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CURRICULUM VITAE

Karl W. Broman

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EDUCATION

1997 – 1999	Postdoctoral Fellow, Center for Medical Genetics, Marshfield Medical Research Foundation, Marshfield, Wisconsin (Advisor: James L. Weber)
1997	PhD, Statistics, University of California, Berkeley (Advisor: Terry Speed; thesis: *Identifying quantitative trait loci in experimental crosses*)
1991	BS, *Summa Cum Laude*, Mathematics, University of Wisconsin–Milwaukee

PROFESSIONAL POSITIONS

2009 – present	Professor, Department of Biostatistics and Medical Informatics, School of Medicine and Public Health, University of Wisconsin–Madison
2007 – 2009	Associate Professor, Department of Biostatistics and Medical Informatics, School of Medicine and Public Health, University of Wisconsin–Madison
2002 – 2007	Associate Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University, Baltimore, Maryland
1999 – 2002	Assistant Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University, Baltimore, Maryland
1999	Associate Research Scientist, Center for Medical Genetics, Marshfield Medical Research Foundation, Marshfield, Wisconsin

ADDITIONAL PROFESSIONAL APPOINTMENTS

Affiliate faculty member, Department of Statistics, University of Wisconsin–Madison
Faculty trainer, Biostatistics Training Program, Cellular and Molecular Pathology Graduate Program, Computation and Informatics in Biology and Medicine Training Program, Genetics PhD Program, Genomic Sciences Training Program, Master of Public Health Program, Plant Breeding and Plant Genetics Program, and Population Health Graduate Program, University of Wisconsin–Madison

RESEARCH INTERESTS

My research concerns statistical issues arising in problems in genetics and genomics. I focus particularly on the characterization of meiotic recombination and the development of improved methods for detecting and identifying genes contributing to variation in complex phenotypes in experimental organisms.

SCIENTIFIC ADVISORY BOARDS

2009 – 2016 Nature Source Genetics, Ithaca, New York

2010 – 2011 Wisconsin Genomics Initiative

HONORS AND AWARDS

Fellow of the American Statistical Association (2016)
Graduate of the Last Decade Award, University of Wisconsin–Milwaukee Alumni Association (2001)
Best Paper in *Genetic Epidemiology* in 1999, International Genetic Epidemiology Society (2000)
John Wasmuth Fellowship in Genomic Analysis, National Human Genome Research Institute (1998)
Evelyn Fix Prize for great promise in statistical research, University of California, Berkeley (1997)
Outstanding Graduate Student Instructor, University of California, Berkeley (1997)
University Fellowship, University of California, Berkeley (1994)
Phi Beta Kappa Society (1991)
General Chemistry Award, University of Wisconsin–Milwaukee (1989)
Wisconsin All-State Scholar (1988)

PROFESSIONAL SOCIETY MEMBERSHIPS

American Association of University Professors
American Statistical Association
Genetics Society of America
Institute of Mathematical Statistics
International Biometric Society (ENAR)

EDITORIAL ACTIVITIES

Editorial Board Membership

2016 – 2021 Senior Editor, *Genetics*

2016 – 2021 Editorial Board, *BMC Biology*

2017 – 2019 Academic Editor, *PeerJ*

2004 – 2010 Associate Editor, *Genetics*

2006 – 2009 Associate Editor, *Journal of the American Statistical Association*, Applications and Case Studies

2004 – 2007 Associate Editor, *Biostatistics*

Peer Review Activities

Referee for American Journal of Epidemiology; American Journal of Human Genetics; American

Statistician; Annals of Applied Statistics; Annals of Human Genetics; Annals of Statistics; Arteriosclerosis, Thrombosis, and Vascular Biology; Bioinformatics; Biometrics; Biostatistics; BMC Bioinformatics; BMC Biology; BMC Genetics; BMC Genomics; BMC Medical Research Methodology; BMC Proceedings; BMC Research Notes; Cancer Research; Circulation Research; Computational Statistics & Data Analysis; Crop Science; eLife; European Journal of Human Genetics; Evolution; G3 (Bethesda); Gene; Genes, Brain, and Behavior; Genes & Immunity; Genetic Epidemiology; Genetica; Genetical Research; Genetics; Genetics Research; Genetics Selection Evolution; Genome; Genome Research; Genomics; Growth, Development, & Aging; Harvard Data Science Review; Heredity; Human Genetics; Human Heredity; Human Molecular Genetics; IEEE/ACM Transactions on Computational Biology and Bioinformatics; Journal of Agricultural, Biological, and Environmental Statistics; Journal of the American Society of Nephrology; Journal of the American Statistical Association; Journal of Applied Genetics; Journal of Bioinformatics and Computational Biology; Journal of Computational and Graphical Statistics; Journal of Fish Biology; Journal of Heredity; Journal of Immunology; Journal of Neuroscience; Journal of Open Source Software; Journal of Statistical Distributions and Applications; Journal of Statistical Planning and Inference; Journal of Statistical Software; Mammalian Genome; Methods in Ecology and Evolution; Molecular Biology and Evolution; Molecular Ecology Resources; Molecular Genetics and Genomics; Molecular Informatics; Nature Communications; Nature Genetics; Nature Methods; Nature Protocols; Nature Reviews–Genetics; Nucleic Acids Research; Ophthalmic Epidemiology; Pacific Symposium on Biocomputing; Physical Review Letters; Physiological Genomics; Plant Cell; Plant Physiology; PLoS Biology; PLoS Computational Biology; PLoS Genetics; PLoS ONE; Proceedings of the National Academy of Sciences USA; R Journal; Scandinavian Journal of Immunology; Science; Statistical Applications in Genetics and Molecular Biology; Statistics; Theoretical Population Biology; and Trends in Genetics

Book reviewer for Arnold Publishers, Chapman & Hall/CRC, Columbia University Press, Oxford University Press, Princeton University Press, Springer–Verlag, and Taylor & Francis

Review Panels

2010 – 2015	Center for Inherited Disease Research (CIDR) Access Committee, National Human Genome Research Institute, National Institutes of Health (*Chair*, 2014 – 2015)
2006 – 2010	Genomics, Computational Biology, and Technology Study Section (GCAT), Center for Scientific Review, National Institutes of Health

Ad hoc Review of Proposals

Center for Inherited Disease Research Access Committee; Clinical Research Review Committee, National Center for Research Resources; Genomics, Computational Biology, and Technology Study Section (NIH); Hatch grant competition, College of Agriculture and Life Sciences, University of Wisconsin–Madison; Johns Hopkins Center for Alternatives to Animal Testing; Mammalian Genetics Study Section (NIH); Microsoft Research European Fellowship Programme; National Cancer Institute Special Emphasis Panel (NIH); National Institute of Environmental Health Sciences Special Emphasis Panel (NIH); National Institute on Aging Special Emphasis Panel (NIH); National Science Council (Republic of China); National Science Foundation; National Sciences and Engineering Research Council (Canada); Council for Earth and Life Sciences, Netherlands Organization for Scientific Research; Neurological Sciences and Disorders A Study Section (NIH); and Telethon (Italy)

PUBLICATIONS

Books

Broman KW, Sen Ś (2009) *A Guide to QTL Mapping with R/qtl.* Springer (ISBN: 978-0-387-92124-2)

Journal Articles

Trotter C, Kim H, Farage G, Prins P, Williams RW, **Broman KW**, Sen Ś (2021) Speeding up eQTL scans in the BXD population using GPUs. *G3 (Bethesda)*, to appear

2021 Tran Q, **Broman KW** (2021) Treatment of the X chromosome in mapping multiple quantitative trait loci. *G3 (Bethesda)* 11:jkab005 doi:10.1093/g3journal/jkab005

Hassold T, Maylor-Hagen H, Wood A, Gruhn J, Hoffmann E, **Broman KW**, Hunt P (2021) Failure to recombine is a common feature of human oogenesis. *Am J Hum Genet* 108:16–24 doi:10/gm56

2020 Linke V, Overmyer KA, Miller IJ, Brademan DR, Hutchins PD, Trujillo EA, Reddy TR, Russell JD, Cushing EM, Schueler DL, Stapleton DS, Rabaglia ME, Keller MP, Gatti DM, Keele GR, Pham D, **Broman KW**, Churchill GA, Attie AD, Coon JJ (2020) A large-scale genome-lipid association map guides lipid identification. *Nat Metab* 2:1149–1162 doi:10/gk5cn6

Schwerbel K, Kamitz A, Krahmer N, Hallahan N, Jähnert M, Gottmann P, Lebek S, Schallschmidt T, Arends D, Schumacher F, Kleuser B, Haltenhof T, Heyd F, Gancheva S, **Broman KW**, Roden M, Joost HG, Chadt A, Al-Hasani H, Vogel H, Jonas W, Schürmann A (2020) Immunity-related GTPase induces lipophagy to prevent excess hepatic lipid accumulation. *J Hepatol* 73:771–782 doi:10/gjpnzk

Broman KW (2020) Reproducibility report: Identifying essential genes by mutagenesis. *ReScience C* 6(1): #12 doi:10.5281/zenodo.3959516

Rodriguez-Gil JL, Watkins-Chow DE, Baxter LL, Elliot G, Harper UL, Wincovitch SM, Wedel JC, Incao AA, Huebecker M, Boehm FJ, Garver WS, Porter FD, **Broman KW**, Platt FM, Pavan BJ (2020) Genetic background modifies phenotypic severity and longevity in a mouse model of Niemann-Pick Disease Type C1. *Dis Model Mech* 13:dmm042614 doi:10.1242/dmm.042614

2019 Keller MP, Rabaglia ME, Schueler KL, Stapleton DS, Gatti DM, Vincent M, Mitok KA, Wang Z, Ishimura T, Simonett SP, Emfinger CH, Das R, Beck T, Kendziorski C, **Broman KW**, Yandell BS, Churchill GA, Attie AD (2019) Gene loci associated with insulin secretion in islets from non-diabetic mice. *J Clin Invest* 130:4419–4432 doi:10.1172/JCI129143

Kemis JH, Linke V, Barrett KL, Boehm FJ, Traeger LL, Keller MP, Rabaglia ME, Schueler KL, Stapleton DS, Gatti DM, Churchill GA, Amador-Noguez D, Russell JD, Yandell BS, **Broman KW**, Coon JJ, Attie AD, Rey FE (2019) Genetic determinants of gut microbiota composition and bile acid profiles in mice. *PLoS Genet* 15: e1008073 doi:10.1371/journal.pgen.1008073

Boehm FJ, Chesler EJ, Yandell BS, **Broman KW** (2019) Testing pleiotropy vs. separate QTL in multiparental populations. *G3 (Bethesda)* 9:2317–2324 doi:10.1371/journal.pgen.1008073

Boehm F, Yandell B, **Broman KW** (2019) qtl2pleio: Testing pleiotropy vs. separate QTL in multiparental populations. *J Open Source Software* 4(38):1435 doi:10.21105/joss.01435

Broman KW, Gatti DM, Svenson KL, Sen Ś, Churchill GA (2019) Cleaning genotype data from Diversity Outbred mice. *G3 (Bethesda)* 9:1571–1579 doi:10.1534/g3.119.400165

Broman KW, Gatti DM, Simecek P, Furlotte NA, Prins P, Sen Ś, Yandell BS, Churchill GA (2019) R/qtl2: software for mapping quantitative trait loci with high-dimensional data and multi-parent populations. *Genetics* 211:495–502 doi:10.1534/genetics.118.301595

2018 Palus M, Sohrabi Y, **Broman KW**, Strnad H, Šíma M, Růžek D, Volkova V, Slapničková M, Vojtíšková J, Mrázková L, Salát J, Lipoldová M (2018) A novel locus on mouse chromosome 7 that influences survival after infection with tick-borne encephalitis virus. *BMC Neurosci* 19:39 doi:10/gm57

Keller MP, Gatti DM, Schueler KL, Rabaglia ME, Stapleton DS, Simecek P, Vincent M, Allen S, Broman AT, Bacher R, Kendziorski C, **Broman KW**, Yandell BS, Churchill GA, Attie AD (2018) Genetic drivers of pancreatic islet function. *Genetics* 209:335–356 doi:10.1534/genetics.118.300864

Broman KW, Woo KH (2018) Data organization in spreadsheets. *Am Stat* 72:2–10 doi:10/gdz6cm

Keele GR, Prokop JW, He H, Holl K, Littrell J, Deal A, Francic S, Cui L, Gatti DM, **Broman KW**, Tschannen M, Tsaih S-W, Zagloul M, Kim Y, Baur B, Fox J, Robinson M, Levy S, Flister MJ, Mott R, Valdar W, Solberg Woods LC (2018) Genetic fine-mapping and identification of candidate genes and variants for adiposity traits in outbred rats. *Obesity* 26:213–222 doi:10.1002/oby.22075

2017 Florek NW, Kamlangdee A, Mutschler JP, Kingstad-Bakke B, Schultz-Darken N, **Broman KW**, Osorio JE, Friedrich TC (2017) A modified vaccinia Ankara vaccine vector expressing a mosaic H5 hemagglutinin reduces viral shedding in rhesus macaques. *PLoS ONE* 12:e0181738 doi:10.1371/journal.pone.0181738

Wang RJ, Gray MM, Parmenter MD, **Broman KW**, Payseur BA (2017) Recombination rate variation in mice from an isolated island. *Mol Ecol* 26:457–470 doi:10.1111/mec.13932

2016 Keller MP, Paul PK, Rabaglia ME, Stapleton DS, Schueler KL, Broman AT, Ye SI, Leng N, Brandon CJ, Neto EC, Plaisier CL, Simonett SP, Kebede MA, Sheynkman GM, Klein MA, Baliga NS, Smith LM, **Broman KW**, Yandell BS, Kendziorski C, Attie AD (2016) The transcription factor *Nfatc2* regulates β-cell proliferation and genes associated with type 2 diabetes in mouse and human islets. *PLoS Genet* 12:e1006466 doi:10.1371/journal.pgen.1006466

Parmenter MD, Gray MM, Hogan CA, Ford IN, **Broman KW**, Vinyard CJ, Payseur BA (2016) Genetics of skeletal evolution in unusually large mice from Gough Island. *Genetics* 204:1559–1572 doi:10.1534/genetics.116.193805

Zigler JS Jr, Hodgkinson CA, Wright M, Klise A, Sundin O, **Broman KW**, Hejtmancik F, Huang H, Patek B, Sergeev Y, Hose S, Brayton C, Xaiodong J, Vasquez D, Maragakis N, Mori S, Goldman D, Hoke A, Sinha D (2016) A spontaneous missense mutation in branched chain keto acid dehydrogenase kinase in the rat affects both the central and peripheral nervous systems. *PLoS ONE* 11:e0160447 doi:10.1371/journal.pone.0160447

Sloan Z, Arends D, **Broman KW**, Centeno A, Furlotte N, Nijveen H, Yan L, Zhou X, Williams RW, Prins P (2016) GeneNetwork: framework for web-based genetics. *J Open Source Software* 1(2):25 doi:10.21105/joss.00025

De Simone M, Spagnuolo L, Lorè NI, Cigana C, De Fino I, **Broman KW**, Iraqi FA, Bragonzi A (2016) Mapping genetic determinants of host susceptibility to Pseudomonas aeruginosa lung infection in mice. *BMC Genomics* 17:351 doi:10/gdsf9t

Tian J, Keller MP, Broman AT, Kendziorski C, Yandell BS, Attie AD, **Broman KW** (2016) The dissection of expression quantitative trait locus hotspots. *Genetics* 202:1563–1574 doi:10.1534/genetics.115.183624

Gruhn JR, Al-Asmar N, Fasnacht R, Maylor-Hagen H, Peinado V, Rubio C, **Broman KW**, Hunt PA, Hassold T (2016) Correlations between synaptic initiation and meiotic recombination: A study of humans and mice. *Am J Hum Genet* 98:102–115 doi:10.1016/j.ajhg.2015.11.019

Kwak I-L, Moore CR, Spalding EP, **Broman KW** (2016) Mapping quantitative trait loci underlying function-valued traits using functional principal component analysis and multi-trait mapping. *G3 (Bethesda)* 6:79–86 doi:10.1534/g3.115.024133

2015 Tian J, Keller MP, Oler AT, Rabaglia ME, Schueler KL, Stapleton DS, Broman AT, Zhao W, Kendziorski C, Yandell BS, Hagenbuch B, **Broman KW**, Attie AD (2015) Identification of the bile acid transporter *Slco1a6* as a candidate gene that broadly affects gene expression in mouse pancreatic islets. *Genetics* 201:1253–1262 doi:10.1534/genetics.115.179432

Broman KW, Keller MP, Broman AT, Kendziorski C, Yandell BS, Sen Ś, Attie AD (2015) Identification and correction of sample mix-ups in expression genetic data: A case study. *G3 (Bethesda)* 5:2177–2186 doi:10.1534/g3.115.019778

Gray MM, Parmenter M, Hogan C, Ford I, Cuthbert RJ, Ryan PG, **Broman KW**, Payseur BA (2015) Genetics of rapid and extreme size evolution in island mice. *Genetics* 201:213–228 doi:10.1534/genetics.115.177790

Whitney KD, **Broman KW**, Kane NC, Hovick SM, Randell RA, Rieseberg LH (2015) Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. *Mol Ecol* 24:2194–2211 doi:10.1111/mec.13044

Broman KW (2015) R/qtlcharts: Interactive graphics for quantitative trait locus mapping. *Genetics* 199:359–361 doi:10.1534/genetics.114.172742

2014 Florek NW, Weinfurter JT, Jegaskanda S, Brewoo JN, Powell TD, Young GR, Das SC, Hatta M, **Broman KW**, Hungnes O, Dudman SG, Kawaoka Y, Kent SJ, Stinchcomb DT, Osorio JE, Friedrich TC (2014) Modified vaccinia Ankara encoding influenza virus hemagglutinin induces heterosubtypic immunity in macaques. *J Virol* 88:13418–13428 doi:10.1128/JVI.01219-14

Gatti DM, Svenson KL, Shabalin A, Wu L-Y, Valdar W, Simecek P, Goodwin N, Cheng R, Pomp D, Palmer A, Chesler EJ, **Broman KW**, Churchill GA (2014) Quantitative trait locus mapping methods for Diversity Outbred mice. *G3 (Bethesda)* 4:1623–1633 doi:10.1534/g3.114.013748

Street VA, Kujawa SG, Manichaikul A, **Broman KW**, Kallman JC, Shilling DJ, Iwata AJ, Robinson LC, Robbins CA, Li J, Liberman MC, Tempel BL (2014) Resistance to noise-induced hearing loss in 129S6 and MOLF mice: Identification of independent, overlapping, and interacting chromosomal regions. *J Assoc Res Otolaryngol* 15:721–738 doi:10/f6hwgk

Kwak I-Y, Moore CR, Spalding EP, **Broman KW** (2014) A simple regression-based method to map quantitative trait loci underlying function-valued phenotypes. *Genetics* 197: 1409–1416 doi:10.1534/genetics.114.166306

Broman KW (2014) Fourteen years of R/qtl: Just barely sustainable. *J Open Res Softw* 2(1):e11 doi:10.5334/jors.at

Rowsey R, Gruhn J, **Broman KW**, Hunt PA, Hassold T (2014) Examining variation in recombination levels in the human female: A test of the production line hypothesis. *Am J Hum Genet* 95:108–112 doi:10.1016/j.ajhg.2014.06.008

Huang BE, Raghavan C, Mauleon R, **Broman KW**, Leung H (2014) Efficient imputation of missing markers in low-coverage genotyping-by-sequencing data from multi-parent crosses. *Genetics* 197:401–404 doi:10.1534/genetics.113.158014

Baier B, Hunt P, **Broman KW**, Hassold T (2014) Variation in genome-wide levels of meiotic recombination is established at the onset of prophase in mammalian males. *PLoS Genet* 10:e1004125 doi:10.1371/journal.pgen.1004125

2013 Gruhn JR, Rubio C, **Broman KW**, Hunt PA, Hassold T (2013) Cytological studies of human meiosis: sex-specific differences in recombination originate at, or prior to, establishment of double-strand breaks. *PLoS ONE* 8:e85075 doi:10.1371/journal.pone.0085075

Moore CR, Johnson LS, Kwak IY, Livny M, **Broman KW**, Spalding EP (2013) High-throughput computer vision introduces the time axis to a quantitative trait map of a plant growth response. *Genetics* 195:1077–1086 doi:10.1534/genetics.113.153346

Bautz DJ, **Broman KW**, Threadgill DW (2013) Identification of a novel polymorphism in X-linked sterol-4-alpha-carboxylate 3-dehydrogenase (Nsdhl) associated with reduced HDL cholesterol levels in I/LnJ mice. *G3 (Bethesda)* 3:1819–1825 doi:10.1534/g3.113.007567

Harris M, Burns CM, Becker EA, Braasch AT, Gostick E, Johnson RC, **Broman KW**, Price DA, Friedrich TC, O'Connor SL (2013) Acute-phase CD8 T cell responses that select for escape variants are needed to control live attenuated simian immunodeficiency virus. *J Virol* 87:9353–9364 doi:10.1128/JVI.00909-13

Maenner MJ, Baker MW, **Broman KW**, Tian J, Barnes JK, Atkins A, McPherson E, Hong J, Brilliant MH, Mailick MR (2013) *FMR1* CGG expansions: Prevalence and sex ratios. *Am J Med Genet **B** Neuropsychiatr Genet* 162:466–473 doi:10.1002/ajmg.b.32176

2012 **Broman KW**, Kim S, Sen Ś, Ané C, Payseur BA (2012) Mapping quantitative trait loci onto a phylogenetic tree. *Genetics* 192:167–179 doi:10.1534/genetics.112.142448

Rice CA, Riehl J, **Broman K**, Soukup JW, Gengler WR (2012) Comparing the degree of exothermic polymerization in commonly used acrylic and provisional composite resins for intraoral appliances. *J Vet Dent* 29: 78–83 doi:10/gm58

Galvan A, Colombo F, Noci S, Pazzaglia S, Mancuso M, Manenti G, **Broman KW**, Saran A, Dragani TA (2012) The *Lsktm1* locus modulates lung and skin tumorigenesis in the mouse. *G3 (Bethesda)* 2:1041–1046 doi:10.1534/g3.112.003525

Greene JM, Chin EN, Budde ML, Lhost JJ, Hines PJ, Burwitz BJ, **Broman KW**, Nelson JE, Friedrich TC, O'Connor DH (2012) *Ex vivo* SIV-specific CD8 T cell responses in heterozygous animals are primarily directed against peptides presented by a single MHC haplotype. *PLoS ONE* 7:e43690 doi:10.1371/journal.pone.0043690

Neto EC, Keller MP, Broman AF, Attie AD, Jansen RC, **Broman KW**, Yandell BS (2012) Quantile-based permutation thresholds for quantitative trait loci hotspots. *Genetics* 191:1355–1365 doi:10.1534/genetics.112.139451

King EG, Merkes CM, McNeil CL, Hoofer SR, Sen S, **Broman KW**, Long AD, Macdonald SJ (2012) Genetic dissection of a model complex trait using the *Drosophila* Synthetic Population Resource. *Genome Res* 22:1558–1566 doi:10.1101/gr.134031.111

Wang CY, Stapleton DS, Schueler KL, Rabaglia ME, Oler AT, Keller MP, Kendziorski CM, **Broman KW**, Yandell BS, Schadt EE, Attie ED (2012) *Tsc2*, a positional candidate gene underlying a quantitative trait locus for hepatic steatosis. *J Lipid Res* 53:1493–1501 doi:10.1194/jlr.M025239

Arends D, van der Velde KJ, Prins P, **Broman KW**, Möller S, Jansen RC, Swertz MA (2012) xQTL workbench: a web based environment for xQTL analysis. *Bioinformatics* 28:1042–1044 doi:10.1093/bioinformatics/bts049

Amlin-Van Schaick JC, Kim S, **Broman KW**, Reilly KM (2012) *Scram1* is a modifier of spinal cord resistance for astrocytoma on mouse chromosome 5. *Mamm Genome* 23:277–285 doi:10/fwbzj7
Broman KW (2012) Genotype probabilities at intermediate generations in the construction of recombinant inbred lines. *Genetics* 190:403–412 doi:10.1534/genetics.111.132647

Broman KW (2012) Haplotype probabilities in advanced intercross populations. *G3 (Bethesda)* 2:199–202 doi:10.1534/g3.111.001818

Collaborative Cross Consortium [97 authors] (2012) The genome architecture of the Collaborative Cross mouse genetic reference population. *Genetics* 190:389–401 doi:10.1534/genetics.111.132639

Amlin-Van Schaick JC, Kim S, DiFabio C, Lee M-H, **Broman KW**, Reilly KM (2012) *Arlm1* is a male-specific modifier of astrocytoma resistance on mouse chr 12. *Neuro Oncol* 14:160–174 doi:10.1093/neuonc/nor206

Davis RC, Van Nas A, Castellani LW, Zhao Y, Zhou Z, Wen P, Yu S, Qi H, Rosales M, Schadt EE, **Broman KW**, Peterfy M, Lusis AJ (2012) Systems genetics of susceptibility to obesity-induced diabetes in mice. *Physiol Genomics* 44:1–13 doi:10/djfhjh

2011 Weinfurter JT, Brunner K, Capuano SV III, Li C, **Broman KW**, Kawaoka Y, Friedrich T (2011) Cross-reactive T cells are involved in rapid clearance of 2009 pandemic H1N1 influenza virus in nonhuman primates. *PLoS Pathog* 7:e1002381 doi:10.1371/journal.ppat.1002381

Aylor DL, Valdar W, Foulds-Mathes W, Buus RJ, Verdugo RA, Baric RS, Ferris MT, Frelinger JA, Heise M, Frieman MB, Gralinski LE, Bell TA, Didion JD, Hua K, Nehrenberg DL, Powell CL, Steigerwalt J, Xie Y, Kelada SNP, Collins F, Yang IV, Schwartz DA, Branstetter LA, Chesler EJ, Miller DR, Spence J, Liu EY, McMillan L, Sarkar A, Wang J, Wang W, Zhang Q, **Broman KW**, Korstanje R, Durrant C, Mott R, Iraqi FA, Pomp D, Threadgill D, Pardo-Manuel de Villena F, Churchill GA (2011) Genetic analysis of complex traits in the emerging Collaborative Cross. *Genome Res* 21:1213–1222 doi:10.1101/gr.111310.110

Greene JM, Wiseman RW, Lank SM, Bimber BN, Karl JA, Burwitz BJ, Lhost JJ, Hawkins OE, Kunstman KJ, **Broman KW**, Wolinsky SM, Hildebrand WH, O'Connor DH (2011) Differential MHC class I expression in distinct leukocyte subsets. *BMC Immunol* 12:39 doi:10/bg6j8r

Bradley KM, Breyer JP, Melville DB, **Broman KW**, Knapik EW, Smith JR (2011) A SNP-based linkage map for zebrafish reveals sex determination loci. *G3 (Bethesda)* 1:3–9 doi:10.1534/g3.111.000190

Moreland AJ, Guethlein LA, Reeves RK, **Broman KW**, Johnson RP, Parham P, O'Connor DH, Bimber BN (2011) Characterization of killer immunoglobulin-like receptor genetics and comprehensive genotyping by pyrosequencing in rhesus macaques. *BMC Genomics* 12:295 doi:10/b2h9p7

Svetec N, Werzner A, Wilches R, Pavlidis P, Álvarez-Castro JM, **Broman KW**, Metzler D, Stephan W (2011) Identification of X-linked quantitative trait loci affecting cold tolerance in *Drosophila melanogaster* and fine-mapping by selective sweep analysis. *Mol Ecol* 20:530–544 doi:10/d9782h

2010 Murdoch B, Owen N, Shirley S, Crumb S, **Broman KW**, Hassold T (2010) Multiple loci contribute to genome-wide recombination levels in male mice. *Mamm Genome* 21:550–555 doi:10/bgkc62

Billings T, Sargent EE, Szatkiewicz JP, Leahy N, Kwak, I-Y, Bektassova N, Walker M, Hassold T, Graber JH, **Broman KW**, Petkov PM (2010) Patterns of recombination activity on mouse chromosome 11 revealed by high resolution mapping. *PLoS ONE* 5:e15340 doi:10.1371/journal.pone.0015340

Arends D, Prins P, Jansen RC, **Broman KW** (2010) R/qtl: High-throughput multiple QTL mapping. *Bioinformatics* 26:2990–2992 doi:10.1093/bioinformatics/btq565

Bader HL, Ruhe AL, Wang LW, Wong AK, Walsh KF, Packer RA, Mitelman J, Robertson KR, O'Brien DP, **Broman KW**, Shelton GD, Apte SS, Neff MW (2010) An *ADAMTSL2* founder mutation causes Musladin-Lueke Syndrome, a heritable disorder of beagle dogs, featuring stiff skin and joint contractures. *PLoS ONE* 5:e12817 doi:10.1371/journal.pone.0012817

Jurisic G, Sundberg JP, Bleich A, Leiter EH, **Broman KW**, Buechler G, Alley L, Vestweber D, Detmar M. (2010) Quantitative lymphatic vessel trait analysis suggests *Vcam1* as candidate modifier gene of inflammatory bowel disease. *Genes Immun* 11:219–231 doi:10.1038/gene.2010.4

Burrage LC, Baskin-Hill AE, Sinasac DS, Singer JB, Croniger CM, Kirby A, Kulbokas EJ, Daly MJ, Lander ES, **Broman KW**, Nadeau JH (2010) Genetic resistance to diet-induced obesity in chromosome substitution strains of mice. *Mamm Genome* 21:115–129 doi:10/b2drrk

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SOFTWARE AND OTHER RESOURCES

R/qtl	An R package for mapping genes contributing to variation in quantitative traits in experimental crosses (`rqtl.org`).
R/qtl2	A reimplementation of the R package R/qtl, to better handle high-dimensional data and complex cross designs. (`kbroman.org/qtl2`).
R/qtl2convert	An R package for converting QTL data (`cran.r-project.org/package=qtl2convert`).
R/qtl2fst	An R package for storing genotype probabilities (`cran.r-project.org/package=qtl2fst`).

R/qtlcharts	An R package to create interactive data visualizations for quantitative trait locus mapping data (`kbroman.org/qtlcharts`).
d3panels	A CoffeeScript library of interactive graphics panels (`kbroman.org/d3panels`).
R/simcross	An R package for simulating general experiemental crosses (`kbroman.org/simcross`).
R/lineup	An R packages for identifying sample mixups in QTL data (`cran.r-project.org/package=lineup`).
R/lineup2	An R packages for identifying sample mixups in QTL data, rewritten to not be tied to the R/qtl package (`cran.r-project.org/package=lineup2`).
R/negenes	An R package for estimating the number of essential genes by random transposon mutagenesis (`cran.r-project.org/package=negenes`).
R/xoi	An R package for the analysis of crossover interference (`cran.r-project.org/package=xoi`).
R/broman	An R package with miscellaneous tools for graphics, statistics, and data analysis (`cran.r-project.org/package=broman`).
R/mbmixture	An R package for assessing mixtures in microbiome samples (`cran.r-project.org/package=mbmixture`).
aRxiv	An R package for searching arXiv, a repository of electronic preprints for computer science, mathematics, physics, quantitative biology, quantitative finance, and statistics (`github.com/ropensci/aRxiv`).
git/GitHub guide	Online tutorial on the git version control system and its use with GitHub (`kbroman.org/github_tutorial`).
knitr in a knutshell	Online tutorial on knitr, a tool for creating documents that mix code and text (`kbroman.org/knitr_knutshell`).
minimal make	Online tutorial on GNU Make, for automating computational tasks (`kbroman.org/minimal_make`).
R package primer	Online tutorial on writing packages for the R statistical software (`kbroman.org/pkg_primer`).
simple site	Online tutorial on constructing simple websites with GitHub Pages (`kbroman.org/simple_site`).
RelCheck	Software for the verification of relationships between individuals with use of autosomal genotype data.
Marshfield genetic maps	Genetic maps of the human genome, with internet-based tools for the search for genetic markers and semi-automated map construction.

EDUCATIONAL ACTIVITIES

PhD Advisees

Quoc Tran, PhD student, Statistics, University of Wisconsin–Madison

Fred Boehm, PhD student, Statistics, University of Wisconsin–Madison (Thesis: *Testing pleiotropy vs. separate QTL in multiparental populations*), 2019

Jianan Tian, PhD, Statistics, University of Wisconsin–Madison (Thesis: *Dissection and fine-mapping of* trans*-eQTL hotspots*), 2015

Il-Youp Kwak, PhD, Statistics, University of Wisconsin–Madison (Thesis: *Regression-based methods to map quantitative trait loci underlying function-valued phenotypes*), 2014

Ani Manichaikul, PhD, Biostatistics, Johns Hopkins Bloomberg School of Public Health (Thesis: *Statistical methods for mapping quantitative trait loci in experimental crosses*), 2007

Wei-Min Chen, PhD, Biostatistics, Johns Hopkins Bloomberg School of Public Health (Thesis: *Robust quantitative trait linkage analysis in extended human pedigrees*), 2004

Master's Advisees

Sungjin Kim, MS, Statistics, University of Wisconsin–Madison, 2011

Laura C. Plantinga, ScM, Biostatistics, Johns Hopkins Bloomberg School of Public Health (Thesis: *Inference of clusters of related individuals with dominant genetic marker data*), 2001

Undergraduate Advisees

Alexandra Lobo, summer student, Biomedical Data Science Summer Research Program, University of Wisconsin–Madison, summer, 2017

Janel Barnes, summer student, Integrated Biological Sciences Summer Research Program, University of Wisconsin–Madison, summer, 2012

Leah Fehr, summer student, Integrated Biological Sciences Summer Research Program, University of Wisconsin–Madison, summer, 2008

Academic Advisees, University of Wisconsin–Madison

2018 – 2020	Alexandra Spicer	MS candidate, Biomedical Data Science

Academic Advisees, Johns Hopkins University

2006 – 2007	Sheng-Chih Jin	ScM candidate, Biostatistics
2005 – 2007	Ani Manichaikul	PhD candidate, Biostatistics
2005 – 2006	Alex Phan	candidate for MHS in Bioinformatics
2005 – 2006	Jichao Chen	candidate for MHS in Bioinformatics
2004 – 2006	Snaebjorn Gunnsteinsson	PhD candidate, Biostatistics
2003 – 2007	Benilton Carvalho	PhD candidate, Biostatistics
2003 – 2005	Wenyi Wang	PhD candidate, Biostatistics
2000 – 2004	Wei-Min Chen	PhD candidate, Biostatistics
2000 – 2003	Michelle Shardell	PhD candidate, Biostatistics

1999 – 2001	Sora Kim	ScM candidate, Biostatistics

Doctoral Thesis Committees, University of Wisconsin–Madison

2021 – present	Zihao Zheng	Statistics
2021 – present	Chenyang Dong	Statistics
2018 – present	Qijun Zhang	Cellular and Molecular Pathology
2018 – present	Michael Kartje	Genetics
2017 – present	Christopher McAllester	Genetics
2019 – 2021	Athena Golfinos	Cellular and Molecular Pathology
2017 – 2021	Jeremy Lange	Genetics
2016 – 2021	April Peterson	Genetics
2015 – 2021	Quentin Sprengelmeyer	Genetics
2018 – 2020	Theeva Chandereng	Statistics
2012 – 2019	Molly McDevitt	Biochemistry
2017 – 2018	Kyubin Lee	Computer Sciences
2015 – 2018	René Welch	Statistics
2012 – 2017	Michelle Parmenter	Genetics
2014 – 2017	Alessandra York	Genetics
2013 – 2017	Richard Wang	Genetics
2013 – 2016	Shuang Huang	Statistics
2011 – 2013	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics
2010 – 2015	Katie Clowers	Genetics
2010	Jingfang Zhang	Oncology
2010 – 2011	Michael White	Genetics
2010	Elias Chaibub Neto	Statistics
2007 – 2010	Beth Dumont	Genetics

Doctoral Thesis Committees, Johns Hopkins University

2006 – 2007	Meera Venkatesan	Molecular Microbiology and Immunology
2006 – 2007	Ching-Yu Cheng	Epidemiology
2005 – 2007	Robert Wojciechowski	Epidemiology
2004 – 2007	Tanya Teslovich	Human Genetics (School of Medicine)
2004 – 2005	Katherine Swanson	Molecular Microbiology and Immunology
2003 – 2004	Shin Lin	Human Genetics (School of Medicine)
2003 – 2004	Adele Mitchell	Human Genetics (School of Medicine)
2002 – 2003	Rivka Glaser	Human Genetics (School of Medicine)
2002	Shawn Soutiere	Environmental Health Sciences
2001 – 2004	Sadeep Shresthra	Epidemiology
2001 – 2002	Rasika Mathias	Epidemiology
1999 – 2002	Cynthia James	Human Genetics (School of Medicine)

Oral Exams, University of Wisconsin–Madison

2021	Zihao Zheng	Statistics
	Quoc Tran	Statistics
	Chenyang Dong	Statistics
2020	Qijun Zhang	Cellular and Molecular Pathology
	Athena Golfinos	Cellular and Molecular Pathology
2019	Michael Kartje	Genetics

2018	Christopher McAllester	Genetics
	Thevaa Chandereng	Statistics
2017	Constanza Rojo	Statistics
	Quentin Sprengelmeyer	Genetics
	Jeremy Lange	Genetics
	Kyubin Lee	Computer Sciences
	Fred Boehm	Statistics
2016	April Peterson	Genetics
	Alessandra York	Genetics
2015	René Welch	Statistics
2014	Shuyun Ye	Statistics
	Michelle Parmenter	Genetics
	Jeea Choi	Statistics
2013	Jianan Tian	Statistics
	Richard Wang	Genetics
	Shuang Huang	Statistics
	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics
	Molly McDevitt	Biochemistry
2012	Katie Clowers	Genetics
2011	Il Youp Kwak	Statistics
2010	Jee Young Moon	Statistics
	John Dawson	Statistics
	Elias Chaibub Neto	Statistics
	Qinglin Pei	Statistics
	Jingfang Zhang	Oncology
2008	Beth Dumont	Genetics

Oral Exams, Johns Hopkins University

2006	Lindsey Garver	Molecular Microbiology and Immunology
	Benilton Carvalho	Biostatistics
	Yen-Yi Ho	Biostatistics
	Lindsey Enewold	Epidemiology
	Renee Gardner	Environmental Health Sciences
2005	Ani Manichaikul	Biostatistics
	Wenyi Wang	Biostatistics
	Meera Venkatesan	Molecular Microbiology and Immunology
	Audrey Grant	Epidemiology
2004	Katherine Swanson	Molecular Microbiology and Immunology
2003	Sadeep Shrestha	Epidemiology
	Wei-Min Chen	Biostatistics

2002	Marie-Hélène Roy-Gagnon	Epidemiology
2001	Leslie Cope	Mathematical Sciences (School of Engineering)
	Vivian Yuan	Mathematical Sciences (School of Engineering)
	Jean-Paul Chretien	Epidemiology
2000	Xin Liu	Epidemiology
	Tsuo-Hung Lan	Epidemiology
	Halcyon Skinner	Epidemiology
1999	David Kaufman	Epidemiology

Doctoral Thesis Defenses, University of Wisconsin–Madison

2021	Jeremy Lange	Genetics
	Quentin Sprengelmeyer	Genetics
	April Peterson	Genetics
2020	Thevaa Chandereng	Statistics
2019	Constanza Rojo	Statistics
	Fred Boehm	Statistics
	Molly McDevitt	Biochemistry
2018	Kyubin Lee	Computer Sciences
	René Welch	Statistics
2017	Richard Wang	Genetics
	Michelle Parmenter	Genetics
2016	Shuang Huang	Statistics
2015	Jianan Tian	Statistics
	Katie Clowers	Genetics
2014	Il-Youp Kwak	Statistics
2013	Qinglin Pei	Statistics
2012	John Dawson	Statistics
2011	Michael White	Genetics
2010	Beth Dumont	Genetics
	Elias Chaibub Neto	Statistics
2009	YounJeong Choi	Statistics

Doctoral Thesis Defenses, Johns Hopkins University

2007	Ani Manichaikul	Biostatistics
2005	Katherine Swanson	Molecular Microbiology and Immunology
	Laura LaRosa	Environmental Health Sciences

	Ji Wan Park	Epidemiology
	Martina Johannesson	Lund University, Sweden
2004	Wei-Min Chen	Biostatistics
	Marie-Hélène Roy-Gagnon	Epidemiology
2001	Alison Klein	Epidemiology
	Tsuo-Hung Lan	Epidemiology

Master's Thesis Defenses, University of Wisconsin–Madison

2013	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics

Master's Thesis Reading, Johns Hopkins University

2001	Jane Peredo, MS	Genetic Counseling
2000	Jennifer Mulle, MHS	Epidemiology
	Heping Hu, MHS	Epidemiology
	Rita Peila, ScM	Epidemiology

Classroom Instruction, University of Wisconsin–Madison

2020 – 2021	BMI 881	Biomedical Data Science Scholarly Literature 1
	BMI 882	Biomedical Data Science Scholarly Literature 2
	BMI 883	Biomedical Data Science Professional Skills 1 (*new*)
	BMI 884	Biomedical Data Science Professional Skills 2 (*new*)
2019 – 2020	BMI 881	Biomedical Data Science Scholarly Literature 1 (*new*)
	BMI 882	Biomedical Data Science Scholarly Literature 2 (*new*)
	BMI 826-001	Advanced Data Analysis (*new*)
2018 – 2019	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Kendziorski, Lu, Dewey, Newton, Keles, Roy, Ané, and Tang)
2017 – 2018	Agronomy 957	Plant Breeding and Plant Genetics seminar (jointly with Brian Yandell)
2016 – 2017	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Kendziorski, Larget, Ané, Newton, Roy, Keles, Wang, and Craven)
2015 – 2016	BMI 826-003	Tools for Reproducible Research
2014 – 2015	BMI 826-003	Tools for Reproducible Research
2013 – 2014	BMI 826-003	Tools for Reproducible Research (*new*)
	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
2012 – 2013	BMI 826-001	Statistical Methods for QTL Mapping

2011 – 2012	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
2010 – 2011	Statistics 992-001	Statistical Methods for QTL Mapping (*new*)
2009 – 2010	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
	Population Health 904-003	Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Meyers)
2008 – 2009	Statistics 371-003	Introductory Applied Statistics for the Life Sciences
2007 – 2008	Statistics 992-002	Statistical Methods in Molecular Biology (*new*) (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, and Keles)
	Population Health 904-003	Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Skinner)

Classroom Instruction, Johns Hopkins University

2006 – 2007	Biostatistics 140.668	Special Topics in Genetics and Genomics
2005 – 2006	Biostatistics 140.615–616	Statistics for Laboratory Scientists
	Epidemiology 340.631	Methods in Genetic Epidemiology I (jointly with Dr. Beaty)
2004 – 2005	Biostatistics 140.776	Statistical Computing (jointly with Drs. Caffo, Irizarry, and Ruczinski)
	Biostatistics 140.668	Special Topics in Genetics and Genomics (jointly with Dr. Ruczinksi)
	Biostatistics 140.615–616	Statistics for Laboratory Scientists
	Epidemiology 340.631	Methods in Genetic Epidemiology I (jointly with Dr. Beaty)
2003 – 2004	Biostatistics 140.776	Statistical Computing (*new*) (jointly with Drs. Caffo, Irizarry, and Ruczinski)
	Biostatistics 140.615–616	Statistics for Laboratory Scientists
2002 – 2003	Biostatistics 140.668	Special Topics in Genetics and Genomics (*new*) (jointly with Dr. Parmigiani)
	Biostatistics 140.615–616	Statistics for Laboratory Scientists
2001 – 2002	Biostatistics 140.615	Statistics for Laboratory Scientists (*new*)
2000 – 2001	Biostatistics 140.778	Advanced Statistical Computing (*new*)
	Biostatistics 140.667	Genetics for Statisticians
	Biostatistics 140.668	Statistical Genetics
1999 – 2000	Biostatistics 140.846	Genetics for Statisticians (*new*)
	Biostatistics 140.668	Statistical Genetics (*new*)

Classroom Instruction, University of California, Berkeley

Summer, 1994	Statistics 131A	Introductory Statistics for Social and Life Scientists

Classroom Instruction, University of Wisconsin–Milwaukee

1991 – 1992	Mathematics 095	Basic Algebra

Other teaching

2021	Lectures on "QTL mapping in MAGIC populations with R/qtl2 in Horticulture 615 (Genetic Mapping), University of Wisconsin–Madison
2021	Lecture on "Steps toward reproducible research" for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2018 – 2021	Lecture on "Data management" to KL2 scholars, Institute for Clinical and Translational Research, School of Medicine and Public Health, University of Wisconsin–Madison
2008 – 2021	Lecture on my consulting experiences in Statistical Consulting (Stat 998), Department of Statistics, University of Wisconsin–Madison
2020	Lecture on "Steps toward reproducible research" in BMI 877 (Statistical Methods for Molecular Biology), Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2020	Lectures on "Steps toward reproducible research" and "Exploratory data analysis" in BMI 773 (Clinical Research Informatics), Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2019 – 2020	Lecture on "Steps toward reproducible research" to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison
2018	Instructor, Workshop on Advanced R and R/qtl, ICRISAT, Hyderabad, India
2018	Lecture on "Steps toward reproducible research" for the Cellular and Molecular Pathology Graduate Program, University of Wisconsin–Madison
2017 – 2018	Workshop on Reproducible Research, Summer Institute in Statistics for Big Data, Seattle, Washington
2017 – 2018	Lecture on "Steps toward reproducible research" for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2016 – 2018	Instructor, Data Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison
2013 – 2018	Lecture on "Creating effective figures and tables" to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison
2017	Instructor, Data Carpentry workshop, National Society of Black Engineers Professional Development Conference, Chicago, Illinois

2017	Workshop on Systems Genetics of Neurodegeneration, Frauenchiemsee, Germany
2017	Workshop on R/qtl and R/qtl2 software, Complex Trait Community meeting, Memphis, Tennessee
2017	Workshop on "Steps toward reproducible research" as part of a Data Science and Plant Breeding Simulation Workshop, University of Minnesota, St. Paul, Minnesota
2017	Lecture to AP Statistics students, Madison East High School, Madison, Wisconsin
2017	Lecture on "Genetics of extreme body size evolution in mice from Gough Island" for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2008 – 2017	Periodic seminars on "Creating effective figures and tables" in the Department of Pathology and Laboratory Medicine, University of Wisconsin–Madison
2016	Lecture on "Creating effective figures and tables" at the Demography Training Seminar, Center for Demography of Health and Aging, University of Wisconsin–Madison
2008 – 2016	Instructor and co-organizer, Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, Maine
2015	R/qtl workshop, Texas A&M, College Station, Texas
2015	Lecture on "Reproducible Research" for undergraduate researchers in the Summer Institute for Training in Biostatistics (SIBS), University of Wisconsin–Madison
2015	Instructor, Software Carpentry workshop, Washington State University, Pullman, Washington
2014 – 2015	Instructor, Software Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison
2014	Lecture on "Creating effective figures and tables" in a manuscript writing workshop, Institute for Clinical and Translational Research, University of Wisconsin–Madison
2013	Lecture on "A brief introduction to git and GitHub" to graduate students, Department of Statistics, University of Wisconsin–Madison
2013	Lecture on "Why aren't all of our graphs interactive?" to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2012	Instructor, Training Course on Field Trials & QTL Analysis using R and R/qtl, ICRISAT, Hyderabad, India
2012	Lecture on "Introduction to QTL mapping in model organisms" for undergraduate researchers in the Summer Institute for Training in Biostatistics (SIBS), University of Wisconsin–Madison
2012	Lecture on "Programming style" to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison

2010	Lecture on "How to give a scientific presentation" to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2008	Lecture on "Recombination and linkage" in Human Emphasis Group Graduate Student Seminar (NS 881, Schoeller), Nutritional Sciences, University of Wisconsin–Madison
2008	Lecture on "Recombination and linkage" in Genetic Epidemiology (PHS 904, Engelman), Population Health Sciences, University of Wisconsin–Madison
2007	Instructor, NeuroproMiSe Training Course in Genetic Analysis and Bioinformatics, Lund University, Lund, Sweden
2001 – 2007	Instructor and co-organizer, Short Course on Complex Trait Analysis, The Jackson Laboratory, Bar Harbor, Maine
2000 – 2007	Lecture on quantitative genetics in Advanced Topics in Human Genetics (Reeves and Feinberg) Human Genetics, Johns Hopkins School of Medicine
2004 – 2006	Lecture on "Statistical epigenomics" in Epigenetics (ME260.710, Feinberg), Johns Hopkins University School of Medicine
2003 – 2006	Lecture on "Experimental design and sample size determination for animal-based research", Johns Hopkins University Animal Care and Use Committee seminar series
2002 – 2006	Instructor, QTL Mapping II module, Summer Institute in Statistical Genetics, formerly at North Carolina State University, now held at the University of Washington, Seattle
2003 – 2005	Lecture on "Perl for human linkage analysis" in Biocomputing I: Perl for Biocomputing (140.636, Pineda), Johns Hopkins Bloomberg School of Public Health
2004	Lecture on experimental design, statistics, and sample size determination, as part of an on-line course on Enhancing Humane Science—Improving Animal Research
1999 – 2000	Special studies course in longitudinal data analysis for Xin Liu, PhD candidate, Epidemiology

ACADEMIC LEADERSHIP AND PROGRAM DEVELOPMENT

2017 – 2020	Director, Biomedical Data Science PhD Program, University of Wisconsin–Madison
2004 – 2007	Co-Director, MHS Program in Bioinformatics, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

SERVICE ACTIVITIES

International and National

2017	Program Committee, Complex Trait Community 15th Annual Meeting (Memphis, Tennessee)

2016 – 2017	John M. Chambers Statistical Software Award Committee, Statistical Computing Section, American Statistical Association
2013 – 2014	Personalized Medicine Research Project (PMRP) Oversight Committee, Marshfield Clinic Research Foundation, Marshfield, Wisconsin
2013	Co-organizer, Complex Trait Community 12th Annual Meeting (Madison, Wisconsin)
2003 – 2004	ENAR Distinguished Student Paper Awards Committee
2003	IMS Contributed Papers Chair, ENAR/IMS Annual Meeting (Tampa, Florida)

University

2020– present	Executive Committee, Plant Breeding and Plant Genetics PhD Program, University of Wisconsin–Madison
2017 – present	Faculty Senator, University of Wisconsin–Madison
2018	Review Committee for Biometry Master of Science Program, College of Agricultural and Life Sciences, University of Wisconsin–Madison
2016	Genomics Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison
2012 – 2015	Faculty Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison
2011 – 2015	University Library Committee, University of Wisconsin–Madison (*Chair*, 2014 – 2015)
2012 – 2014	Steering Committee, Medical Scientist Training Program, School of Medicine and Public Health, University of Wisconsin–Madison
2009 – 2012	Master of Public Health Program Curriculum Committee, School of Medicine and Public Health, University of Wisconsin–Madison
2009 – 2012	Curriculum Planning Committee, Biological Sciences Division, University of Wisconsin–Madison
2008 – 2012	Faculty Senator, University of Wisconsin–Madison
2002 – 2007	Maintainer of the Faculty Senate web site, Johns Hopkins Bloomberg School of Public Health
2001 – 2004	Faculty Senate representative to the Committee on Information Technology, Johns Hopkins Bloomberg School of Public Health
2001 – 2003	Organizer of a monthly discussion forum for junior faculty, Johns Hopkins Bloomberg School of Public Health
2001 – 2002	Secretary of the Faculty Senate, Johns Hopkins Bloomberg School of Public Health
2000 – 2002	Faculty Senator, Johns Hopkins Bloomberg School of Public Health

2000 – 2001 Biochemistry and Molecular Biology Strategic Plan Committee, Johns Hopkins Bloomberg School of Public Health

Departmental

2015 – present Scientific Advisory and Steering Committee, Biostatistics Computing Group, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2014 – present Steering Committee, Biomedical Data Science MS Program, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2010 – 2020 Chair, Education and Curriculum Committee, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2015 – 2016 Co-chair, Faculty Search Committee, Biostatistics and Medical Informatics, University of Wisconsin–Madison

2010 – 2013 Seminar organizer, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2010 – 2012 Steering Committee, Biomedical Computing Group, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2008 Committee for Information Technology Assessment, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

2004 – 2007 Intellectual and Social Environment Committee, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

2000 – 2002 Biostatistics Information Technology Committee, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

2000 – 2001 Seminar organizer, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

GRANT SUPPORT

Current Grant Support

System Genetic Analysis of Multi-Parent Crosses NIH/NIGMS
co-PI with Gary Churchill (Jackson Laboratory) 07/01/15 – 07/31/23 (25%)
Develop statistical methods and software for the analysis of multi-parent crosses, such as the mouse Diversity Outcross population and the Collaborative Cross.
Role: Co-Principal investigator

NIAID Centers of Excellence for Influenza Research and Surveillance NIH/NIAID
Yoshihiro Kawaoka, PI 04/01/14 – 08/31/21 (8%)
In a genetics study with Diversity Outbred (DO) mice, identify host genes that, in the context of a functional Mx1 *gene, affect the outcome of H5N1 influenza virus infections.*
Role: Co-investigator

A Program of Research in Population Cytogenetics NIH/NICHD
Terry Hassold (Washington State), PI 12/01/10 – 07/31/21 (8%)
Study meiosis in human oocytes and spermatocytes to examine the way in which homologous chromosomes find and synapse with each other and how these processes relate to the formation of crossovers, and to compare the recombination processes between human males and females, including the contribution of chromatin structure and interference to sex-specific differences in recombination rates.
Role: Co-investigator

A Unified High-Performance Web Service for Systems Genetics and Precision Medicine NIH/NIGMS
Robert W. Williams and Saunak Sen, PIs 04/15/17 – 07/31/25 (10%)
Develop and improve the web services framework GeneNetwork 2, a modular high-performance computational resource that provides statistical and genetic tools to analyze and integrate massive omics datasets jointly with information on disease risk and severity.
Role: Co-investigator

Previous Grant Support

Evolution of the Genome-wide Recombination Rate in Mice NIH/NIGMS
Bret Payseur, PI 05/15/17 – 03/31/21 (5%)
Develop a portrait of natural genetic variation in recombination rate across multiple evolutionary scales by measuring polymorphism and divergence in genome-wide recombination rate during oogenesis and spermatogenesis, and by profiling natural genetic variation in molecular processes that lead to crossovers, including the generation of double-strand breaks.
Role: Co-investigator

Genetics of the Island Rule NIH/NIGMS
Bret Payseur, PI 09/10/12 – 02/28/21 (5%)
This project aims to functionally characterize and fine-map quantitative trait loci (QTL) for body size in Gough Island mice and map QTL for extreme body size evolution in a second island population from Papa Westray.
Role: Co-investigator

Collaborative Cross of the Microbiome and Metabolic Disease NIH/NIDDK
Federico Rey, PI 09/23/15 – 08/31/20 (5%)
Identify genes and pathways that modulate gut microbial composition and abundance, and their association to disease, in the mouse Diversity Outcross.
Role: Co-investigator

Alexander Disease: Mechanisms, Modifiers, and Therapeutics NIH/NIHD
Albee Messing, PI 09/20/14 – 07/31/19 (5%)
Identify genomic regions, and ultimately specific genes, that contribute to GFAP *accumulation and toxicity in a mouse model of Alexander disease.*
Role: Co-investigator

The Collaborative Cross Project of Diabetes NIH/NIDDK
Alan Attie, PI 04/01/14 – 01/31/19 (5%)
Identify genes involved in type 2 diabetes using two mouse populations derived from the same set of eight founder strains: the Diversity Outcross and the Collaborative Cross. The project includes detailed phenotyping to identify genes and pathways associated with beta cell functions.
Role: Co-investigator

Genome Dynamics: Evolution, Organization, and Function NIH/NIGMS
Gary Churchill (Jackson Laboratory), PI 04/01/06 – 06/30/16 (9%)
In a project led by Petko Petkov and Ken Paigen, characterize recombination by detailed mapping of recombination events on a single chromosome in a larger mouse backcross.
Role: Co-Investigator

Statistical Methods for Analysis and Integration in Genomic Studies of Disease NIH/NIGMS
Christina Kendziorski, PI 08/01/12 – 04/30/16 (7%)
This project aims to develop and disseminate statistical methods to address challenges that arise in genomic based studies of disease, with particular focus on methods that integrate data across multiple platforms and scales to both identify as well as comprehensively characterize genomic features affecting an individual's disease course and/or likelihood of response to treatment.
Role: Co-investigator

Systems Genetic Analysis of Methamphetamine's Motivational Effects in Mouse AIL NIH/NIDA
Abraham Palmer (U Chicago), PI 07/01/11 – 12/31/15 (10%)
Investigate the genetic underpinnings of the methamphetamine preference in mouse advanced intercross lines (AIL) and develop improved statistical methods and software for system genetics analysis in AIL.
Role: Co-investigator

Statistical Methods and Software for QTL Mapping NIH/NIGMS
Karl Broman, PI 06/01/05 – 05/31/15 (30%)
Develop improved model selection methods of multiple QTL mapping in experimental crosses, develop improved methods for the analysis of recombinant inbred lines and related strains, develop and disseminate the R/qtl software for QTL mapping.
Role: Principal Investigator

Genes and Gene Networks Associated with Obesity and Diabetes NIH/NIDDK
Alan Attie (UW–Madison), PI 12/01/09 – 11/30/14 (5%)
Identify genes and gene networks that play a role in the development of obesity-induced type 2 diabetes in a large mouse intercross with detailed clinical phenotypes and gene expression data on multiple tissues.
Role: Co-investigator

Genetic Complexity and Modifiers of Hirschsprung Disease NIH/NIDDK
Michelle Southard-Smith (Vanderbilt University), PI 07/01/07 – 06/30/12 (8%)
The goal of the proposed studies is to identify additional genes and gene interactions that impact aganglionosis in the $Sox10^{Dom}$ *model.*
Role: Co-Investigator

Statistical Methods for Experimental Genome Populations NIH/NIGMS
Saunak Sen (UCSF), PI 07/01/07 – 06/30/12 (10%)
The goal of this proposed research is to develop statistical design and analysis methods that will reduce experimental cost, make efficient use of existing resources, and better infer causation when we have incomplete control over the assignment of genetic factors to individual organisms.
Role: Co-Investigator

Genetic Basis of WNV Competence in *Culex tarsalis* NIH/NIAID
Jason Rasgon (Johns Hopkins University), PI 07/01/07 – 10/31/11 (2%)
Identify genetic loci contributing to variation in West Nile virus vector competence in susceptible and refractory colonis of Culex tarsalis.
Role: Co-Investigator

Genetic Basis of Nanophthalmos and Axial Hyperopia NIH/NEI
Olof Sundin (Texas Tech), PI 09/01/09 – 08/31/11 (10%)
Investigate the genetic and phenotypic diversity of extreme hyperopia, and identify common hypomorphic alleles of MFRP, the gene that causes nanophthalmos, and determine their effect on ocular structure.
Role: Co-investigator

Mechanism of Inflammation-Induced Airway Hyperactivity NIH/NHLBI
Wayne Mitzner (Johns Hopkins University), PI 12/01/04 – 6/30/07 (3%)
Identify genetic loci contributing to variation in inflammation-induced airway hyperactivity in mice.
Role: Co-Investigator

Center for Epigenetics of Common Human Diseases NIH/NHGRI
Andrew Feinberg, PI 04/01/04 – 06/30/07 (10%)
Develop tools for medical epigenetics, including epigenome discovery, its quantitative analysis, and its application to medicine.
Role: Co-Investigator

Epigenetic Variation and its Determinants in Depression NIH/NIMH
James Potash, PI 04/01/05 – 06/30/07 (10%)
Establish the connection between genetic, environmental, and epigenetic factors and susceptibility to depression.
Role: Co-Investigator

Genetic Mechanisms of Autoimmune Myocarditis NIH/NHLBI
Noel Rose, PI 07/01/04 – 06/30/07 (4%)
Identify genetic loci contributing to susceptibility to autoimmune myocarditis in mice.
Role: Co-Investigator

Catecol-O-methyltransferase and Breast Cancer NIH/NCI
James Yager, PI 09/21/04 – 06/30/07 (2.5%)
The goal of this project is to conduct a rigorous experimental investigation of the hypothesis that decreased COMT activity results in increased DNA damage that contributes to increased cell transformation and breast cancer.
Role: Co-Investigator

Core Center Grant: Biostatistical Center NIH/NEI
Sheila West, PI 07/01/04 – 06/30/07 (5%)
Provide biostatistics support for epidemiological research in ophthalmology.
Role: Senior Biostatistician

Older Americans Independence Center NIH/NIA
Linda Fried, PI 06/01/03 – 06/30/07 (1.5%)
The Center is dedicated to developing the next generation of research to determine the causes and treatments for frailty in older adults.
Role: Advisory Board Member

Statistical Methods for Genetic Epidemiology NIH/NIGMS
Kung-Yee Liang, PI; Karl Broman, acting PI 12/01/00 – 11/30/05 (25%)
Develop and implement new statistical methodology useful for genetic epidemiologic studies of complex chronic diseases.
Role: Co-Investigator

Portable Software for Mapping Quantitative Traits NIH/NHGRI
Ken Manly, PI 09/24/04 – 08/31/05 (5%)
Design and test a graphical user interface for software R/qtl and ensure that the GUI makes the proper connections with the core program.
Role: Co-Investigator

Center for Craniofacial Development and Disorders NIH/NIDR
Terri Beaty, PI 08/01/01 – 08/01/04 (5%)
Biostatistical Core for program project on the genetics of craniofacial disorders.
Role: Co-Investigator

Mouse QTL in Endotoxic Shock — NIH
Roger Reeves, PI — 08/01/01 – 07/30/05 — (10%)
Identify genomic regions contributing to susceptibility to endotoxic shock in mice.
Role: Co-Investigator

Genetic Basis of Nanophthalmos — NIH/NEI
Olof Sundin, PI — 08/15/01 – 06/30/04 — (10%)
Identify the gene responsible for nanophthalmos in a single large pedigree.
Role: Co-Investigator

Center for Craniofacial Development and Disorders — NIH/NIDR
Ethylin Jabs, PI — 08/01/99 – 04/30/04 — (10%)
Map and identify genes contributing to susceptibility to craniofacial disorders by linkage in multiplex families.
Role: Co-Investigator

The Genetics of Age Related Cataract in Salisbury — NIH/NIA
Nathan Congdon, PI — 09/30/00 – 08/31/03 — (10%)
Identify genes contributing to susceptibility to cataract
Role: Co-Investigator

JHSPH Faculty Innovation Fund grant — JHSPH
Karl Broman, PI — 05/01/01 – 04/30/02 — (30%)
Applications of tree-based models to identify epistatic interactions between QTLs in model organisms.
Role: Principal Investigator

INVITED PRESENTATIONS

Scientific Meetings

2021 csv,conf (*online*)
Data Mishaps Night (*online*)

2019 RStudio Conference, Austin, Texas
American Association for the Advancement of Science (AAAS) annual meeting, Washington, DC
Michigan State Plant Breeding, Genetics, and Biotechnology (PBGB) Symposium, East Lansing, Michigan

2018 Complex Trait Community meeting, Glasgow, Scotland
Purdue Symposium on Statistics, West Lafayette, Indiana

2017 Complex Trait Community meeting, Memphis, Tennessee

2016 Genome and Gene Mapping Satellite, Queenstown Research Week, Nelson, New Zealand
Joint Statistical Meetings, Chicago, Illinois
Conference on Learning Tools to Promote Reproducible Research and Open Science, Chicago Chapter, American Statistical Association, Chicago, Illinois

2015 Plant breeding symposium, Texas A&M, College Station, Texas
Joint Statistical Meetings, Seattle, Washington
BioC 2015 (Bioconductor annual meeting), Seattle, Washington
Complex Trait Community annual meeting, Portland, Oregon
The Challenge of Inference from Genome to Phenome, CSIRO Chief Executive Cutting Edge Symposium, Brisbane, Australia
American Association for the Advancement of Science (AAAS) annual meeting, San Jose, California

2014 Fourth Symposium on Biological Data Visualization, Boston, Massachusetts
Scholarly Publishing Symposium, University of Wisconsin–Madison

2013 Open Access, Open Data @ UW, University of Wisconsin–Madison
Workshop on MAGIC-type populations, Cambridge, United Kingdom
Kansas State University Plant Breeding and Genetics Symposium, Manhattan, Kansas
International Biometric Society/ENAR Annual Meeting, Orlando, Florida

2012 EvoSysBio meeting, Wisconsin Institutes for Discovery, University of Wisconsin – Madison
EURATRANS annual meeting, Tutzing, Germany

2011 Quantitative Biology and Bioinformatics in Modern Medicine, Dublin, Ireland

2010 Fourteenth QTL-MAS Workshop, Poznań, Poland

2008 Emerging Statistical Challenges in Genome and Translational Research, Banff, Canada

2007 Systems Medicine Workshop, NHLBI, Bethesda, Maryland

2005 Fifth Australiasian Human Gene Mapping Conference, Mt. Buller, Australia
Joint Statistical Meetings, Minneapolis, Minnesota
CSPS/IMS Joint Meeting, Beijing, China

2004 Taipei Symposium on Statistical Genomics, Academia Sinica, Taipei, Taiwan
Seventh Annual Conference on Computational Genomics, Reston, Virginia
Complex Trait Consortium Third Annual Meeting, Bar Harbor, Maine
Nobel Symposium on Epigenetic Reprogramming in Development and Disease, Stockholm, Sweden
Workshop on the Analysis of Complex Genetic Traits, Mathematical Sciences Research Institute, Berkeley, California

2002 Royal Statistical Society, London, England

2001 Classification Society of North America meeting, St. Louis, Missouri
Modifier Analysis in Cancer Genetics of Experimental Mammals Workshop, Madison, Wisconsin

1996 WNAR/IMS Western Regional Conference, Pullman, Washington

Seminars

2021 Department of Biomedical Informatics, University of Pittsburgh (*online*)
NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome (online)

2020 Center for Quantitative Methods and Data Science, Tufts Medical Center (*online*)

2019 Providence/Boston Center for AIDS Research Biostatistics Core, Boston University
Department of Mathematics, Statistics, and Computer Science, St. Olaf College, Northfield, Minnesota

2018 Department of Statistics, Colorado State University, Fort Collins, Colorado
qBio seminar series, Wisconsin Institute for Discovery, University of Wisconsin–Madison
BBC seminar series, University of California, San Francisco

2017 Department of Bioinformatics and Genomics, University of North Carolina at Charlotte
Berkeley Institute for Data Science, University of California, Berkeley
Genetics Program, North Carolina State University, Raleigh, North Carolina

2016 Department of Genetics, Genomics, and Informatics, University of Tennessee Health Science Center, Memphis, Tennessee
Department of Statistics, University of Auckland, Auckland, New Zealand
Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, New York
Graduate Researchers interested in Data (GRiD), University of Massachusetts, Amherst, Massachusetts
Bioinformatics and Computational Biology, Genentech, South San Francisco, California

2015 Holz Series in Research Data Management, University of Wisconsin–Madison
Division of Biostatistics, Department of Preventive Medicine, University of Tennessee Health Science Center, Memphis, Tennessee
Bioinformatics Division, Walter & Eliza Hall Institute for Medical Research, Melbourne, Australia

2014 Delta Program, University of Wisconsin–Madison
Department of Biostatistics, Harvard School of Public Health, Boston, Massachusetts
Danforth Plant Science Center, St. Louis, Missouri

2013 Graphics Working Group, Department of Statistics, Iowa State University, Ames, Iowa

2012 Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland

2011 Department of Biostatistics, University of Washington, Seattle
Department of Statistics, George Mason University, Fairfax, Virginia
Groningen Bioinformatics Centre, University of Groningen, Groningen, The Netherlands
Department of Biostatistics, Columbia University, New York

2010 Institute of Mathematics and Computer Sciences, Wrocław University of Technology, Wrocław, Poland
Department of Genetics and Animal Breeding, Wrocław University of Environmental and Life Sciences, Wrocław, Poland
Quantitative Biology and Modeling Initiative Program, Michigan State University, East Lansing, Michigan
Integrative Genomics Seminar Series, Vanderbilt University, Nashville, Tennessee
Evolution Seminar Series, University of Wisconsin–Madison
Curriculum in Genetics and Molecular Biology, University of North Carolina at Chapel Hill

2009 Department of Human Genetics, University of California, Los Angeles
Laboratory of Genetics, University of Wisconsin–Madison
Department of Statistics, University of Wisconsin–Madison
Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
Groningen Bioinformatics Centre, University of Groningen, Groningen, The Netherlands
Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom

2008 Annual Retreat, Genomic Sciences Training Program, University of Wisconsin–Madison
Division of Human Genetics, Cincinnati Children's Hospital, Cincinnati, Ohio
Computation and Informatics in Biology and Medicine (CIBM), University of Wisconsin–Madison
Evolution Seminar Series, University of Wisconsin–Madison
Department of Animal Sciences, University of Wisconsin–Madison
2007 Department of Human Genetics, University of Chicago
Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
Statistics Program, St. Olaf College, Northfield, Minnesota
Center for Interdisciplinary Research, St. Olaf College, Northfield, Minnesota
Annual Retreat, Laboratory of Genetics, University of Wisconsin–Madison
Division of Statistics, Northern Illinois University, DeKalb, Illinois
Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison
Department of Human Genetics, University of California, Los Angeles

Department of Statistics, University of California, Berkeley
The Jackson Laboratory, Bar Harbor, Maine
Department of Biostatistics, University of Michigan, Ann Arbor

2006 Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland
Department of Biostatistics, University of Michigan, Ann Arbor
Laboratory of Genetics, University of Wisconsin–Madison
Department of Biostatistics, University of Washington, Seattle

2005 Department of Statistics, University of California, Davis
Department of Genetics, School of Medicine, University of Pennsylvania, Philadelphia
Department of Mathematics and Statistics, University of Maryland, Baltimore County
Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
Section for Medical Inflammation Research, Department of Cell and Molecular Biology, Lund University, Lund, Sweden

2004 Department of Biostatistics, Yale University, New Haven, Connecticut
Marshfield Clinic Research Foundation, Marshfield, Wisconsin
Genetics and Genomic Biology, Hospital for Sick Children, Toronto, Canada
Genetic Interest Group, Center for Human Genetic Research, Vanderbilt University, Nashville, Tennessee
Department of Biostatistics, University of Buffalo
Immunogenetics, Universität Rostock, Germany
Department of Epidemiology and Biostatistics, Memorial Sloan–Kettering Cancer Center, New York

2003 Departments of Statistics and Biostatistics & Medical Informatics, University of Wisconsin–Madison
Department of Statistics, University of California, Los Angeles
Department of Mathematics, Haverford College, Pennsylvania
Department of Biostatistics, University of North Carolina, Chapel Hill
Department of Biostatistics, University of California, San Francisco

2002 Section on Statistical Genetics, University of Alabama, Birmingham
Department of Statistics, University of California, Berkeley
Department of Biostatistics, Johns Hopkins University
Department of Molecular and Cellular Biology, Roswell Park Cancer Institute, Buffalo, New York
Department of Mathematics and Statistics, American University, Washington, DC

2001 Department of Statistics, Yale University
Department of Mathematical Sciences, University of Wisconsin–Milwaukee

2000 Biometric Research Branch, National Cancer Institute, Bethesda, Maryland
The Jackson Laboratory, Bar Harbor, Maine

1999 Department of Biostatistics, Johns Hopkins University
Department of Biostatistics, University of Washington, Seattle
Gemini Research, Cambridge, England
Department of Biostatistics, Johns Hopkins University
Department of Statistics, University of California, Berkeley
Department of Molecular and Cell Biology, University of California, Berkeley

1998 Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
Queensland Institute for Medical Research, Brisbane, Australia
Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
deCODE Genetics, Reykjávik, Iceland
Biostatistics Department, University of Michigan, Ann Arbor

Department of Statistics, University of California, Berkeley
Department of Mathematical Sciences, University of Wisconsin–Milwaukee

1997 Department of Statistics, University of Chicago
Department of Statistics, University of Wisconsin–Madison
Department of Statistics, University of California, Berkeley
Department of Statistics, Stanford University, Palo Alto, California