CURRICULUM VITAE

Karl W. Broman

Work

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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: <i>Identifying quantitative trait loci in experimental crosses</i>)
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

Faculty member, Computational Systems Biology Cluster, University of Wisconsin–Madison Affiliate faculty member, Department of Statistics, University of Wisconsin–Madison Member, Genome Center of Wisconsin, 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 Statistical Association Genetics Society of America Institute of Mathematical Statistics International Biometric Society (ENAR)

EDITORIAL ACTIVITIES

Editorial Board Membership

2017 - present Academic Editor, PeerJ
2016 - present Senior Editor, Genetics
2016 - present Editorial Board, BMC Biology
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; 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; European Journal of Human Genetics; Evolution; 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; 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 Planning and Inference; Journal of Statistical Software; Mammalian Genome; Molecular Biology and Evolution; Molecular Ecology Resources; Molecular Genetics and Genomics; 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; 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 Heath (<i>Chair</i> , 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

- 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
- 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

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

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

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

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

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

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* 6:79–86

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

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. *G*3 5:2177–2186

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

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

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

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

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. *G*3 4:1623–1633

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

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

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

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

- 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
- 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
- 2013 Gruhn JR, Rubio C, **Broman KW**, Hunt PA, Hassold T (2013) Cytological studies of human meiosis: sexspecific differences in recombination originate at, or prior to, establishment of double-strand breaks. PLOS ONE 8:e85075
 - 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
 - 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* 3:1819–1825
 - 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
 - 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
- 2012 **Broman KW**, Kim S, Sen Ś, Ané C, Payseur BA (2012) Mapping quantitative trait loci onto a phylogenetic tree. *Genetics* 192:167–179
 - 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
 - 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* 2:1041–1046
 - 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
 - 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
 - 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
 - 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
 - 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
 - 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
 - **Broman KW** (2012) Genotype probabilities at intermediate generations in the construction of recombinant inbred lines. *Genetics* 190:403–412

Broman KW (2012) Haplotype probabilities in advanced intercross populations. G3 2:199-202

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

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

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

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

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

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

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* 1:3–9

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

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

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

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

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

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 *ADAMTSL*2 founder mutation causes Musladin-Lueke Syndrome, a heritable disorder of beagle dogs, featuring stiff skin and joint contractures. *PLOS ONE* 5:e12817

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

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

Greene JM, Lhost JJ, Burwitz BJ, Budde ML, Macnair CE, Weiker MK, Gostick E, Friedrich TC, **Broman KW**, Price DA, O'Connor SL, O'Connor DH (2010) Extralymphoid CD8⁻T cells resident in tissue from Simian Immunodeficiency Virus SIVmac239Δnef-vaccinated macaques suppress SIVmac239 replication *ex vivo*. *J Virol* 84:3362–3372

Wong AK, Ruhe AL, Dumont BL, Robertson KR, Guerrero G, Shull SM, Ziegle JS, Millon LV, **Broman KW**, Payseur BA, Neff MW (2010) A comprehensive linkage map of the dog genome. *Genetics* 184:595–605

2009 Shavit JA, Manichaikul A, Lemmerhirt HL, **Broman KW**, Ginsburg D (2009) Modifiers of von Willebrand factor identified by natural variation in inbred strains of mice. *Blood* 114:5368–5374

Cheng EY, Hunt PA, Naluai-Cecchini TA, Fligner CL, Fujimoto VY, Pasternack TL, Schwartz JM, Woodruff TJ, Cherry SM, Hansen TA, Vallente RU, **Broman KW**, Hassold TJ (2009) Meiotic recombination in human oocytes. *PLOS Genet* 5:e1000661

Fledel-Alon A, Wilson DJ, **Broman KW**, Wen W, Ober C, Coop G, Przeworski M (2009) Broad-scale recombination patterns underlying proper disjunctions in humans. *PLOS Genet* 5:e1000658

Cox A, Ackert-Bicknell CL, Dumont BL, Ding Y, Bell, JT, Brockmann GA, Wergedal JE, Bult C, Paigen B, Flint J, Tsaih S-W, Churchill GA, **Broman KW** (2009) A new standard genetic map for the laboratory mouse. *Genetics* 182:1335–1344

Dumont BL, **Broman KW**, Payseur BA (2009) Variation in genomic recombination rates among heterogeneous stock mice. *Genetics* 182:1345–1349

Manichaikul A, **Broman KW** (2009) Binary trait mapping in experimental crosses with selective genotyping. *Genetics* 182:863–874

Venkatesan M, **Broman KW**, Sellers M, Rasgon JL (2009) An initial linkage map of the West Nile Virus vector *Culex tarsalis*. *Insect Mol Biol* 18:453–463

Sen Ś, Johannes F, **Broman KW** (2009) Selective genotyping and phenotyping strategies in a complex trait context. *Genetics* 181:1613–1626

Manichaikul A, Moon JY, Sen Ś, Yandell BS, **Broman KW** (2009) A model selection approach for the identification of quantitative trait loci in experimental crosses, allowing epistasis. *Genetics* 181:1077–1086 [Erratum: *Genetics* 184:607, 2010]

Shao H, Burrage LC, Sinasac DS, Hill AE, Ernest SR, O'Brien W, Courtland HW, Jepsen KJ, Kirby A, Kulbokas EJ, Daly MJ, **Broman KW**, Lander ES, Nadeau JH (2008) Genetic architecture of complex traits: Large phenotypic effects and pervasive epistasis. *Proc Natl Acad Sci USA* 105:19910–19914

Hill M, **Broman KW**, Stupka E, Smith W, Jiang D, Sidow A (2008) The *C. savignyi* genetic map and its integration with the reference sequence facilitates insights into chordate genome evolution. *Genome Res* 18:1369–1379

Lupi I, **Broman KW**, Tzuo S-C, Gutenberg A, Martino E, Caturegli P (2008) Novel autoantigens in autoimmune hypophysitis. *Clin Endocrinol* 69:269–278

Paigen K, Szatkiewicz JP, Sawyer K, Leahy N, Parvanov ED, Ng SH, Graber JH, **Broman KW**, Petkov PM (2008) The recombinational anatomy of a mouse chromosome. *PLOS Genet* 4(7): e1000119

Bjornsson HT, Albert TJ, Ladd-Acosta CM, Green RD, Rongione MA, Middle CM, Irizarry RA, **Broman KW**, Feinberg AP (2008) SNP-specific array-based allele-specific expression analysis. *Genome Res* 18:771–779

Peirce JL, **Broman KW**, Lu L, Chesler EJ, Zhou G, Airey DC, Birmingham AE, Williams RW (2008) Genome Reshuffling for Advanced Intercross Permutation (GRAIP): Simulation and permutation for advanced intercross population analysis. *PLOS ONE* 3(4):e1977

Roy-Gagnon M-H, Mathias RA, Fallin MD, Jee SH, **Broman KW**, Wilson AF (2008) An extension of the regression of offspring on mid-parent to test for association and estimate locus-specific heritability: The revised ROMP method. *Ann Hum Genet* 72:115–125

Sinha D, Klise A, Sergeev Y, Hose S, Bhutto IA, Hackler L Jr, Malpic-Ilanos T, Samtani S, Grebe R, Goldberg MF, Hejtmancik JF, Nath A, Zack DJ, Fariss RN, McLeod DS, Sundin O, **Broman KW**, Lutty GA, Zigler JS Jr (2008) β A3/A1-crystallin in astroglial cells regulates retinal vascular remodeling during development. *Mol Cell Neurosci* 37:85–95

2007 Rajagopal SK, Ma Q, Obler D, Shen J, Manichaikul A, Tomita-Mitchell A, Boardman K, Briggs C, Garg V, Srivastava D, Goldmuntz E, **Broman KW**, Benson DW, Smoot LB, Pu WT (2007) Spectrum of heart disease associated with murine and human *GATA4* mutation. *J Mol Cell Cardiol* 43:677–685

Manichaikul A, Palmer AA, Sen Ś, **Broman KW** (2007) Significance thresholds for quantitative trait locus mapping under selective genotyping. *Genetics* 177:1963–1966

Petkov PM, **Broman KW**, Szatkiewicz JP, Paigen K (2007) Crossover interference underlies sex differences in recombination rates. *Trends Genet* 23:539–542

Peirce JL, **Broman KW**, Lu L, Williams RW (2007) A simple method for combining genetic mapping data from multiple crosses and experimental designs. *PLOS ONE* 2(10):e1036

Teuscher F, **Broman KW** (2007) Haplotype probabilities for multiple-strain recombinant inbred lines. *Genetics* 175:1267–1274

Sen Ś, Satagopan JM, **Broman KW**, Churchill GA (2007) R/qtlDesign: Inbred line cross experimental design. *Mamm Genome* 18:87–93

Lemmerhirt HL, **Broman KW**, Shavit JA, Ginsburg D (2007) Genetic regulation of plasma von Willebrand factor levels: QTL analysis in a mouse model. *J Thromb Haemost* 5:329–335

Nichols KM, **Broman KW**, Sundin K, Young JM, Wheeler PA, Thorgaard GH (2007) Quantitative trait loci by maternal cytoplasmic environment interaction for development rate in *Oncorhynchus mykiss*. *Genetics* 175:335–347

2006 **Broman KW**, Sen Ś, Owens SE, Manichaikul A, Southard-Smith EM, Churchill GA (2006) The X chromosome in quantitative trait locus mapping. *Genetics* 174:2151–2158

Shrestha S, Smith MW, **Broman KW**, Farzadegan H, Vlahov D, Strathdee SA (2006) Multi-person-use of syringes among injection drug users in a needle exchange program: A gene based molecular epidemiological analysis. *J Acquir Immune Defic Syndr* 43:335–343

Kess D, Lindqvist AK, Peters T, Wang H, Zamek J, Nischt R, **Broman KW**, Blakytny R, Krieg T, Holmdahl R, Scharffetter-Kochanek K (2006) Identification of susceptibility loci for skin disease in a murine psoriasis model. *J Immunol* 177:4612–4619

Manichaikul A, Dupuis J, Sen Ś, **Broman KW** (2006) Poor performance of bootstrap confidence intervals for the location of a quantitative trait locus. *Genetics* 174:481–489

Sundin OH, **Broman KW**, Chang HH, Vito ECL, Stark WJ, Gottsch JD (2006) A common locus for lateonset Fuchs corneal dystrophy maps to 18q21.2-q21.32. *Invest Ophthalmol Vis Sci* 47:3919–3926

Feenstra B, Skovgaard IM, **Broman KW** (2006) Mapping quantitative trait loci by an extension of the Haley-Knott regression method using estimating equations. *Genetics* 173:2269–2282

Chadwick LH, Pertz L, **Broman KW**, Bartolomei MS, Willard HF (2006) Genetic control of X chromosome inactivation in mice: definition of the *Xce* candidate interval. *Genetics* 173:2111–2119

Grant GR, Robinson SW, Edwards RE, Clothier B, Davies R, Judah DJ, **Broman KW**, Smith AG (2006) Multiple polymorphic genes determine 'normal' hepatic and splenic iron status in mice. *Hepatology* 44:174–185

Orgogozo V, **Broman KW**, Stern DL (2006) High-resolution QTL mapping reveals sign epistasis controlling ovariole number between two Drosophila species. *Genetics* 173:197–205

Shrestha S, Strathdee SA, **Broman KW**, Smith MW (2006) Unknown biological mixtures evaluation using STR analytical quantification. *Electrophoresis* 27:409–415

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2004 Boyadjiev SA, Dodson JL, Radford CL, Ashrafi GH, Beaty TH, Mathews RI, **Broman KW**, Gearhart JP (2004) Clinical and molecular characterization of the bladder exstrophy-epispadias complex: analysis of 232 families. *BJU International* 94:1337–1343

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2002 **Broman KW**, Speed TP (2002) A model selection approach for the identification of quantitative trait loci in experimental crosses. *J Roy Stat Soc* B 64:641–656

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- 1998 **Broman KW**, Murray JC, Sheffield VC, White RL, Weber JL (1998) Comprehensive human genetic maps: Individual and sex-specific variation in recombination. *Am J Hum Genet* 63:861–869

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Letters

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Proceedings and Book Chapters

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González-Recio O, López de Maturana E, Vega AT, Engelman CD, **Broman KW** (2009) Detecting single-nucleotide polymorphism by single-nucleotide polymorphism interactions in rheumatoid arthritis by a two-step approach with machine learning and a Bayesian threshold least absolute shrinkage and selection operator (LASSO) model. *BMC Proc* 3(Suppl 7):S63

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Weber JL, **Broman KW** (2001) Human whole genome polymorphism scans: Past, present and future. In: Rao DC, Province MA (eds) *Genetic Dissection of Complex Traits*. Vol. 42: *Advances in Genetics*. Academic Press, New York, pp. 77–96

Broman KW (1999) Cleaning genotype data. In: Goldin L, Amos CI, Chase GA, Goldstein AM, Jarvik GP, Martinez MM, Suarez BK, Weeks DE, Wijsman EM, MacCluer JE. Genetics Workshop 11: Analysis of genetic and environmental factors in common diseases. *Genet Epidemiol* 17(Suppl. 1):S79–S83

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Technical Reports

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. Identification of *Slco1a6* as a candidate gene that broadly affects gene expression in mouse pancreatic islets. *bioRxiv* doi: 10.1101/020974.

Broman KW (2010) Genetic map construction with R/qtl. Technical report #214, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison

Broman KW (2006) Use of hidden Markov models for QTL mapping. Working paper 125, Department of Biostatistics, Johns Hopkins University, Baltimore, MD

Blades NJ, **Broman KW** (2002) Estimating the number of essential genes in a genome by random transposon mutagenesis. Technical Report MS02-20, Department of Biostatistics, Johns Hopkins University, Baltimore, MD

Bowman KO, Shenton LR, Kastenbaum MA, **Broman K** (1992) Overdispersion: Notes on discrete distributions. Technical Report ORNL/TM-12167, Oak Ridge National Laboratory

SOFTWARE AND OTHER RESOURCES

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quantitative traits in experimental crosses (www.rqtl.org).

R/qtlcharts An R package to create interactive data visualizations for quantitative

trait locus mapping data (kbroman.org/qtlcharts).

aRxiv An R package for searching arXiv, a repository of electronic preprints

for computer science, mathematics, physics, quantitative biology, quantitative financy, and statistics. (github.com/ropensci/aRxiv).

git/GitHub guide Online tutorial on the git version control system and its use with

GitHub.com (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).

Organizing data in spreadsheets Online tutorial on how to layout experimental data within

spreadsheets, such as Excel (kbroman.org/dataorg).

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

Fred Boehm, PhD student, Statistics, University of Wisconsin-Madison

Jianan Tian, PhD student, 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

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, 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

2015 – present	Quentin Sprengelmeyer	Genetics
2012 – present	Michelle Parmenter	Genetics
2012 – present	Molly McDevitt	Biochemistry
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 Comr	mittees, Johns Hopkins University	
2006 - 2007 $2006 - 2007$ $2005 - 2007$ $2004 - 2007$ $2004 - 2005$ $2003 - 2004$ $2003 - 2004$ $2002 - 2003$ 2002 $2001 - 2004$ $2001 - 2002$ $1999 - 2002$	Meera Venkatesan Ching-Yu Cheng Robert Wojciechowski Tanya Teslovich Katherine Swanson Shin Lin Adele Mitchell Rivka Glaser Shawn Soutiere Sadeep Shresthra Rasika Mathias Cynthia James	Molecular Microbiology and Immunology Epidemiology Epidemiology Human Genetics (School of Medicine) Molecular Microbiology and Immunology Human Genetics (School of Medicine) Human Genetics (School of Medicine) Human Genetics (School of Medicine) Environmental Health Sciences Epidemiology Epidemiology Human Genetics (School of Medicine)
Oral Exams, Universit	y of Wisconsin–Madison	
2017	Kyubin Lee Fred Boehm	Computer Sciences Statistics
2016	April Peterson Alessandra York	Genetics Genetics
2015	René Welch	Statistics
2014	Shuyun Ye Michelle Parmenter Jeea Choi	Statistics Genetics Statistics
2013	Jianan Tian Richard Wang Shuang Huang Raja Farhana Raja Mohd Anuar Molly McDevitt	Statistics Genetics Statistics Plant Breeding and Plant Genetics Biochemistry
2012	Katie Clowers	Genetics
2011	Il Youp Kwak	Statistics
2010	Jee Young Moon John Dawson Elias Chaibub Neto Qinglin Pei Jingfang Zhang	Statistics Statistics Statistics Statistics Oncology
2008	Beth Dumont	Genetics
Oral Exams, Johns Ho	opkins University	
2006	Lindsey Garver Benilton Carvalho Yen-Yi Ho Lindsey Enewold Renee Gardner	Molecular Microbiology and Immunology Biostatistics Biostatistics Epidemiology Environmental Health Sciences

Biostatistics Biostatistics

Ani Manichaikul Wenyi Wang

2005

	Meera Venkatesan Audrey Grant	Molecular Microbiology and Immunology Epidemiology	
2004	Katherine Swanson	Molecular Microbiology and Immunology	
2003	Sadeep Shrestha Wei-Min Chen	Epidemiology Biostatistics	
2002	Marie-Hélène Roy-Gagnon	Epidemiology	
2001	Leslie Cope Vivian Yuan Jean-Paul Chretien	Mathematical Sciences (School of Engineering) Mathematical Sciences (School of Engineering) Epidemiology	
2000	Xin Liu Tsuo-Hung Lan Halcyon Skinner	Epidemiology Epidemiology Epidemiology	
1999	David Kaufman	Epidemiology	
ctoral Thesis Defenses, University of Wisconsin–Madison			
2017	Richard Wang	Genetics	
2016	Shuang Huang	Statistics	
2015	Jianan Tian	Statistics	

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2017	Richard wang	Genetics
2016	Shuang Huang	Statistics
2015	Jianan Tian Katie Clowers	Statistics Genetics
2014	Il-Youp Kwak	Statistics
2013	Qinglin Pei	Statistics
2012	John Dawson	Statistics
2011	Michael White	Genetics
2010	Beth Dumont Elias Chaibub Neto	Genetics Statistics
2009	YounJeong Choi	Statistics

Doctoral Thesis Defenses, Johns Hopkins University

2007	Ani Manichaikul	Biostatistics
2005	Katherine Swanson Laura LaRosa Ji Wan Park Martina Johannesson	Molecular Microbiology and Immunology Environmental Health Sciences Epidemiology Lund University, Sweden
2004	Wei-Min Chen Marie-Hélène Roy-Gagnon	Biostatistics Epidemiology
2001	Alison Klein Tsuo-Hung Lan	Epidemiology 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 Heping Hu, MHS Rita Peila, ScM	Epidemiology Epidemiology Epidemiology

Classroom Instruction, University of Wisconsin-Madison

Spring	g, 2017	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Kendziorski, Larget, Ané, Newton, Roy, Keles, Wang, and Craven)
Spring	g, 2016	BMI 826-003	Tools for Reproducible Research
Spring	g, 2015	BMI 826-003	Tools for Reproducible Research
Spring	g, 2014	BMI 826-003 Statistics 877	Tools for Reproducible Research (<i>new</i>) Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
Fall, 2	.012	BMI 826-001	Statistical Methods for QTL Mapping
Spring	g, 2012	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
Spring	g, 2011	Statistics 992-001	Statistical Methods for QTL Mapping (new)
Sumn	ner, 2010	Population Health 904-003	Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Meyers)
Spring	g, 2010	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
Fall, 2	2008	Statistics 371-003	Introductory Applied Statistics for the Life Sciences
Sumn	ner, 2008	Population Health 904-003	Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Skinner)
Spring	g, 2008	Statistics 992-002	Statistical Methods in Molecular Biology (<i>new</i>) (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, and Keles)

Classroom Instruction, Johns Hopkins University

2006 – 2007	Biostatistics 140.668	Special Topics in Genetics and Genomics
2005 – 2006	Biostatistics 140.615–616 Epidemiology 340.631	Statistics for Laboratory Scientists Methods in Genetic Epidemiology I (jointly with Dr. Beaty)

2004 – 2005	Biostatistics 140.776 Biostatistics 140.668 Biostatistics 140.615–616 Epidemiology 340.631	Statistical Computing (jointly with Drs. Caffo, Irizarry, and Ruczinski) Special Topics in Genetics and Genomics (jointly with Dr. Ruczinksi) Statistics for Laboratory Scientists Methods in Genetic Epidemiology I (jointly with Dr. Beaty)
2003 – 2004	Biostatistics 140.776 Biostatistics 140.615–616	Statistical Computing (<i>new</i>) (jointly with Drs. Caffo, Irizarry, and Ruczinski) Statistics for Laboratory Scientists
2002 – 2003	Biostatistics 140.668 Biostatistics 140.615–616	Special Topics in Genetics and Genomics (<i>new</i>) (jointly with Dr. Parmigiani) Statistics for Laboratory Scientists
2001 – 2002	Biostatistics 140.615	Statistics for Laboratory Scientists (new)
2000 – 2001	Biostatistics 140.778 Biostatistics 140.667 Biostatistics 140.668	Advanced Statistical Computing (new) Genetics for Statisticians Statistical Genetics
1999 – 2000	Biostatistics 140.846 Biostatistics 140.668	Genetics for Statisticians (new) Statistical Genetics (new)
room Instruction,	University of California, Berkeley	<i>'</i>

Classro

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

Classroom Instruction, University of Wisconsin-Milwaukee

1991 – 1992 Mathematics 095 Basic Algebra

Other to

teaching		
2017	Workshop on "Steps towards 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	
2016 – 2017	Instructor, Data Carpentry workshops, Advanced Computing Initiative, 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	
2008 – 2016	Instructor and co-organizer, Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, Maine	
2013 – 2016	Lecture on "Creating effective figures and tables" to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison	
2008 – 2016	Lecture on my consulting experiences in Statistical Consulting (Stat 998), Department of Statistics, 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	
2015	Instructor, 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
2014 – 2015	Instructor, Software Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison
2015	Instructor, Software Carpentry workshop, Washington State University, Pullman, Washington
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 inmodel 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

2004 – 2007 Co-Director, MHS Program in Bioinformatics, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

SERVICE ACTIVITIES

International and National

Interna	International and National		
	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 12 th Annual Meeting (Madison, Wisconsin)	
	2003 - 2004	ENAR Distinguished Student Paper Awards Committee	
	2003	IMS Contributed Papers Chair, ENAR/IMS Annual Meeting (Tampa, Florida)	
Univer	sity		
	2016 – present	Genomics Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison	
	2012 – present	Steering Committee, Medical Scientist Training Program, 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 (<i>Chair</i> , 2014 – 2015)	
	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
Departm	nental	
	2010 – present	Chair, Education and Curriculum Committee, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison
	2015 – present	Scientific Advisory and Steering Committee, Biostatistics Computing Group, 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
	2004 – 2007	Medical Informatics, University of Wisconsin–Madison 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

co-PI with Gary Churchill (Jackson Laboratory)

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

A Program of Research in Population Cytogenetics

NIH/NICHD

Terry Hassold (Washington State), PI

12/01/10 - 7/31/20

(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

NIAID Centers of Excellence for Influenza Research and Surveillance

NIH/NIAID

Yoshihiro Kawaoka, PI

04/01/14 - 03/31/17

(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

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: Ćo-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

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

Previous Grant Support

The Genetics and Evolution of Extreme Body Size in Mice from Gough Island

NIH/NIGMS

Bret Payseur, PI

09/10/12 - 06/30/16

(10%)

This project aims to integrate genetic mapping, comparative morphometrics, and population genetics to provide the first detailed genetic portrait of rapid body size evolution in an island mammal, using the Gough Island wild house mice, which have evolved extreme body size in just hundreds of generations.

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-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

07/01/04 - 06/30/07Sheila West, PI (5%)

Provide biostatistics support for epidemiological research in ophthalmology.

Role: Senior Biostatistician

NIH/NIA Older Americans Independence Center

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

12/01/00 - 11/30/05Kung-Yee Liang, PI; Karl Broman, acting PI (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

09/24/04 - 08/31/05Ken Manly, PI (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

08/01/01 - 07/30/05Roger Reeves, PI (10%)

Identify genomic regions contributing to susceptibility to endotoxic shock in mice.

Role: Co-Investigator

Genetic Basis of Nanophthalmos NIH/NEI 08/15/01 - 06/30/04Olof Sundin, PI (10%)

Identify the gene responsible for nanophthalmos in a single large pedigree.

Role: Co-Investigator

Center for Craniofacial Development and Disorders NIH/NIDR

08/01/99 - 04/30/04Ethylin Jabs, PI (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

09/30/00 - 08/31/03Nathan Congdon, PI (10%)

Identify genes contributing to susceptibility to cataract

Role: Co-Investigator

JHSPH Faculty Innovation Fund grant **JHSPH**

05/01/01 - 04/30/02Karl Broman, PI (30%)

Applications of tree-based models to identify epistatic interactions between QTLs in model organisms.

Role: Principal Investigator

INVITED PRESENTATIONS

Scientific Meetings

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
Semina	ars
2017	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

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