholar Citation List: `http://scholar.google.com/citations?hl=en& user=B4WVzSEAAAAJ`
Email: `doerge@purdue.edu`

Education

B.S. in Mathematics, 1982-1986
    University of Utah, Salt Lake City, Utah

M.Stat. in Mathematics, 1986-1988
    University of Utah, Salt Lake City, Utah
    Advisor: Simon Tavaré
    Thesis: *Information of Fixed Cluster Samples for Genetic Traits Involving Mixtures of Distributions*

Ph.D. in Statistics, 1989-1993
    North Carolina State University, Raleigh, North Carolina
    Minor in Genetics
    Advisor: Bruce Weir
    Dissertation: *Statistical Methods for Locating Quantitative Trait Loci with Molecular Markers*

Postdoctoral Fellow, 1993-1995
    Cornell University, Ithaca, New York
    Sponsor: Gary Churchill (Department of Plant Breeding and Biometry)

Professional Experience

NSF Research Fellow: North Carolina State University, Statistics Department.
    Dates: 8/1990 to 12/1992.
Research Assistant: North Carolina State University, Statistics Department.
    Dates: 12/1992 to 5/1993.
Postdoctoral Associate: North Carolina State University,
    Statistics Department, Dr. Bruce Weir.
    Dates: 5/1993 to 7/1993.
Instructor/Postdoctoral Associate: Cornell University,
    Biometrics Unit, Dr. Gary Churchill.
    Dates: 8/1993 to 7/1995.
Assistant Professor of Statistics (75%) and Agronomy (25%): Purdue University.
    Dates: 8/1995 to 8/2000.
Associate Professor of Statistics and Agronomy: Purdue University.
    Dates: 8/2000 to 8/2003.
Professor of Statistics and Agronomy: Purdue University.
    Dates: 8/2003 to present.
Interim Head, Department of Statistics: Purdue University.
    Dates: 8/2008 to 7/2009.
Associate Head, Department of Statistics: Purdue University.
    Dates: 7/2009 to 6/2010.
Head, Department of Statistics: Purdue University.
    Dates: 7/2010 to 06/30/15.
Trent and Judith Anderson Distinguished Professor of Statistics.
    Date: 10/2011 to present.

Teaching Experience

1993-1995 Cornell University, Biometrics Unit. Course: Introduction to Statistical Methods,
    Text: Devore and Peck.
1993-1995 Cold Spring Harbor Laboratory Course. Cold Spring Harbor, NY: Molecular
    Markers for Plant Genetics and Plant Breeding (with Ben Burr and Scott Tingey).
1995-2002 Purdue University, Statistics Dept. Courses: Applied Regression Analysis (service course for non-majors (ST512), graduate level statistics course (ST525)),
    Text: Neter, Kutner, Nachtsheim, and Wasserman.
1996 The International Potato Center. Lima, Peru: Molecular Markers for Potato Germplasm
    Management and Enhancement Course (with Scott Tingey).
1995-2005 The (abroad) Summer Institute in Statistical Genetics. North Carolina State
    University, Raleigh, NC.
1998 Purdue University, Statistics Dept: Introduction to Statistics and Probability (ST511),

Text: Devore.

1999-present (every other year) STAT 549. Purdue University, "An Applied Introduction to QTL Mapping in Experimental Populations",
Text: Lynch and Walsh.

1999-present Purdue University, Statistics Dept: Bioinformatics/Statistical Bioinformatics Seminar Series.

2003 Purdue University, Statistics Dept.: "Discovering Genomics, Proteomics, and Bioinformatics", Text: Campbell and Heyer.

2005 Purdue University, Statistics Dept. Course: Applied Regression Analysis (ST525), Text: Kutner, Nachtsheim, Neter, and Li.

2006-present The (abroad) Summer Institute in Statistical Genetics. University of Washington, Seattle, WA.

2010-2015 First Year Graduate Student Seminar. Fall semesters only.

Purdue University and Departmental Service

Department of Statistics:

- 1995-present Job/Career Coordinator (web site: `http://www.stat.purdue.edu/`$\tilde{j}obs$)
- 1995-2000 Teaching Policy Committee
- 1995-2010 Harassment Liaison
- 1995-2010 Graduate Placement Coordinator
- 1998, 2003, 2012 6th - 8th Purdue Symposium on Statistics Organizing Committee
- 1999 Member of Statistics Department Head 5 year review committee
- 1999-2002 Comprehensive Examination Committee
- 1999-2000 Graduate Admissions Committee
- 2000-Fall 2005, Fall 2006-2008, Fall 2009-present Chair of the Graduate Admissions Committee
- 2003-present Member of the Statistics Primary Committee
- 2004-present Member of the Statistics Graduate Committee
- 2005-present Member of the Statistics Promotion Committee
- 2006-2008 Member of the Ph.D. Qualifying Exam Committee
- 2006-2015 Member of the Executive and Personnel Committee
- 2007 Interim Chair Graduate Committee
- 2008 Interim Head, Department of Statistics
- 2009 Associate Head, Department of Statistics
- 2010-2015 Head, Department of Statistics

Purdue University:

- 1997-2003 Chair, Advisory Committee for Genomics Facility
- 1998-2003 Advisory Committee for Computational Genomics Facility
- 2001 Member of President Jischke's Policy Advisory Group on New University Facilities
- 2001-2002 Computing Research Institute Faculty Advisory Committee
- 2002-2006 Member of the Discovery Park Advisory Committee
- 2003-2006, 2007 Chair of the Bioinformatics COALESCE Area, College of Science
- 2004-2012 Director of the Statistical Bioinformatics Center
- 2005, 2007 College of Science Faculty Scholar Selection Committee
- 2005-2007 Member of the Bindley Biosciences Director Search Committee
- 2005-2015 College of Science Area Promotion Committee
- 2007 Organizing Committee: Convergence of Genomics and the Land Grant Mission
- 2008-2009 Dean of Science Search Committee, Purdue University
- 2008-present Executive Advisory Board Discovery Park Bindley Biosciences
- 2008-present Executive Committee, International Breast Cancer and Nutrition Research Team
- 2009-2010 Purdue University, Provost Steering Committee on Sustaining New Synergies
- 2009-2010 College of Science Strategic Planning Oversight Committee
- 2009-2010 College of Science Faculty Council
- 2011 Selection Committee for the Outstanding Faculty Mentoring Award
- 2011 Discovery Park Director/Administrative Officer Review Committee
- 2011-2015 ADVANCE-Purdue Council of Department Heads
- 2011-2014 Chair, Purdue University Mediation Committee
- 2012-2013 Task Force on Computing and Information Science, Engineering and Technology
- 2012-present Faculty Advisory Committee of the Bioinformatics Core
- 2013-2014 Provost Search Committee, Purdue University
- 2014-2015 Director of Discovery Park Search Committee, Purdue University
- 2015-2016 Director of Regenstrief Center for Healthcare Engineering Search Committee, Purdue University
- 2015-2018 Member, Purdue University Faculty Senate
- 2015-2016 President's Fellow, Big Data and Simulation, Purdue University

Ph.D. Students

Completed (23):

1. Dr. Brian Munneke: August 2001. *Null model methods for cluster analysis of gene expression data.* Current position: Senior Biostatistician; Genomic Health, Redwood City, CA, USA.

2. Dr. Jayson Wilbur: (co-advised with Jayanta Ghosh) December 2001. *Variable selection in high-dimensional multivariate binary data.* Current position: Senior Scientist; Metrum Research Group, Tariffville, CT, USA.

3. Dr. Michael Black: August 2002. *Statistical issues in the design and analysis of spotted microarray experiments.* Current position: Associate Professor (equivalent to Full Professor in US); Department of Biochemistry, University of Otago, Dunedin, New Zealand.

4. Dr. Dachuang Cao: (co-advised with Bruce Craig) May 2004. *Quantitative trait locus mapping in polyploids.* Current position: Research Scientist; Division of Statistics, Eli Lilly and Company, Indianapolis, IN, USA.

5. Dr. Hongmei Jiang: December 2004. *A two-step procedure for multiple pairwise comparisons in microarray experiments.* Current position: Associate Professor; Department of Statistics, Northwestern University, Evanston, IL, USA.

6. Dr. John Stevens: May 2005. *Meta-analytic approaches for microarray data.* Current position: Associate Professor; Department of Mathematics and Statistics, Utah State University, Logan, UT, USA.

7. Dr. Lianbo Yu: May 2006. *Statistical issues in protein microarray analysis.* Current position: Biostatistical Scientist; Center for Biostatistics, College of Medicine, and Research Assistant Professor of Biostatistics, School of Public Health, The Ohio State University, Columbus, OH, USA.

8. Dr. Martina Muehlbach Bremer: December 2006. *Identifying regulated genes through the correlation structure of time dependent microarray data.* Current position: Associate Professor; Department of Mathematics, San Jose State University, San Jose', CA, USA.

9. Dr. Kyunga Kim: May 2007. *Statistical issues in mapping genetic determinants for expression level polymorphisms.* Current position: Assistant Professor; Department of Statistics, Sookmyung Women's University, Seoul, South Korea.

10. Dr. Riyan Cheng (co-advised with Jun Xie): December 2007. *Statistical methods for mapping multiple complex traits.* Current position: Research Fellow, Justin Borevitz Lab; Research School of Biology, The Australian National University, Acton, Australia.

11. Dr. Lingling An: August 2008. *Dynamic clustering of time series gene expression.* Current position: Assoc. Professor; Department of Agricultural and Biosystems Engineering; University of Arizona, Tucson, AZ, USA.

12. Dr. Suk-Young Yoo: December 2008. *Statistical methods for integrating epigenomic results.* Current position: Research Statistical Analyst; MD Anderson Cancer Center, Houston, TX, USA.

13. Dr. Cherie Ochsenfeld (co-advised with Kristopher Jennings): August 2009. *Mixed models in quantitative trait loci and association mapping with bootstrap thresholds.* Current position: Statistical Geneticist; Dow AgroSciences, Indianapolis, IN, USA.

14. Dr. Alexander Lipka (co-advised with George McCabe): December 2009. *Associating single nucleotide polymorphisms (SNPs) with binary traits.* Current position: Assistant Professor; Department of Crop Sciences, University of Illinois Champagne-Urbana, Urbana, IL, USA.

15. Dr. Gayla Hobbs Olbricht (co-advised with Bruce Craig): August 2010. *Incorporating genome annotation in the statistical analysis of genomic and epigenomic tiling array data.* Current position: Assistant Professor; Department of Mathematics, Missouri University of Science and Technology, Ralla, MO, USA.

16. Dr. Andrea Rau: August 2010. *Reverse engineering gene networks using genomic time-course data.* Current position: Assistant Professor; Institut National de la Recherche Agronomique (GABI / PSGen) Domaine de Vilver, Jouy-en-Josas, France.

17. Dr. Paul Livermore Auer: August 2010. *Statistical design and analysis of next-generation sequencing data.* Current position: Assistant Professor; Department of Biostatistics, School of Public Health, University of Wisconsin, Milwaukee, Milewaukee, WI, USA.

18. Dr. Tilman Achberger: May 2011. *Selecting subsets of traits for quantitative trait loci analysis.* Current position: Statistician; Google Inc. World Headquarters - Mountain View, CA, USA.

19. Dr. Douglas Baumann: December 2012. *Annotation-informed integration of omic data in next-generation sequencing.* Current position: Assistant Professor; University of Wisconsin, La Crosse, La Crosse, WI, USA.

20. Dr. Xiongzhi (Chee) Chen: December 2012. *General methods for adaptive control and estimation of false discovery rate.* Current position: Postdoctoral Fellow, John Storey Lab; The Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, USA.

21. Dr. Sanvesh Srivastava: August 2013. *Hierarchical Bayesian modeling strategies for analyzing high-dimensional data.* Current position: Assistant Professor; Department of Statistics, University of Iowa, Iowa City, IA, USA.

22. Dr. Ani Elias (Agronomy; co-advised with Mitch Tuinstra): August 2013. *Understanding environmental variables influencing hybrid maize performance across the United States corn belt.* Current position: Research Scientist; Monsanto, Saint Louis, MO, USA.

23. Dr. Jeremiah Rounds: August 2015. *Inference using multi-level genomic features sets and models in RNA-seq experiments.* Current position: Applied Statistics & Computational Modeling Group; Pacific Northwest National Laboratory, National Security Directorate.

Active (3) Ph.D. students:

1. **Mr. Emery Goossens (Projected graduation: May 2018)
2. *Mr. Patrick Medina (Projected graduation: December 2016)
3. *Ms. Faye Zheng (Projected graduation May 2016)

* students funded by R.W. Doerge; ** students funded by fellowship

Professional Society Memberships and Programs

American Society of Plant Biologists
American Association for the Advancement of Science
American Statistical Association
Genetics Society of America
International Biometric Society
Institute of Mathematical Statistics

Professional Service

External departmental reviews:

- 2002 (Chair) University of Minnesota, Program in Biostatistics
- 2007 University of Nevada-Reno, Department of Biochemistry (USDA-review)
- 2010 Statistical and Applied Mathematical Sciences Institute (SAMSI; NSF-review)
- 2013 University of Nebraska-Lincoln, Department of Statistics
- 2015 University of Pittsburgh, Department of Statistics

Federal grant review panel:

- 1997 United States Department of Agriculture Plant Genome Panel
- 1999 United States Department of Agriculture Animal Genetic Mechanisms Panel
- 2000 National Science Foundation Biocomplexity Panel
- 2001 United States Department of Agriculture (IFAFs) Panel
- 2002 United States Department of Agriculture (NRI) Bioinf. Panel Manager
- 2006 National Institute of Health (NIH) Software Maintenance and Dev. Panel
- 2012 National Science Foundation Biology; Plant Genome Panel
- 2015 National Science Foundation Division of Mathematical Sciences Panel

Grant reviews for:

- USDA, NSF, NIH, Welcome Trust, Howard Hughes

Manuscript reviews for:

- Biometrics, Cell, Crop Science, Evolution, Genetics, Genetical Research,
- Genome Research, JASA, Journal of Quantitative Trait Loci, Molecular Breeding,
- Nature, Nature Reviews Genetics, Plant Breeding Reviews,
- Plant Physiology, Plant Cell, PLoS One, Science, Statistical Science,
- Statistical Applications in Genetics and Molecular Biology, Theoretical and Applied Genetics,
- Theoretical and Population Biology, Trends in Genetics,
- The Plant Cell, The Proceedings of the National Academy of Sciences USA.

Book review for:

- 1999 Applied Linear Regression Models, Fourth Edition. Authors: Neter, Kutner, Nachtsheim, and Wasserman
- 2006 Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Authors: Gentleman, Carey, Huber, Irizarry, and Dudoit (eds): Biometrics. 62:4 (1270-1271)
- 2009 A Guide to QTL Mapping with R/qtl. Authors: Broman and Sen. Biometrics (invited)

Conference organization/participation:

- Invited talks for major Genetics, Plant Breeding, and Statistical conferences.
- Organized Statistical Genetics session for the 1996, 1997 Joint Statistical Meetings.
- 1998 Organized the Statistical Genetics Workshop, 6th Purdue Symposium on Statistics.
- 1998-2005 Organizing Committee for The International Plant and Animal Genome Meeting, San Diego, CA.
- 2003 Co-Chair, Gordon Conference on Quantitative Genetics and Genomics, Ventura, CA.
- 2003 Organized the Bioinformatics and Microarray Workshop, 7th Purdue Symposium on Statistics.
- 2005 Chair, Gordon Conference on Quantitative Genetics and Genomics, Ventura, CA.
- 2009 Co-Chair (with Jaya Satagopan), Joint Statistics Meeting (JSM) session on Epigenomics, Washington DC.
- 2009-2012 Member of the Statistical Practice Conference Planning Committee, American Statistical Association (2012).

- 2010-2012 Member, International Advisory Committee (IAC) for the Fourth International Conference on Quantitative Genetics, Edinburgh, Scotland; June 2012.

- 2011-2012 Member, Organizing and Program Committee for the 8th International Purdue Symposium on Statistics "Diversity in the Statistical Sciences for the 21st Century", West Lafayette, IN; June 2012.

- 2013 Member, Organizing Committee "Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics Conference", Seattle, WA; November 2013.

- 2014-2016 Member, International Advisory Committee (IAC) for the Fifth International Conference on Quantitative Genetics, University of Wisconsin, Madison; June 2016.

Editorial Positions, Advisory Boards, Professional Committees

1996-2000 Co-Editor, *Journal of Agricultural Genomics (JAG)*: http://www.ncgr.org/ag/jag/

2002-2012 Associate Editor, *Statistical Applications in Genetics and Molecular Biology*: http://www.bepress.com/sagmb/

2003-2009 Associate Editor, *GENETICS*: http://www.genetics.org

2003-2008 Associate Editor, *The Plant Cell*: http://www.plantcell.org

2006-2012 University of Florida Genomics Institute Advisory Board (Advisors to Ken Burns)

2006-2010 American Association for Cancer Research Epigenomics Task Force (Advisors to Peter Jones)

2007-2010 Samuel S. Wilks Memorial Medal Committee of the American Statistical Association

2007-2012 Cold Spring Harbor Laboratory External Advisory Board on Quantitative Biology

2008-2013 Associate Editor, *Genetics Research*

2008-present Associate Editor, *Epigenomics*

2009-2012 Advisory Board (University of South Carolina) NSF ESPCoR Cyberinfrastructure research Infrastructure project (PI: Jim Bottom)

2010-2015 Advisory Board (German Ministry of Research and Education) Synbreed: Synergistic plant and animal breeding (PI: Chris Schoen)

2010-2012 Cavell Brownie Scholars Mentoring Program Committee

2011-2015 American Statistical Association Committee on Women in Statistics

2011-present Associate Editor, *G3: Genes—Genomes—Genetics*

2012-present Member, Board of Trustees, National Institute of Statistical Sciences (NISS)

2012 American Statistical Association Gertrude Cox Scholarship Award Committee

2012 National Institute of Statistical Sciences Jerome Sacks Award Committee

2013-present Member, Statistical and Mathematical Sciences Institute (SAMSI) National Advisory Committee

2013-2014 Chair, American Statistical Association Gertrude Cox Scholarship Award Committee

2014-present Member, Board of Trustees Mathematical Biosciences Institute, The Ohio State University

2014 Chair, National Institute Statistical Science Awards Committee

2014-present Associate Editor, Journal of the American Statistical Association (JASA) Theory and Methods

2015 Snedecor Awards Committee of the American Statistical Association

2015-2019 Advisory Board, Global Open-Source Breeding Informatics Initiative (GOBII), Cornell University

Honors and Awards

1990-1993 NSF Fellowship in Mathematics and Molecular Biology (UC Berkeley)

1990-1992 Gertrude Cox Fellowship (NC State University)

1991 Mu Sigma Rho membership (NC State University)

1992 Cold Spring Harbor Laboratory award to attend Molecular Markers for Plant Breeding

1994 Instit. for Math. and its Appl. award to attend the Mol. Bio. program (Univ. MN)

1996 Teaching for Tomorrow Award (Purdue University)

1997 Outstanding Asst Prof. for Excellence in Teaching and Research (Science, Purdue)

1998 Outstanding Teacher of Undergrads, School of Science (Purdue University)

1998-1999 Who's Who Among America's Teachers (student nominated, Purdue University)

2001 Elected Member Gamma Sigma Delta

2002 James Madison University Visiting Scholar

2001-2006 University Scholar (Purdue University)

2007 College of Science Graduate Student Mentoring Award (Purdue University)

2007 Elected Member Sigma Xi

2007 Elected Fellow of the American Statistical Association

2007 Elected Fellow of the American Association for the Advancement of Science (AAAS)

2009 Fellow, Committee on Institutional Cooperation (CIC)

2010 Provost's Award for Outstanding Graduate Faculty Mentor (Purdue University)

2011 Trent and Judith Anderson Distinguished Professor of Statistics (Purdue University)

2015 College of Science Leadership Award (Purdue University)

Grant History: Completed, Current, and Pending Grants

Completed Grants:

***Academic salary (a.s.) as stated.

**Doerge is PI, otherwise PI is indicated by *.

Sponsor	Title	Duration	Amount	Home
USDA/CSRC NRI Plant Genome	Quantitative Trait Mapping: A New Statistical Approach	1994-1997	$80K	Cornell to Purdue
Pioneer Hi-Bred International Research Grant	Attaching Biological Function to Genes Using Statistical Genetics	1997-2000	$70K	Purdue
USDA/CSRC NRI Plant Genome	Statistical Genetics in Agriculture	1998-1999	$2K	Purdue
NSF Major Research Instrumentation	Acquisition of Equipment for a Comprehensive Agricultural Genomics Laboratory at Purdue University (with Drs. Bennetzen* and Martin)	1998-1999	$1.3M	Purdue
Purdue Research Foundation	Rhizosphere Microbial Community Succession	1999-2001	$23K	Purdue
USDA/CSRC NRI Plant Genome	Complex Trait Mapping: Statistical Methodology and Significance	1998-2002	$175K	Purdue
USDA/CSRC NRI Soils and Soil Biology	Microbial Community Dynamics in the Rhizosphere of Zea mays L. and Glycine max L (with Drs. Brouder* and Nakatsu)	1998-2002	$250K	Purdue
NSF Computational Biology	Binary Trait Analysis (with Dr. McIntyre*)	1998-2003	$350K	Purdue
Purdue	Agricultural Genomics Core Facility (with Drs. Bennetzen and Mackenzie)	1999-2003	$600K	Purdue

Completed Grants (continued):

***Academic salary (a.s.) as stated.

**Doerge is PI, otherwise PI is indicated by *.

Sponsor	Title	Duration	Amount	Home
Showalter Grant Research & Tech.	Functional Genomics for Animal Research Center (with Drs. Bidwell*, McIntyre, Moody, Aref, Spurlock)	2001-2002	$83K	Purdue
NIH (mouse genomics)	Susceptibility and Resistance Loci in EAE (with Dr. Cory Teuscher*) (subcontract)	1999-2004 Doerge:	$2.3M (15% a.s.) ($133K)	Univ. Vermont
USDA NRI Plant Genome	Conference Grant: Bioinformatics	2003-2004	$5K	Purdue
USDA/IFAFS	Statistical Genomics in Agriculture (with Drs. McIntyre and Kontoyiannis)	2001-2004	$500K (10% a.s.)	Purdue
NSF (Plant Genome)	Functional Genomics in Plant Polyploids (with Drs. Osborn*, Birchler, Chen, Comai, Martienssen)	2000-2005 Doerge:	$5M (5%a.s.) ($250K)	Wisc.
Purdue	Genomics Database Facility Bioinformatics (with Drs. McIntyre*, Aref et al.)	2001-2005	$480K	Purdue reinvest
NSF 2010	Functional Genomics of Quantitative Traits (with Drs. St. Clair* and Michelmore)	2001-2006 Doerge:	$2.4M (20% a.s.) ($300K)	UC Davis
Orion Genomics, LLC	DNA Methylation (12 month RA)	2004-2006	$25K/yr Ph.D. student	Purdue
NIH (R03)	Regulation of Apical Polarity in Breast Cancer (with Dr. LeLievre*)	2005-2007 Doerge:	$50K (5%a.s.) ($11K)	Purdue

Completed Grants (continued):

***Academic salary (a.s.) as stated.

**Doerge is PI, otherwise PI is indicated by *.

Sponsor	Title	Duration	Amount	Home
Purdue	Target Connexin 43 to Prevent Breast Cancer Development from early pre-neoplastic stages (with Dr. Lelievre*)	2006-2007 Doerge:	$50K (0%a.s.) ($20K)	Purdue
Purdue Research Foundation	Statistical Issues in Epigenetics	2007-2008	$15K (Ph.D. student)	Purdue
Bilsland Fellowship	Combining Epigenomic Data	2007-2008	$15K (Ph.D. student)	Purdue
NIH (R01)	Molecular Analysis of Synaptic Transmission Mutants (with Dr. Pak* and Broadie)	2006-2010 Doerge:	$1.25M (10%a.s.) ($150K)	Purdue
NSF	Plant Science Cyberinfrastructure (with Dr. Jorgensen et al.*)	2008-2010 Doerge:	$50M (20%a.s.) ($200K)	Univ. AZ
Komen Breast Cancer Foundation	Focus on Apical Polarity to Develop Breast Cancer Prevention Therapies (with Dr. Lelievre*)	2007-2010 Doerge: Ph.D. student	$350K (0%a.s.) ($60K)	Purdue
NSF Plant Genome	Functional Genomics of Plant Polyploids (with Dr. Comai* et al.):	2005-2011 Doerge:	$8M (20%a.s.) ($1.2M)	UC Davis
Dow Agro Sciences	Modeling of GxE Interactions Using Environmental Data From Weather Stations to Improve Prediction (with Dr. M. Tuinstra*)	2009-2012 Doerge: Ph.D. student	$171,150 (0%a.s.) ($0)	Purdue
USDA AFRI	Partnership for Research & Education in Plant Breeding and Genetics (with Dr. H. Ohm* et al.)	2010-2014 Doerge:	$497,672 (0%a.s.) ($0)	Purdue

Current Federal and Industry Grants:

***Academic salary (a.s.) as stated.
**Doerge is PI, otherwise PI is indicated by *.

Sponsor	Title	Duration	Amount	Home
NSF Plant Genome	Genetic and Genomic Approaches to Understanding Long-distance Transport and Carbon Partitioning in Plants (with Dr. D. Braun* et al.)	2010-2015 Doerge:	$5.8M (10%a.s.) ($690K)	Univ. MO
NSF MCTP	Sophomore Transitions: Bridges into a statistics major and big data research experiences via learning communities (with Dr. Mark Ward* et al.)	2014-2018 Doerge:	$1.5M (0%)	Purdue

Pending Grants:

***Academic salary (a.s.) as stated.
**Doerge is PI, otherwise PI is indicated by *.

Sponsor	Title	Duration	Amount	Home
NIH	Vitamin D Regulation of Metastasis (with Teegarden* et al.)	2016-2020 Doerge:	$1M (5% a.s.) ($250K)	Purdue University
NIH	Impact of Tissue Geometry on Nuclear Organization and Function (with Lelievre* et al.)	2015-2019 Doerge:	$1.2M (1 su mo) ($300K)	Purdue University

Refereed Book Chapters, Proceedings, and Publications (130)

Books (2); Reviewed Book Chapters (7); Reviewed Proceedings (29); Journal Publications (92)
Current and former Purdue graduate students denoted by *

[1] G.A. Churchill and R.W. Doerge. 1994. Empirical threshold values for quantitative trait mapping. Genetics. 138:963-971.

[2] R.W. Doerge. 1995. Testing for linkage: phase known/phase unknown. Journal of Heredity. 86(1):61-62.

[3] R.W. Doerge. 1995. The relationship between the LOD score and the analysis of variance F-statistic when detecting QTL using single markers. Appendix 1: Locating genes associated with root morphology and drought avoidance in rice via linkage to molecular markers. M.C. Champoux, G. Wang, S. Sarkarung, D.J. Mackill, J.C. O'Toole, N. Huang, S.R. McCouch. Theoretical and Applied Genetics. 90:969-981.

[4] S.R. McCouch and R.W. Doerge. 1995. QTL mapping in rice. Trends in Genetics. 11(12):482-487.

[5] R.W. Doerge and G.A. Churchill. 1996. Permutation tests for multiple loci affecting a quantitative character. Genetics. 142:285-294.

[6] R.W. Doerge and A. Rebaï. 1996. Significance thresholds for QTL interval mapping tests. Heredity. 76:459-464.

[7] M.A. Mutschler, R.W. Doerge, J.P. Kuai, S.C. Liu, B. Liedl, and Y. Shapiro. 1996. QTL analysis of the production of acylsugars responsible for pest resistance in the wild tomato *lycopersicon pennellii*. Theoretical and Applied Genetics. 92:709-719.

[8] R.W. Doerge. 1996. Constructing genetic maps by rapid chain delineation. Journal of Quantitative Trait Loci. Volume 2. Article 6. http://probe.nalusda.gov:8000/otherdocs/jqtl

[9] R.W. Doerge, Z-B. Zeng, and B.S. Weir. 1997. Statistical issues in the search for genes affecting quantitative traits in experimental populations. Statistical Science. 12(3):195-219.

[10] C. Teuscher, D.M. Rhein, K.D. Livingstone, R.A. Paynter, R.W. Doerge, S.M. Nicholson, and R.W. Melvold. 1997. Evidence that Tmevd2 and eae3 may represent either a common locus or gene complex controlling susceptibility to immunologically mediated demyelination in mice1. Journal of Immunology. 159:4930-4934.

[11] G.A. Churchill and R.W. Doerge. 1997. Mapping Quantitative Trait Loci in Experimental Populations. In: *Molecular Dissection of Complex Traits*. A.H. Paterson (ed). CRC Press: New York.

[12] R.J. Roper, R.W. Doerge, S.B. Call, K.S.K. Yung, W.F. Hickey, and C. Teuscher. 1998. Autoimmune orchitis, epididymitis, and vastis are immunogenetically distinct lesions. The American Journal of Pathology. 152(5):1337-1345.

[13] R.J. Roper, J.S. Griffith, C.R. Lyttle, R.W. Doerge, A.W. McNabb, R.E. Broadbent, and C. Teuscher. 1998. Interacting quantitative trait loci control phenotypic variation in murine estradiol-regulated responses. Endocrinology. 2(140):556-561.

[14] R.W. Doerge. 1998. Statistical threshold values for locating quantitative trait loci. Proceedings of the Tenth Annual Conference on Applied Statistics in Agriculture, Kansas State University. Edited by George Milliken. 10:84-95.

[15] J. Weis, B. McCracken, Y. Ma, D. Fairbairn, R. Roper, J. Weis, J. Zachery, R.W. Doerge, and C. Teuscher. 1999. Identification of quantitative trait loci governing arthritis severity and humoral responses in the murine model of Lyme disease. Journal of Immunology. 162:948-956.

[16] R.J. Butterfield, E.P. Blankenhorn, R.J. Roper, J.F. Zachary, R.W. Doerge, J. Sudweeks, J. Rose, and C. Teuscher. 1999. Genetic analysis of disease subtype and sexual dimorphism in mouse EAE: Relapsing-remitting and monophasic remitting/nonrelapsing EAE are immunogenetically distinct. Journal of Immunology. 162(5):3096-3102.

[17] S.A. Fennimore, G.E. Shaner, W.E. Nyquist, R.W. Doerge, and M.E. Foley. 1999. A genetic model and molecular markers for wild oat (*Avena fatua* L.) seed dormancy. Theoretical and Applied Genetics. (3-4):711-718.

[18] C. Teuscher, R.J. Butterfield, R. Ma, J. Zachary, R.W. Doerge, and E.P. Blankenhorn. 1999. Sequence polymorphisms in the chemokines *scya1* (TCA-3), *scya2* (Monocyte chemattractant protein (MCP-1)), and *scya12* (MCP-5) are candidate genes for *eae 7*, a locus controlling the susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis. Journal of Immunology. 163:2262-2266.

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[127] I. Pardo, H.A. Lillemoe, R.J. Blosser, M. Choi, C.A.M. Sauder, D.K. Doxey, T. Mathieson, B.A. Hancock, D. Baptiste, R. Atale, M. Hickenbotham, J. Zhu, J. Glasscock, A.M.V. Storniolo, F. Zheng, R.W. Doerge, Y. Liu, S. Badve, M. Radovich, and S.E. Clare. 2014. Next-generation transcriptome sequencing of the premenopausal breast epithelium using specimens from a normal human breast tissue bank. Breast Cancer Research. 16(2):R26

[128] F. Lin, M. Zhao, D.D. Baumann, J. Ping, L. Sun, Y. Liu, B. Zhang, Z. Tang, E. Hughes, R.W. Doerge, T.J. Hughes and J. Ma. 2014. Molecular response to the pathogen phytophthora sojae among ten soybean near isogenic lines revealed by comparative transcriptomics. BMC Genomics. 15(1):18

[129] D.D. Baumann and R.W. Doerge. 2014. MAGI: Methylation analysis using genome information. Epigenetics. 9(5):0-1.

[130] M. Bremer* and R.W. Doerge. 2015. Using R at the Bench: Step-by-Step Analytics for Biologists. Cold Spring Harbor Press. Cold Spring Harbor, NY.

Manuscripts/Chapters Submitted for Publication (8)

Current and former Purdue graduate students denoted by *

[1] M. Tanurdzic, P. L. Auer*, P. Finigan, E. Ernst, B. Dilkes, L. Comai, B. Meyers, M. Vaughn, R.W. Doerge, R. Martienssen. Transposon instability in inter-species hybrids is mediated by RNA interference. Science (under revision).

[2] J. Cardenas-Mora, C. Plachot, L. An*, D. Baumann*, J. Stanley*, H. Adissu, A. Schafer, A. Lipka*, K. Hodges, S. Badve, R.W. Doerge, S. Lelievre. Disruption of tissue polarity modifies the expression of key genes for breast homeostasis and identifies phospholipid synthase, CDS1, as a new candidate in breast cancer. Journal of Pathology.

[3] S. Srivastava* and R.W. Doerge. 2015. Latent process decomposition of high-dimensional count data. Biostatistics.

[4] S. Srivastava* and R.W. Doerge. 2015. Dynamic latent process decomposition of genomic time-course data. Biostatistics.

[5] A.A. Elias*, K.R. Robbins, R.W. Doerge, and M. R. Tuinstra. Half a century of studying genotype by environment interactions in plant breeding experiments. Crop Science.

[6] X. Chen* and R.W. Doerge. 2015. Estimating proportion of nonzero means under certain strong covariance dependence. Electronic Journal of Statistics.

[7] X. Chen* and R.W. Doerge. 2015. Generalized estimators for multiple testing: proportion of true nulls and false discovery rate. Electronic Journal of Statistics.

[8] J.H. Oh*, F. Zheng*, R.W. Doerge, H. Chun. 2015. Kernel partial correlation: A novel approach to capturing conditional independence in graphical models for noisy data. Computational Statistics and Data Analysis.

Manuscripts, Book Chapters, and Books in Progress (4)

Current and former Purdue graduate students denoted by *

[1] C. Ochsenfeld*, K. Jennings, and R.W. Doerge. Bootstrap thresholds for mixed model QTL and association mapping. Genetics.

[2] C. Ochsenfeld*, K. Jennings, and R.W. Doerge. Mixed models for QTL mapping.

[3] M. Bogdan, D.O. Siegmund, P.A. Szulc, H. Tang. 2013. Are "Hot-spots" an indication of complex interactions?

[4] F. Zheng* and R.W. Doerge. Statistical considerations of single-cell sequencing experiments.

Published Abstracts, Non-Refereed Publications, and Conference Proceedings (43)

Current and Purdue graduate students denoted by *

[1] R.W. Doerge. 1988. *Information of Fixed Cluster Samples for Genetic Traits Involving Mixtures of Distributions.* Master of Statistics in Mathematics, University of Utah.

[2] M.M. Shoukri, R.H. Ward, R.W. Doerge. 1989. Statistical inference from the genetic mixture of normal distributions, Proceedings of the 47th Session of the International Statistical Institute.

[3] R.D. Sederoff, D. Grattapaglia, P. Wilcox, J. Chaparro, D. O'Malley, S. McCord, R. Whetten, L. McIntyre, B. Weir, R.W. Doerge, F. Bridgewater, S. Thorpe. 1992. Use of PCR-based RAPD markers for genetic mapping in conifers. Abstracts of papers of the American Chemical Society. 203: 73-BTEC, Part 3.

[4] B.S. Weir and R.W. Doerge. 1992. Statistical issues in the search for QTLs. XVI International Biometric Conference Proceedings, Contributed Papers p. 164.

[5] B.S. Weir and R.W. Doerge. 1993. Biometrical issues in the search for genes affecting quantitative traits. American Statistical Association Annual Meeting Abstracts p311.

[6] R.W. Doerge. 1993. *Statistical Methods for Locating Quantitative Trait Loci with Molecular Markers.* Ph.D. Dissertation. Department of Statistics. North Carolina State University, Raleigh, NC.

[7] G.A. Churchill and R.W. Doerge. 1994. Mapping quantitative trait loci in experimental populations. Proceedings of the Biometric Conference. Ontario, Canada.

[8] R.W. Doerge and G.A. Churchill. 1994. Analysis of molecular marker data. Issues in genetic mapping of quantitative trait loci. Proceedings of the ASHA/CSSA 2nd Joint Plant Breeding Symposium. Corvallis, Oregon.

[9] R.W. Doerge, Z-B. Zeng and B.S. Weir. 1994. Statistical issues in the search for genes affecting quantitative traits in populations. Proceedings of the ASHA/CSSA 2nd Joint Plant Breeding Symposium. Corvallis, Oregon.

[10] R.W. Doerge. 1996. Locating genes in plants, animals and humans using Statistics and Genetics. Sequel. Purdue University School of Science publication.

[11] R.W. Doerge. 1998. Characterizing germplasm collections using molecular markers. Abstracts Proceedings of the American Statistical Association.

[12] R.W. Doerge. 1999. Risk communication for locating quantitative trait loci (QTL) in experimental populations. Abstracts Proceedings of the American Statistical Associa-

tion.

[13] S.M. Brouder, C.H. Nakatsu and R.W. Doerge. 1999. Microbial community dynamics in the rhizosphere of Zea mays L. and Glycine max. Amer. Soc. Agronomy, Salt Lake City, UT (Oct. 31 - Nov. 5, 1999).

[14] C.H. Nakatsu, S.M. Brouder, F. Wanjau, J.D. Wilbur*, and R.W. Doerge. 2000. Impact of tillage and crop rotation on corn development and its associated microbial community. Proceedings of the 15th Conference of the International Soil Tillage Research Organization (ISTRO). July 2-7, 2000. Fort Worth, TX (CD-ROM).

[15] J.D. Wilbur*, S.M. Brouder, C.H. Nakatsu, and R.W. Doerge. 2000. Statistical analysis of rhizosphere microbial communities. In Proceedings of Interface 2000. The 32nd Symposium on the Interface: Computing science and statistics. New Orleans, LA (CD-ROM).

[16] F.M Wanjau, S.M Brouder, C.H. Nakatsu, and R.W. Doerge. 2000. Influence of crop rotation and tillage practices on root architecture of corn and soybean. American Society of Agronomy Abstracts. Minneapolis, MN.

[17] R.J. Roper, R.W. Doerge, K.S.K. Tung, C. Teuscher. 2000. Genetic loci controlling thymectomy-induced autoimmune ovarian dysgenesis. NIH Workshop on The Ovary, Gensis, Function and Failure (Bethesda, MD).

[18] M.A. Black*, B.A. Craig, M.J. Tanurdzic*, and R.W. Doerge. 2001. A Bayesian approach to the analysis of cDNA microarray data. Proceedings of the 33rd Symposium on the Interface.

[19] D.A. Bulinski*, C.H. Nakatsu, J.D. Wilbur*, S. M. Brouder, and R.W. Doerge. 2001. Rhizosphere Microbial population dynamics over three field seasons. American Society of Agronomy Abstracts. Charlotte, NC.

[20] H.-S. Lee, J. Wang, L. Tian, L. Lukens, A. Madlung, M.A. Black*, L. Comai and R.W. Doerge. 2002. Genome-wide expression analysis of orthologous genes in *Arabidopsis* and *Brassica* polyploids. Plant Biology 2002. Denver, CO.

[21] T.C. Osborn, L. Lukens, J.C. Pires, Z.J. Chen, L. Comai, R.W. Doerge, R.A. Martienssen. 2002. Why become a polyploid? Plant and Animal Genome X, p65.

[22] T.C. Osborn, L. Lukens, J.C. Pires, M.E. Schranz, H.-S. Lee, Z.J. Chen, R.W. Doerge. 2002. Gene expression studies in Brassica. 13th Crucifer Genet Workshop Abstracts, p71.

[23] M.A. Black*, B.A. Craig, J. Deely, R.W. Doerge. 2002. Bayesian analysis of cDNA microarray data. Joint Statistical Meetings, p271.

[24] J.D. Wilbur*, J.K. Ghosh, C.H. Nakatsu, S.M. Brouder, R.W. Doerge. 2002. An application of empirical bayes model selection to microbial community fingerprint analysis. Joint Statistical Meetings, p272.

[25] A. Madlung, B. Watson, R. Masuelli, Z. Lippman, V. Colot, R. Martienssen, R.W. Doerge, M. Black, L. Comai, L. 2003. Genetic and epigenetic changes in synthetic allopolyploids of *Arabidopsis thaliana*. Plant and Animal Genome XI, p63.

[26] D. Cao*, B.A. Craig, R.W. Doerge. 2003. A maximum likelihood-based interval mapping model for autopolyploids. Joint Statistical Meetings, p27.

[27] K. Kim* and R.W. Doerge. 2003. Statistical issues in dissecting regulatory networks associated with complex traits: genetic mapping of gene expression levels. Joint Statistical Meetings, p27.

[28] B.A. Craig and R.W. Doerge. 2003. Gene expression data: The technology and statistical analysis. Joint Statistical Meetings, p67.

[29] A. Madlung, B. Watson, H. Jiang*, T. Kagochi, R.W. Doerge, L. Comai, R. Martienssen. 2004. Transposon activation in Arabidopsis neopolyploids. Arabidopsis Meeting, Berlin, Germany.

[30] J. Chen, J. Wang, L. Tian, E. Weil, M. Chen, S. Rao, R.W. Doerge, H. Jiang*, L. Comai, B. Watson. 2005. Transcriptome divergence and mechanisms of non-additive gene regulation in Arabidopsis allopolyploids. International Botanical Congress.

[31] M. Bogdan, J. K. Ghosh, R.W. Doerge, P. Biecek, A. Baierl, A. Futschik, F. Frommlet. 2005. Modified version of Schwarz Bayesian Information Criterion for localization of multiple interacting quantitative trait loci. Paris, France. Annals of Human Genetics.

[32] M. Bogdan, J.K. Ghosh, R.W. Doerge, P. Biecek, A. Baierl, A. Futschik, F. Frommlet. 2005. Modified version of Bayesian Information criterion for localization of multiple interacting quantitative trait loci. Ann. Hum. Gen. 69:765.

[33] M. Vaughn, M. Tanurdzic, Z. Lippman, H. Jiang*, V. Colot, R.W. Doerge, and R. Martienssen. 2005. Epigenomic profiling of Arabidopsis Thaliana. Cold Spring Harbor Laboratory Genome Informatics Meeting. Cold Spring Harbor, NY.

[34] R.A. Martienssen, M. Zaratiegui, D. Irvine, D. Goto, K. Slotkin, M. Tanurdzic, Z. Lippman, M. Vaughn, B. May, Z. Cande, V. Colot, and R.W. Doerge. 2007. Silent running: RNA interference and heterochromatic modification. Chromosome Research 15:20-21 Supplement 2.

[35] R.A. Martienssen, M. Tanurdzic, K. Slotkin, P. Finigan, K. Creasey, P. Auer*, M. Vaughn, J.-P. Vielle-Calzada, and R.W. Doerge. 2011. Heterochromatin reprogramming by small RNA regulates germ cell fate in Arabidopsis. Plant Epigenome Work-

shop. Plant and Animal Genome Conference. San Diego, CA.

[36] J.M. Cardenas-Mora, A. Schafer, C. Plachot, J. Stanley, D. Stegelman, A. Lipka*, D. Baumann*, K. Hodges, K. McDole, L. An*, R.W. Doerge, and S.A. Lelievre. 2011. CDS1, a potential novel marker of breast cancer development. 3rd Annual National Predoctoral Clinical Research Training Program Meeting. St Louis, MO.

[37] S. Chudalyandi, R.W. Doerge, S. Srivastava*, and J. Birchler. 2011. Gene expression profiling in normal and interploidy endosperms of maize. ASPB Plant Biology Meeting.

[38] M. Tanurdzi, P. Auer*, P. Finigan, E. Ernst, B. Dilkes, L. Comai, B.C. Meyers, M.W. Vaughn, R.W. Doerge, R.A. Martienssen. 2011. Small RNA mediate transposon instability in plant inter-specific hybrids in a parent-specific manner. European Science Foundation (ESF) European Molecular Biology Organization (EMBO) "Epigenetics in Context: From Ecology to Evolution". Sant Feliu de Guixols, Spain.

[39] R.J. Roper, C. Billingsley, J. Allen, J. Blazek, D. Baumann, A, Newbauer, A. Darrah1, B.C. Long, B. Young, M. Clement, and R.W. Doerge. 2011. Non-trisomic homebox gene AND sox9 expression alters craniofacial development in a down syndrome mouse model. Mouse Genetics Conference. Washington, D.C.

[40] A.A. Elias, K.R. Robbins, Dev Niyogi, James J. Camberato, R.W. Doerge, and M.R. Tuinstra. 2011. Estimation and prediction of hybrid maize performance in mega-environments and changing climate American Society of Agronomy. San Antonio, TX.

[41] R.A. Martienssen, M. Tanurdzic, P. Baduel, J. Calarco, K. Creasey, F. vanEx, Y. Jacob, P.L. Auer, J.-P. Vielle-Calzada, and R.W Doerge. 2011. RNA interference, heterochromatin reprogramming and germ cell fate. Conference on epigenetics and the inheritance of acquired states. Boston, MA.

[42] R.A. Martienssen, M. Tanurdzic, P.L. Auer, P.E. van Ernst, B.P. Dilkes, L. Comai,B.C. Meyers, M. Vaughn, R.W. Doerge. 2012. Transposon activation in Arabidopsis allopolyploids is mediated by RNA interference. Plant and Animal Genome XX, San Diego, CA.

[43] R.W. Doerge. 2012. Statistical issues and the analysis of next-generation sequencing data. Plant and Animal Genome XX, San Diego, CA.

Invited Presentations/Chaired (1992-present total: 237) 2002-present: 157

Total: Purdue University Presentations (51); Non-Purdue Presentations (186)

[1] Determining Statistically Significant Changes in Gene Expression. (February 2002). Advances in Genome Biology and Technology, Marco Island, FL (invited).

[2] Determining Statistically Significant Changes in Gene Expression. (April 2002). Sloan Kettering Cancer Center, New York, NY (invited).

[3] Determining Statistically Significant Changes in Gene Expression. (May 2002). Evry Genomics Institute and Genoscope, Evry, France (invited).

[4] Determining Statistically Significant Changes in Gene Expression. (May 2002). USDA, Stoneville, MS (invited).

[5] Challenges in Bioinformatics. (June 2002). Workshop on the National Plant Genome Initiative: 2003-2008. National Academy of Sciences, Washington, DC (invited).

[6] Locating QTL. (June 2002, 3 days). The Statistical Genetics Institute, Department of Statistics, North Carolina State University. Raleigh, NC (invited).

[7] QTL Analysis Meets Microarray Analysis. (August 2002). The Joint Statistics Meetings. New York City, NY (invited).

[8] What in the World Does a Statistician Know About Genetics, Farming, and Microbes? (August 2002). Indiana Top Farmers. Purdue University, West Lafayette, IN (invited).

[9] QTL Analysis Meets Microarray Analysis. (August 2002). Bioinformatics Seminar, Purdue University, West Lafayette, IN (invited).

[10] Design and Analysis of Microarray Experiments. (September 2002). National Science Foundation Plant Genome Meeting, Washington, DC (invited).

[11] Old Methods for New Technology. (October 2002). Genomics Conference. Purdue University, West Lafayette, IN (invited).

[12] Determining Statistically Significant Changes in Gene Expression. (October 2002). Worchester Polytech. Institute, Worchester, MA (invited).

[13] Locating and Understanding Genes in Plants Using Statistics. (October 2002). James Madison University, Harrisonburg, VA (invited).

[14] An Introduction to Statistical Genetics/Genomics. (October 2002). VIGRE Seminar: Explore Statistics and Mathematics Research, Purdue University, West Lafayette, IN (invited).

[15] Determining Statistically Significant Changes in Gene Expression. (October 2002). Department of Statistics, University of Georgia, Athens, GA (invited).

[16] Locating QTL. (December 2002, 3 days). The Statistical Genetics Institute, Trinity College, Dublin, Ireland (invited).

[18] Bioinformatics: An Opportunity for Statisticians to Have an Impact on Biology. (December 2002). Department of Statistics, National University of Ireland, Galway, Ireland (invited).

[19] QTL Analysis for Gene Expression Studies. (January 2003). Department of Statistics, University of New Mexico, Albuquerque, NM (invited).

[20] Statistical Genetics. (February 2003). Chaired Session. Gordon Conference on Quantitative Genetics and Genomics. Ventura, CA (invited).

[21] Old Methods for New Ideas: Expression Level Polymorphisms. (March 2003). Stadler Genetics Symposium. University of Missouri, Columbia (invited).

[22] Tutorial on microarray analysis (with Bruce Craig). (June 2003). 7th Purdue Symposium on Statistics, West Lafayette, IN (invited).

[23] Locating QTL. (June 2003, 3 days). The Statistical Genetics Institute, Department of Statistics, North Carolina State University. Raleigh, NC (invited).

[24] Locating QTL. (July 2003, 2 days). The Southern Statistical Genetics Institute, Genetics Congress, University of Melbourne, Australia (invited).

[25] Functional genomics of quantitative traits: expression level polymorphism of QTL. (August 2003) Joint Statistical Meetings, San Francisco, CA (invited).

[26] Using Statistics to Understand the Location and Behavior of Genes. (September 2003). VIGRE Seminar, Purdue University, West Lafayette, IN (invited).

[27] The importance of experimental design and statistical analysis when analyzing microarray data. (September 2003). National Science Foundation, Washington, DC (invited).

[28] Old Methods for New Ideas: Expression Level Polymorphism. (September 2003). Michigan State University, Lancing, MI (invited).

[29] Using expression level polymorphism (ELP) to elucidate regulatory regions in Arabidopsis. (November 2003). American Society for Human Genetics. Los Angles, CA (invited).

[30] Functional genomics of quantitative traits: old methods for new ideas. (January 2004). The International Plant and Animal Genome Conference. San Diego, CA (invited).

[31] Using functional genomics to identify candidate genes. (February 2004). Wyethe. Boston, MA (invited).

[32] QTL mapping in experimental systems. (February 2004). USDA-ARS, University of California, Davis, CA (invited).

[33] Functional genomics of quantitative traits. (March 2004). University of Edinburgh, Edinburgh, Scotland (invited).

[34] Statistical Bioinformatics: Molecular dissection of quantitative trait loci. (March 2004). Purdue University Presidential Reviews of the School of Science. (invited).

[35] QTL mapping. (June 2004). Summer Institute in Statistical Genetics, NC State

University, Raleigh, NC (invited).

[36] New methods for old ideas: expression level polymorphism. (June 2004). Symposium Honoring Bruce Weir, NC State University, Raleigh, NC (invited).

[37] QTL mapping. (July 2004). European Summer Institute in Statistical Genetics, University of Faro, Faro, Portugal (invited).

[38] Locating genes using Statistics. (September 2004). VIGRE Kick-off Seminar, Purdue University, WL, IN (invited).

[39] Identifying determinants of expression level polymorphism. (September 2004). CIGENE - Centre for Integrative Genetics, Agricultural University of Norway, Oslo, Norway (invited).

[40] Identifying determinants of expression level polymorphism. (October 2004). 12th New Phyt Symposium. Gatlinburg, TN (invited).

[41] Mapping Gene Regulation: QTLs and Microarrays. (December 2004). Banbury Center. CSHL, NY (invited).

[42] Meta-analysis combines Affymetrix microarray results across laboratories. (January 2005). The International Plant and Animal Genome Conference. San Diego, CA (invited).

[43] Microarray analysis for Polyploids. (April 2005). Banbury Center. CSHL, NY (invited).

[44] Statistical Analysis of Microarray Data. What are we really testing? (June 2005). American Association for Cancer Research. Focus Group. Landsdowne Resort, VA (invited).

[45] Statistical Bioinformatics. (May 2005). Dean of Science, Purdue University, Advisory Board. (invited).

[46] QTL mapping. (June 2005). Summer Institute in Statistical Genetics, NC State University, Raleigh, NC (invited).

[47] QTL mapping. (July 2005). Asian Summer Institute in Statistical Genetics, Yonsei University, Seoul, Korea (invited).

[48] Using statistics to understand the location and behavior of genes. (October 2005). BYU -Idaho, Idaho Falls, Idaho (invited).

[49] New Advances in Detecting Cancer. (November 2005). Dean of Science and Women in Science Program, Purdue University (invited).

[50] Functional genomics of quantitative traits: Expression level polymorphisms of QTLs affecting disease resistance pathways in arabidopsis. (April 2006). Cold Spring Harbor Laboratory In House (invited).

[51] QTL mapping, permutation thresholds, and e-QTLs. (June 2006). Noble Foundation (invited).

[52] QTL mapping. (June 2006). Summer Institute in Statistical Genetics, University of

Washington, Seattle, WA (invited).

[53] QTL mapping. (July 2006). European Summer Institute in Statistical Genetics, University of Aarhus, Aarhus, Denmark (invited).

[54] Functional genomics of quantitative traits: Expression level polymorphisms of QTLs affecting disease resistance pathways in Arabidopsis. (September 2006). Department of Biostatistics, Washington University, St. Louis, MO (invited).

[55] QTL mapping, permutation thresholds, and e-QTLs. (October 2006). USDA Ag. Station, Lubbock, TX (invited).

[56] Functional genomics of quantitative traits: Expression level polymorphisms of QTLs affecting disease resistance pathways in Arabidopsis. (November 2006). Wellcome Trust Conference on Crop Genomics Trait Analysis and Breeding, Hinxton, UK (invited).

[57] Statistical Issues in Identifying Epigenomic Changes. (January 2007). Genentech, So. San Francisco, CA (invited).

[58] Functional Genomics of Quantitative Traits: Expression Level Polymorphisms of QTLs Affecting Disease Resistance Pathways in Arabidopsis (eQTL). (February 2007). Department of Statistics, Indiana University, Bloomington, IN (invited).

[59] Functional genomics of quantitative traits: Expression level polymorphisms of QTLs affecting disease resistance pathways in Arabidopsis. (February 2007). Gordon Conference on Quantitative Genetics and Genomics, Ventura, CA (invited).

[60] Introduction to QTL mapping. (April 2007). Applied Statistics in Agriculture Keynote Speaker, Kansas State University, Manhattan, KS (invited).

[61] Statistical Issues in the Analysis of Epigenetic Data. (May 2007). The International Conference on Polyploidy, Heterosis, and Epigenetics. Beijing, China (invited).

[62] Functional Genomics of Quantitative Traits: Expression Level Polymorphisms of QTLs Affecting Disease Resistance Pathways in Arabidopsis (eQTL). (May 2007). Workshop: Addiction, Microarrays, and Gene Discovery. National Institute on Drug Abuse (NIDA). Washington, DC (invited).

[63] QTL mapping. (June 2007). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[64] QTL mapping. (August 2007). Asian Summer Institute in Statistical Genetics, National University, Seoul, Korea (invited).

[65] QTL mapping. (September 2007). European Summer Institute in Statistical Genetics, University of Leige, Leige, Belgium (invited).

[66] Part 1: How to Find, Apply, and Interview for a Job (Academic, Industry, etc.). (September 2007). Bioinformatics Seminar. Purdue University (Graduate Student Organization invited).

[67] What Does Statistics Have to do with Genetics? (October 2007). Dean's Honor Semi-

nar, Purdue University (invited).

[68] Statistical Issues in Identifying Epigenomic Changes. (November 2007). First Year Statistics Graduate Seminar, Purdue University (invited).

[69] Functional Genomics of Quantitative Traits: Expression Level Polymorphisms of QTLs Affecting Disease Resistance Pathways in Arabidopsis (eQTL). (November 2007). Department of Statistics, Clemson University, SC (invited).

[70] Statistics in the Era of 'Omics. (November 2007). American Society of Agronomy, New Orleans, LA (invited).

[71] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis (November 2007). Dupont. Wilmington, DE (invited).

[72] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis (November 2007). Cornell University, Ithaca, NY (invited).

[73] Part 2: How to Preparation, Interview, Negotiate, and Accept/Decline a Job (Academic, Industry, etc.). (December 2007). Bioinformatics Seminar. Purdue University (Graduate Student Organization invited).

[74] Statistical Issues When Analyzing Epigenetic Data. (February 2008). 4th Course on Epigenetics. Institute Curie, Paris, France (invited).

[75] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis. (March 2008). South African Genetics Congress. University of Pretoria, Pretoria, South Africa (invited).

[76] Interdisciplinary Research and the Importance of Networking. (April 2008). Women in Science Program. Purdue University (invited).

[77] Statistical Issues When Analyzing Epigenomic Data. (April 2008). Epigenetics Workshop. Foundation des Treilles. Chemin des Treilles, France (invited).

[78] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis. (June 2008). Women in Genomics Science (WIGS). University of Washington, Seattle, WA.

[79] QTL mapping. (June 2008). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[80] The Importance of Statistics in the Era of 'Omics. (September 2008). 9th New Phytologist Symposium - Physiological Sculpture of Plants: new visions and capabilities for crop development. Timberline Lodge, Mount Hood, OR.

[81] What Does Statistics Have to do with Genetics? (October 2008). Dean's Honor Seminar, Purdue University (invited).

[82] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis. (November 2008). Australiasia Microarray and Associated Technology meeting. Dunedin, New Zealand.

[83] QTL mapping. (December 2008). Summer Institute in Statistical Genetics, University of Auckland, Auckland, NZ (invited).

[84] Whole Genome Expression Quantitative Trait Loci (eQTL) Analysis of Arabidopsis. (January 2009). Dow Agro Sciences, Indianapolis, IN (invited).

[85] Statistical Issues in the Analysis of Epigenomic Data Gained From Array Technologies. (January 2009). Plant and Animal Genome Meeting. San Diego, CA (invited).

[86] Introduction to QTL Mapping in Experimental Populations. (February 2009.) Bioinformatics Seminar. Purdue University, West Lafayette, IN (invited).

[87] eQTL Mapping in Arabidopsis. (February 2009). Bioinformatics Seminar. Purdue University, West Lafayette, IN (invited).

[88] The Design and Analysis of Gene Expression Experiments in Maize Polyploids. (May 2009). International Conference on Polyploidy, Hybridization and Biodiversity. Palais du Grand Large, Saint Malo, France (invited).

[89] QTL mapping. (June 2009). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[90] Statistical Challenges in Modelling Expression Quantitative Traits and Gene Networks. (July 2009). 24th International Workshop on Statistical Modelling. Cornell University, Ithaca, NY (invited).

[91] Developing Statistics Programs for Majors Outside of Statistics and Expanding Interdisciplinary Cooperation. (August 2009) Heads/Chairs Workshop, American Statistical Association. Arlington, VA (invited).

[92] Statistical Issues and Challenges of Epigenomics. (August 2009). Impact of High-Dimensional Data on Molecular Epidemiology and Statistical Genomics Invited Session. Joint Statistics Meetings, Washington, DC (invited).

[93] QTL mapping. (September 2009). Summer Institute in Statistical Genetics, University of Liege. Liege, Belgium (invited).

[94] Gene networks from eQTL; Are We There Yet? (September 2009). Genes, Systems and Phenotypes, Modelling Networks from Sequence to Consequence GENESYS meeting at ECCS09 (keynote speaker). University of Warwick, Warwick, UK.

[95] Statistics, Epigenomics, and Cancer. (September 2009). Exploring Statistical Sciences Research Seminar. Purdue University (invited).

[96] What is a Statistician and What Do They Do? And What does it have to do with genetics? (November 2009). Freshman Mathematics Seminar. Purdue University (invited).

[97] What is the Difference Between CVs and Resumes? (January 2010). Women In Science Program (WISP), Purdue University (invited).

[98] Part 1: Beginning a Job Search: Academic, Industry, Government... (January 2010).

Bioinformatics Seminar, Purdue University (invited).

[99] Part 2: The Job Interview and What to do When You Get an Offer (Academic, Industry, etc.). (March 2010). Bioinformatics Seminar, Purdue University (invited).

[100] QTL mapping. (June 2010). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[101] Modeling Differential Expression in RNA-Seq Data. (August 2010). Impact of Statistics on Next Generation Sequencing, Joint Statistics Meetings, Vancouver, BC (invited).

[102] QTL mapping. (August 2010). Summer Institute in Statistical Genetics, Peking University, Beijing, China (invited).

[103] Statistical Issues When Modeling RNA-Seq Data for Differential Expression. (October 2010). Department of Biostatistics, Indiana University Purdue University, Indianapolis (IUPUI), IN (invited).

[104] Statistical Issues When Modeling RNA-Seq Data for Differential Expression. (November 2010). Department of Applied and Computational Mathematics and Statistics, Notre Dame University, South Bend, IN (invited).

[105] Statistical Issues When Modeling RNA-Seq Data for Differential Expression. (November 2010). Cold Spring Harbor Laboratory. Cold Spring Harbor, NY (invited).

[106] Statistical Issues When Modeling RNA-Seq Data for Differential Expression. (January 2011). Next Generation Sequencing Symposium. Indianapolis, IN (invited).

[107] Statistical Issues When Modeling RNA-Seq Data for Differential Expression. (March 2011). International Biometrics Society Eastern North American Region meeting. Miami, FL (invited).

[108] High-dimensional QTL mapping in Arabidopsis. (March 2011). Kavli Royal Society International Centre, Buckinghamshire, UK (invited).

[109] A Two-Stage Poisson Model for Testing RNA-Seq Data. (April 2011). Departments of Plant Science and Statistics; University of Missouri, Columbia, MO (invited).

[110] A Two-Stage Poisson Model for Testing RNA-Seq Data. (April 2011). Department of Biological Statistics and Computational Biology. Cornell University, Ithaca, NY (invited).

[111] QTL mapping. (June 2011). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[112] Part 1: Beginning a Job Search: Academic, Industry, Government... (August 2011). Bioinformatics Seminar, Purdue University, West Lafayette, IN (invited).

[113] Part 2: The Job Interview and What to do When You Get an Offer (Academic, Industry, etc.). (September 2011). Bioinformatics Seminar, Purdue University, West Lafayette, IN (invited).

[114] QTL mapping. (September 2011). European Summer Institute in Statistical Genetics,

University of Washington, Seattle, WA (invited).

[115] Large Scale Epigenome Analysis. (October 2011). International Breast Cancer and Nutrition Conference. Rennes, France (invited).

[116] Statistics, Technology, Epigenomics and our Future. (October 2011). Department of Mathematics, Trinity University, San Antonio, TX (invited).

[117] Statistical Issues and the Analysis of Next-Generation Sequencing Data. (January 2012). Plant and Animal Genome XX, San Diego, CA (invited).

[118] Modeling Next-Generation Sequencing Data and Related Statistical Issues. (March 2012). Department of Statistics. Iowa State University. Ames, IA (invited).

[119] Modeling Next-Generation Sequencing Data and Related Statistical Issues. (April 2012). Department of Statistics. University of Nebraska, Lincoln, NB (invited).

[120] A Conversation About the Role(s) of Statistical Bioinformatics in a Department of Statistics, and at a University. (April 2012). Department of Statistics. University of Nebraska, Lincoln, NB (invited).

[121] Job Interviewing Skills. (April 2012). Purdue University Graduate Student Association. Purdue University. West Lafayette, IN (invited).

[122] Modeling Next-Generation Sequencing Data and Related Statistical Issues. (May 2012). Department of Statistics. Northwestern University, Evanston, IL (invited).

[123] QTL mapping. (June 2012). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[124] Modeling Next-Generation Sequencing Data and Related Statistical Issues. (August 2012). Department of Statistics and the Department of Genetics. University of Georgia, Athens, GA (invited).

[125] Self Promotion Techniques and Interview Skills. (September 2012). Women in Science Program. Purdue University. West Lafayette, IN (invited).

[126] Statistical Issues in Plant Genomic Data. (January 2013). SAS Plant Genome Workshop. Plant and Animal Genome Conference. San Diego, CA (invited).

[127] Part 1: Beginning a Job Search: Academic, Industry, Government... (January 2013). Bioinformatics Seminar. Purdue University.

[128] Part 2: The Job interview and What to do When You Get an Offer (academic, industry, etc.). (January 2013). Bioinformatics Seminar. Purdue University.

[129] Introduction to Systems Genetics Session. (February 2013). Gordon Conference on Quantitative Genetics and Genomics. Galveston Island, TX (invited).

[130] Statistical Bioinformatics: Statistical Analysis of 'Omic Data. (March 2013). Qatar Computing Research Institute. Doha, Qatar (invited).

[131] The Job Interview and What to do When You Get an Offer (academic, industry, etc.). (March 2013). Postdoctoral Association, Purdue University (invited).

[132] Conversation about Academics. (March 2013). Association for Women in Mathematics. Purdue University.

[133] Modeling Next-Generation Sequencing Data and Related Statistical Issues. (April 2013). Department of Mathematics. Ball State University, Munice, IN (invited).

[134] QTL mapping. (July 2013). Summer Institute in Statistical Genetics, University of Washington, Seattle, WA (invited).

[135] Analyzing Next-Generation Sequencing Data and Related Statistical Issues. (August 2013). Department of Genetics and Department of Statistics. University of Georgia, Athens, GA (invited).

[136] Common Themes in Statistical Bioinformatics Analysis. (August 2013). Joint Statistics Meetings. Montreal, Canada (invited).

[137] Analyzing Next-Generation Sequencing Data and Related Statistical Issues. (November 2013). Synbreed. Munich, Germany (invited).

[138] Correcting for Amplification Bias in Next-Generation Sequencing Data. (November 2013). "Impact of Large scale Omic Data on Statistical and Quantitative Genetics", University of Washington, Seattle, WA (invited).

[139] Correcting for Amplification Bias in Next-Generation Sequencing Data. (December 2013). The Ninth ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data, Hong Kong Baptist University, Hong Kong (invited).

[140] Correcting for Amplification Bias in Next-Generation Sequencing Data. (January 2014). Plant and Animal Genome Meeting. San Diego, CA (invited).

[141] Correcting for Amplification Bias in Next-Generation Sequencing Data. (February 2014). Bioinformatics Seminar Series. Purdue University (invited).

[142] Challenges in Bioinformatics. (April 2014). Indiana Clinical and Translational Science Institute Retreat. Purdue University (invited).

[143] MAGI: Methylation Analysis using Genome Information. (April 2014). Applied Statistics in Agriculture Conference. Kansas State University. Manhattan, KS. (invited).

[144] Growing your Research Program: When, Why, and How. (May 2014). Celebrating Women in Statistics: Know Your Power. Durham, NC. (invited).

[145] Correcting for Amplification Bias in Next-Generation Sequencing Data. (June 2014). Chengdu University. Chengdu, China. (invited).

[146] QTL mapping. (July 2014). Summer Institute in Statistical Genetics, University of Washington. Seattle, WA (invited).

[147] Correcting for Amplification Bias in Next-Generation Sequencing Data. (August 2014). Joint Statistics Meetings. Boston, MA. (invited).

[148] Analyzing Next-Generation Sequencing Data and Related Statistical Issues. (August 2014). Molecular Biology Institute Summer Undergraduate Research Program. The Ohio State University. Columbus, OH.

[149] Wanted: Large Complex Omic Data Seeking Quantitative Reasoning and Analysis. (September 2014). Opening Workshop on Beyond Bioinformatics. Statistics and Applied Mathematics Institute (SAMSI). Durham, NC. (invited).

[150] The Impact of Academic Mentoring on the Work Environment. Provost ASSIST Program. North Carolina State University. Raleigh, NC. (invited).

[151] Correcting for Amplification Bias in Next-Generation Sequencing Data. (September 2014). Department of Genetics, North Carolina State University. Raleigh, NC. (invited).

[152] RASTA: Robust Adjustment of Sequence Tag Abundance in Next-Generation Sequencing Data. (October 2014). Department of Plant Sciences. University of Missouri. Columbia, MO. (invited).

[153] The Path to Success Isnt Always Linear: One Statisticians Not Boring and Nonlinear Story Forward. (November 2014). Department of Statistics, Undergraduate Statistics Club; North Carolina State University. Raleigh, NC. (invited).

[154] The Role and Importance of Modern Interdisciplinary Statistics in Academics. (December 2014). Northeastern University. Boston, MA. (invited).

[155] Part 1: Beginning a Job Search: Academic, Industry, Government... (January 2015). Purdue University (invited).

[156] Wanted: Large Complex Omic Data Seeking Quantitative Reasoning and Analysis. (March 2015). The Challenge of Inference from Genome to Phenome. The Commonwealth Scientific and Industrial Research Organization (CSIRO). Brisbane, Australia (invited).

[157] Introduction to Quantitative Trait Locus (QTL) in Experimental Populations. (March 2015). Bioinformatics Seminar. Purdue University (invited).

Posters (93)

Current and former Purdue graduate students denoted by *

[1] Rapid Chain Delineation (RCD) for mapping genetic markers. 1992. R.W. Doerge. Conference of the Program in Mathematics and Molecular Biology. Santa Fe, NM.

[2] Quantitative trait mapping. 1994. G.A. Churchill and R.W. Doerge. The Second International Conference on the Plant Genome. San Diego, CA.

[3] QTL analysis of the production of acylsugars responsible of pest resistance in the wild tomato, *Lycopersicon Pennellii*. 1995. R.W. Doerge and M.A. Mutschler. The Third International Conference on the Plant Genome. San Diego, CA.

[4] Empirical threshold values for locating QTL. 1995. R.W. Doerge and G.A. Churchill. The Third International Conference on the Plant Genome. San Diego, CA.

[5] Comparative genetic mapping and QTL analysis of *Saccharum* L. (Sugarcane) and its relation to sorghum and maize. 1998. R.W. Doerge. The Sixth International Conference on the Plant and Animal Genome. San Diego, CA.

[6] Locating binary trait loci using regression. 1998. R.W. Doerge. The Sixth International Symposium on Statistics. Statistical Genetics Workshop. West Lafayette, IN.

[7] Interacting quantitative trait loci control phenotypic variation in murine estradiol-regulated responses. 1998. R.W. Doerge. The Sixth International Symposium on Statistics. Statistical Genetics Workshop. West Lafayette, IN.

[8] Evolution of JQTL to JAG. 1999. R.W. Doerge. The VII International Conference on the Plant and Animal Genome. San Diego, CA.

[9] Microbial community dynamics in the rhizosphere of Zea mays L. and Glycine max. J. Wilbur *, S.M. Brouder, C.H. Nakatsu. 1999. Division Z-4, NRICGP Special Poster Session. American Society of Agronomy. Salt Lake City, UT.

[10] Identification of new QTL controlling day three thymectomy induced autoimmune ovarian dysgenesis using new quantitative genetics approaches. R.J. Roper, R.W. Doerge, R.G. Ma, K.S.K. Tung, and C. Teuscher. 1999. FASEB Summer Research Conference on Autoimmunity. Saxton River, VT.

[11] Multiple sexually dimorphic quantitative trait loci (QTL) control histopathology in EAE. R.J. Butterfield, E.P. Blankenhorn, J.F. Zachary, R.J. Roper, R.W. Doerge, and C. Teuscher. 1999. FASEB Summer Research Conference on Autoimmunity. Saxton River, VT.

[12] A novel methodological approach to the genetic analysis of day three thymectomy induced autoimmune ovarian dysgensis. R.J. Roper, R.W. Doerge and C. Teuscher. 1999. University of Illinois 6th Biennial Retreat in Reproductive Biology. Allerton, IL.

[13] Rhizosphere bacterial population dynamics and root architecture. J. Wilbur*, R.W. Doerge, C. Nakatsu, and S. Brouder. 1999. Annual Meetings of the American Society of Agronomy, Crop Science Society of America, and the Soil Science Society of America. Salt Lake City, UT.

[14] Conditional permutation based confidence measures for cluster groupings. B. Munneke*, W.D. Beavis, and R.W. Doerge. 1999. Gene Expression Analysis Conference. Lake Tahoe, CA.

[15] Detection and location of a single binary trait locus in experimental populations. C. Coffman, R.W. Doerge, and L.M. McIntyre. 2000. The VIII International Conference on Plant and Animal Genome. San Diego, CA.

[16] Conditional permutation based confidence measures for cluster groupings. B. Munneke*, W.D. Beavis, and R.W. Doerge. 2000. The VIII International Conference on Plant and

Animal Genome. San Diego, CA.

[17] Statistical analysis of bacterial communities. J. Wilbur*, C. Nakatsu, S. Brouder, J.K. Ghosh, and R.W. Doerge. 2000. 23rd Annual Midwest Biopharmaceutical Statistics Workshop. Muncie, IN.

[18] Calculating the number of per gene replicate spots required for microarray expression experiments. M.A. Black* and R.W. Doerge. 2001. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[19] Compound hypothesis testing in QTL analysis. C. Coffman, R.W. Doerge, and L. McIntyre. 2001. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[20] Detection and localization of multiple binary trait loci in experimental populations. C. Coffman, R.W. Doerge, L. McIntyre, K. Simonsen. 2001. International Biometrics Society Eastern North American Region meeting. Charlotte, NC.

[21] Compound hypothesis testing in QTL analysis. C. Coffman, R.W. Doerge, and L. McIntyre. 2001. International Biometrics Society Eastern North American Region meeting. Charlotte, NC.

[22] A penalized distance measure and permutation based confidence measure applied to gene expression data. B. Munneke*, W. Beavis, K.A. Schlauch, and R.W. Doerge. 2001. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[23] Genetic analysis of immunoregulation using a day three thymectomy model. R.J. Roper, J.O.Biggins, S. Ming, R.D. McAllister, S.D. Michael, K.S.K Tung, R.W. Doerge, and C. Teuscher. 2001. Annual Bar Harbor Short Course. Bar Harbor, ME.

[24] An overview of linear models techniques for the analysis of microarray data. M.A. Black*, B.A. Craig, M.J. Tanurdzic*, J.L. Bennetzen, and R.W. Doerge. 2002. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[25] Detection and localization of multiple binary trait loci in experimental populations. C.J. Coffman, K.L. Simonsen, R.W. Doerge, and L.M. McIntyre. 2002. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[26] Retroarray-microarray analyses of LTR retrotransposons in the maize genome. M.A. Black*, B.A. Craig, M.J. Tanurdzic*, J.L. Bennetzen, O. Vitek*, and R.W. Doerge. 2002. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[27] Development of a database for the functional and expression annotation of sequence tags (FEAST) in the pig. D. Moody, W. Aref, L. McIntyre, M. Mokbel, A. Valova*, R.W. Doerge, and C. Bidwell. 2002. The International Conference on Plant and Animal Genome Research. San Diego, CA.

[28] Quantitative trait locus analysis in polyploids. D. Cao*, B.A. Craig, and R.W. Doerge. 2002. International Biometrics Society Eastern North American Region. Arlington, VA.

[29] Nonparametric discriminant analysis for class prediction using gene expression data. K. Kim* and R.W. Doerge. 2002. International Biometrics Society Eastern North American Region. Arlington, VA.

[30] Quantitative trait locus analysis in polyploids. D. Cao*, B.A. Craig, and R.W. Doerge. 2002. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[31] Nonparametric discriminant analysis for class prediction using gene expression data. K. Kim* and R.W. Doerge. 2002. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[32] Statistical analysis of a macroarray experiment testing differential expression of genes involved in the initial stages of Agrobacterium-mediated transformation. Hongmei Jiang* and R.W. Doerge. 2002. The 25th Anniversary Midwest Biopharmaceutical Statistics Workshop (MBSW). Ball State University. Muncie, IN.

[33] Nonparametric discriminant analysis for class prediction using gene expression data. K. Kim* and R.W. Doerge. 2002. The 25th Anniversary Midwest Biopharmaceutical Statistics Workshop (MBSW). Ball State University. Muncie, IN.

[34] Quantitative trait locus analysis in polyploids. D. Cao*, B.A. Craig, and R.W. Doerge. 2002. The 25th Anniversary Midwest Biopharmaceutical Statistics Workshop (MBSW). Ball State University. Muncie, IN.

[35] Statistical analysis of a macroarray experiment testing differential expression of genes involved in the initial stages of Agrobacterium-mediated transformation. Hongmei Jiang* and R.W. Doerge. 2003. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[36] Expression level polymorphism analysis for dissecting regulatory networks of plant disease resistance: genetic mapping of gene expression levels. Kyunga Kim* and R.W. Doerge. 2003. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[37] Statistical analysis of a macroarray experiment testing differential expression of genes involved in the initial stages of Agrobacterium-mediated transformation. Hongmei Jiang* and R.W. Doerge. 2003. Joint Statistics Meetings. San Francisco, CA.

[38] Functional genomics of plant polyploids: research on the effects of polyploidy in Arabidopsis, Brassica, and corn. J.C. Pires, J. Birchler, Z.J. Chen, L. Comai, R.W. Doerge, R. Martienssen, and T. Osborn. 2004. The International Plant and Animal Genome meeting. San Diego, CA.

[39] Polyploidy dependent transcriptome changes in arabidopsis J. Wang, L. Tian, J. Wang, H.-S. Lee, J.J. Lee, H. Jiang, B. Watson, L. Comai, R.W. Doerge, and Z.J. Chen. 2004. The International Plant and Animal Genome meeting. San Diego, CA.

[40] Meta-Analytic approaches to microarray analysis. John Stevens* and R.W. Doerge. 2004. 16th Kansas State University Conference on Applied Statistics. Manhattan, KS.

[41] Statistical issues of protein microarray analysis. Lianbo Yu* and R.W. Doerge. 2004. 16th Kansas State University Conference on Applied Statistics. Manhattan, KS.

[42] Meta-analysis combines Affymetrix microarray results across laboratories. J. Stevens* and R.W. Doerge. 2004. First Annual Indiana Bioinformatics Conference. IUPUI. Indianapolis, IN.

[43] Statistical issues of protein microarray analysis. Lianbo Yu* and R.W. Doerge. 2004. The Joint Statistical Meetings. Toronto, Canada.

[44] Meta-analysis combines Affymetrix microarray results across laboratories.J. Stevens* and R.W. Doerge. 2004. The Joint Statistical Meetings. Toronto, Canada.

[45] Methylscope and Methylscreen Technologies: Genome-wide DNA methylation biomarker discovery and detection. H. Holemon, Y. Korshunova, J. Ordway, J. Fries, M. Smith, D. Cao*, R.W. Citek., A. Nunberg, D. Robbins, J. Bedell, R.W. Doerge, J.D. McPherson, and J.A. Jeddeloh. 2004. 69th Epigenetics Symposium/ Cold Spring Harbor Laboratory. Cold Spring Harbor, NY.

[46] Progenitor-dependent gene expression and evolution of transcriptome in Arabidopsis allopolyploids. J. Wang, L. Tian, H.-S. Lee, M. Chen, J.J. Lee, J.J. Wang, N.E. Wei, S, Rao, H. Jiang*, B. Watson, A. Madlung, R.W. Doerge, T. Osborn, L. Comai, and Z.J. Chen). 2004. The 15th International Conference on Arabidopsis Research. Berlin, Germany.

[47] Transposon activation in Arabidopsis neopolyploids. A. Madlung, B. Watson, H. Jiang*, T. Kagochi, R.W. Doerge, L. Comai, R. Martienssen. 2004. The 15th International Conference on Arabidopsis Research. Berlin, Germany.

[48] MethylScope and MethylScreen technologies: Genome-wide DNA methylation biomarker discovery and detection. Y. Korshunova, J.M. Ordway, H. Holemon, M. Smith, J.R. Stevens*, J. Fries, R.W. Citek, A. Nunberg, A. Robbins, J.A. Bedell, N. Lakey, J.D. McPherson, R.W. Doerge, and J.A. Jeddeloh. 2004. Chromatin, Chromosomes, and Cancer Epigenetics: An American Association for Cancer Research Special Conference on Cancer Research. Waikoloa, HA.

[49] Non-Host resistance of barley to the septoria tritici blotch pathogen of wheat involves an active defense response. S.B. Goodwin, J.D. Breeden, J.R. Stevens*, and R.W. Doerge. 2005. Plant and Animal Genome Conference. San Diego, CA.

[50] Novel use of Spearman's rank correlation to categorize RNA abundance differences detected on Affymetrix Genechips as expression polymorphisms or sequence polymorphisms. M.A.L. West, K. Kim*, R. Walker, R.W. Michelmore, R.W. Doerge, and D.A. St.Clair. 2005. The International Plant and Animal Genome meeting. San Diego, CA.

[51] Model selection in binary trait locus mapping. C. Coffman, R.W. Doerge, K.Simonsen, K. Nichols, C. Duarte, R Wolfinger, L.M. McIntyre. 2005. Quantitative Genetics and Genomics Gordon Research Conference. Ventura, CA.

[52] Global mapping of expression QTLs in an Arabidopsis RIL population. M.A.L. West,

K. Kim*, H. van Leeuwen, R.W. Michelmore, R.W. Doerge, and D.A. St.Clair. 2006. Plant and Animal Genome Conference. San Diego, CA.

[53] High-density haplotyping with microarray-based single feature polymorphism markers in Arabidopsis. H. van Leeuwen, M.A.L. West, A. Kozik, D.J. Kliebenstein, R.W. Doerge, D.A. St.Clair, and R.W. Michelmore. 2006. Plant and Animal Genome Conference. San Diego, CA.

[54] Gene expression markers: using transcript levels obtained from microarrays to genotype a segregating population. M.A.L. West, H. van Leeuwen, A. Kozik, D.J. Kliebenstein, R.W. Michelmore, R.W. Doerge, and D.A. St.Clair. 2006. Plant and Animal Genome Conference. San Diego, CA.

[55] Faze-O-Matic an algorithm for detecting phased siRNA biogenesis and calculating its probability. M.W. Vaughn, M.J. Ronemus, R.W. Doerge, and R.A. Martienssen. 2006. Cold Spring Harbor Laboratory Symposium on Epigenetics. Cold Spring Harbor, NY.

[56] Multiple trait QTL mapping and its application to expression trait (e-Trait) data. R. Cheng* and R.W. Doerge. 2007. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[57] Combining the results from gene expression, methylation, and ChIP-chip microarray statistical analyses. S.-Y. Yoo* and R.W. Doerge. 2007. Applied Statistics in Agriculture. Kansas State University. Manhattan, KS.

[58] Tiling Microarrays: Possibilities and challenges for the future. G. Olbricht*, H. Walia, L. Comai, and R.W. Doerge. 2008. National Science Foundation GK-12 Annual Meeting. Washington D.C.

[59] Integrating genomic and quantitative trait data. T.Achberger*, I. Baxter, J. Fleet, D. Salt, and R.W. Doerge. 2008. Applied Statistics in Agriculture Conference. Kansas State University. Manhattan, KS.

[60] Copy number variant discovery via analysis of data from the Solexa sequencer. P. Livermore Auer* and R.W. Doerge. 2008. Applied Statistics in Agriculture Conference. Kansas State University. Manhattan, KS.

[61] Affymetrix Tiling Arrays: Challenges for the future. G. Olbricht*, H. Walia, L. Comai, and R.W. Doerge. 2008. Applied Statistics in Agriculture Conference. Kansas State University. Manhattan, KS.

[62] Disruption of apical polarity in mammary epithelium is associated with the transcriptional down regulation of genes linked to cellular homeostasis and breast cancer. C. Plachot, J. Stanley*, L. An*, H. Adissu, R.W. Doerge, and S. Lelievre. 2008. American Society Cell Biology Meeting. San Diego, CA.

[63] Disruption of apical polarity in mammary epithelium is associated with the transcriptional down-regulation of genes linked to cellular homeostasis and breast cancer. J. Cardenas, J. Stanley*, C. Plachot, L. Chaboub, A. Lipka*, L. An*, H. Adissu, R.W. Doerge, and S. Lelievre. 2008. Cancer Prevention Retreat & Poster Session. Purdue

University. West Lafayette, IN.

[64] An empirical bayes approach to inferring genetic regulatory interactions with dynamic Bayesian networks. A Rau*, F. Jaffrezic, J.-L. Foulley, and R.W. Doerge. 2009. Gordon Conference on Quantitative Genetics and Genomics. Galveston Island, TX.

[65] Novel directions in breast cancer prevention: the link between tissue polarity and lipid pathways via CDP-diacylglycerol synthase 1 (CDS1). A. Schafer, J. Cordenas-Mora, C. Plachot, J. Stanley*, K. Hodges, L. An*, A. Lipka*, R.W. Doerge, and S. Lelievre. 2009. Cancer Prevention Retreat & Poster Session. Purdue University. West Lafayette, IN.

[66] New markers of early stages of breast cancer development: significance of apical polarity alterations in glandular structures. D.A. Stegelman, A. Lipka*, J. Cordenas-Mora, J.A. Stanley*, E. Retsek, D.D. Baumann*, H.A. Adissu, R.W. Doerge, and S.A. Lelievre. 2009. Cancer Prevention Retreat & Poster Session. Purdue University. West Lafayette, IN.

[67] Novel directions in breast cancer prevention: the link between tissue polarity and lipid pathways via CDP-diacylglycerol synthase 1 (CDS1). A. Schafer, J. Cordenas-Mora, C. Plachot, J. Stanley*, K. Hodges, L. An*, A. Lipka*, R.W. Doerge, and S.A. Lelievre. 2009. (1st Place Undergraduate Poster Presentation). Purdue Cancer Prevention and Healthcare Retreat. West Lafayette, IN.

[68] Genomics and epigenomics of Arabidopsis interspecies hybrids. M. Tanurdzic, P. Auer*, P. Finigan, M. Vaughn, R.W. Doerge, and R.A. Martienssen. 2010. Keystone Symposia on RNA Silencing Mechanisms in Plants. Santa Fe, NM.

[69] Nutrition-based breast cancer prevention: conjugated linoleic acid influences apical polarity and proliferation modulator sprouty. K. McDole, M. Downey, A. Lipka*, D. Baumann*, R.W. Doerge, and S. Lelievre. 2010. Annual Amelia Project Retreat. University Conference Center, Indiana University. Indianapolis, IN.

[70] Integrating epigenetic information with next-generation sequencing data. D. Baumann* and R.W. Doerge. 2010. Kansas State University Conference on Applied Statistics in Agriculture. Manhattan, KS.

[71] A non-parametric empirical Bayesian approach for estimating tag abundance in next generation sequencing data. S. Srivastava* and R.W. Doerge. 2010. Kansas State University Conference on Applied Statistics in Agriculture. Manhattan, KS.

[72] CDS1: A new marker for nutritional effects on breast cancer development? A. Schafer, J. Cardenas-Mora, C. Plachot, J. Stanley*, D. Stegelman*, A. Lipka*, D. Baumann*, K. Hodges, K. McDole, L. An*, R.W. Doerge, and S.A. Lelievre. 2010. The International Symposium on Breast Cancer Prevention. Purdue University. West Lafayette, IN.

[73] Genome dosage effects on heterosis and gene expression in triploid hybrids of maize. H. Yao, L. An*, R.W. Doerge, and J. Birchler. 2011. Maize Meeting. Chicago, IL.

[74] Comparison of inbreeding depression between diploid and tetraploid maize. H. Yao, S.

Srivastava*, R.W. Doerge, and J. Birchler. 2011. Maize Genetics Meeting. St. Charles, IL.

[75] A hierarchical Bayesian approach for detecting differential expression in unreplicated RNA-sequencing data. S. Srivastava*, and R.W. Doerge. 2011. Gordon Research Conferences in Quantitative Genetics and Genomics, Galveston, TX.

[76] Polarity-dependent genes as targets for the prevention of breast cancer development: The example of CDS1. J. Cardenas-Mora, A. Schafer, K.B. Hodges, A. Lipka*, D. Baumann*, M. Bina, S. Badve, R.W. Doerge, S.A. Lelievre. 2011. The International Symposium on Breast Cancer Prevention Symposium. Rennes, France.

[77] Latent process decomposition of next-generation sequencing data. S. Srivastava* and R.W. Doerge. 2011. Case Studies in Bayesian Statistics and Machine Learning. Carnegie Mellon University, Pittsburgh, PA.

[78] Latent process decomposition of next-generation sequencing data. S. Srivastava* and R.W. Doerge. 2011. BioC Conference. Fred Hutchinson Cancer Research Center, Seattle, WA.

[79] Latent process decomposition of next-generation sequencing data. Srivastava* and R.W. Doerge. 2011. 5th Annual Bayesian Biostatistics Conference, Department of Biostatistics at The University of Texas MD Anderson Cancer Center, Houston, TX.

[80] Latent process decomposition of next-generation sequencing data. S. Srivastava* and R.W. Doerge. 2011. Dow AgroSciences-Purdue Workshop on Utilizing "Omic" Technologies to Accelerate Crop Improvement, Purdue Research Park, West Lafayette, IN.

[81] Random regression models: incorporating weather and soil information for prediction of genotype by environment interactions. A.A. Elias*, K.R. Robbins, D. Niyogi, J.J. Camberato, R.W. Doerge, M.Tuinstra. 2012. Plant and Animal Genome XX. San Diego, CA.

[82] Estimating environmental variables influencing hybrid maize performance across the United State Corn Belt. 2012. A.A. Elias*, K.R. Robbins, D. Niyogi, J.J. Camberato, R.W. Doerge and M.R. Tuinstra. Maize Meeting. Portland, OR.

[83] Identifying targets for the prevention of breast cancer development: How CDS1 came to be known in aggressive forms of breast tumors. 2012. J. Cardenas-Mora, D. Baumann*, K.B. Hodges, K. McDole, D. Stegelman, S. Badve, A. Schafer, A. Lipka*, R.W. Doerge, S.A. Lelievre. Purdue's Office of Interdisciplinary Graduate Programs (OIGP) Spring reception. Purdue University. West Lafayette, IN.

[84] Identification of a novel gene for breast cancer prevention: The rise of CDS1 as an early marker of modifications in breast epithelial homeostasis. 2012. J. Cardenas-Mora; D. Baumann*; K.B. Hodges; K. McDole, D. Stegelman, A. Schafer, A. Lipka*, M. Bina, R.W. Doerge, S. Badve, S.A. Lelievre. The National Clinical and Translational Sciences Predoctoral Programs Meeting Navigating the Path to Translation. Mayo Clinic Campus. Rochester, MN.

[85] Third-Generation Sequencing: The Possibilities and Challenges of Single Molecule Technologies. 2012. F.H. Zheng*, Lin-Yang Cheng*, and R.W. Doerge. Kansas State University Conference on Applied Statistics in Agriculture. Manhattan, KS.

[86] Latent process decomposition of next- generation sequencing data. 2012. S. Srivastava* and R.W. Doerge. Machine Learning: Theory and Computation, Institute of Mathematics and its Applications, University of Minnesota, Minneapolis, MN.

[87] Latent process decomposition of next- generation sequencing data. 2012. S. Srivastava* and R.W. Doerge. 8th International Purdue Symposium on Statistics, Purdue University, West Lafayette, IN.

[88] Latent process decomposition of next- generation sequencing data. 2012. S. Srivastava* and R.W. Doerge. Joint Statistical Meetings, San Diego, CA.

[89] Correcting for amplification bias in next-Generation sequencing data. 2012. D. Baumann* and R.W. Doerge. 8th International Purdue Symposium on Statistics, West Lafayette, IN.

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