

CURRICULUM VITAE

Karl W. Broman

Department of Biostatistics and Medical Informatics
School of Medicine and Public Health
University of Wisconsin–Madison
2126 Genetics-Biotechnology Center
425 Henry Mall
Madison, Wisconsin 53706

Phone: 608-262-4633

Email: broman@wisc.edu

Web: <https://kbroman.org>

EDUCATION

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|-------------|---|
| 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, <i>Summa Cum Laude</i> , Mathematics, University of Wisconsin–Milwaukee |

PROFESSIONAL POSITIONS

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| 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 Statistical Association
 Genetics Society of America
 Institute of Mathematical Statistics
 International Biometric Society (ENAR)

EDITORIAL ACTIVITIES

Editorial Board Membership

- 2016 – present Senior Editor, *Genetics*
 2016 – present 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; 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 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; 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

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| 2010 – 2015 | Center for Inherited Disease Research (CIDR) Access Committee, National Human Genome Research Institute, National Institutes of Health (<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/qt1*. Springer (ISBN: 978-0-387-92124-2)

Journal Articles

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*, to appear

- 2019 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

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

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

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

Broman KW, Gatti DM, Simecek P, Furlotte NA, Prins P, Sen Ś, Yandell BS, Churchill GA (2019) R/qt12: software for mapping quantitative trait loci with high-dimensional data and multi-parent populations. *Genetics* 211:495–502

- 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
- Keller MP, Gatti DM, Schueler KL, Rabaglia ME, Stapleton DS, Simecek P, Vincent M, Allen S, Broman AT, Bacher R, Kendzierski C, **Broman KW**, Yandell BS, Churchill GA, Attie AD (2018) Genetic drivers of pancreatic islet function. *Genetics* 209:335–356
- Broman KW**, Woo KH (2018) Data organization in spreadsheets. *Am Stat* 72:2–10
- 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
- 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
- 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
- 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, Kendzierski 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
- 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
- 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, Kendzierski 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
- 2015 Tian J, Keller MP, Oler AT, Rabaglia ME, Schueler KL, Stapleton DS, Broman AT, Zhao W, Kendzierski 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, Kendzierski C, Yandell BS, Sen Ś, Attie AD (2015) Identification and correction of sample mix-ups in expression genetic data: A case study. *G3* 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. *G3* 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: sex-specific 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, Kendzierski 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

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

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 *ADAMTSL2* founder mutation causes Musladin-Lueke Syndrome, a heritable disorder of beagle dogs, featuring stiff skin and joint contractures. *PLoS ONE* 5:e12817

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

Manichaikul A, Moon JY, Sen S, 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]

2008 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**, Luty 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 S, **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 S, 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 S, 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**, Blakytyn 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 S, **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 late-onset 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
- Reilly KM, **Broman KW**, Bronson RT, Tsang S, Loisel DA, Christy ES, Sun Z, Diehl J, Munroe DJ, Tuskan RG (2006) An imprinted locus epistatically influences *Nstr1* and *Nstr2* to control resistance to nerve sheath tumors in a neurofibromatosis type 1 mouse model. *Cancer Res* 66:62–68
- Sundin OH, Jun AS, **Broman KW**, Liu SH, Sheehan SE, Vito ECL, Stark WJ, Gottsch JD (2006) Linkage of late-onset Fuchs corneal dystrophy to a novel locus at 13pTel-13q12.13. *Invest Ophthalmol Vis Sci* 47:140–145
- 2005 Sundin OH, Leppert GS, Silva ED, Yang J-M, Dharmaraj S, Maumenee IH, Santos LC, Parsa CF, Traboulsi EI, **Broman KW**, DiBernardo C, Sunness JS, Toy J, Weinberg EM (2005) Extreme hyperopia is the result of null mutations in *MFRP*, which encodes a Frizzled-related protein. *Proc Natl Acad Sci USA* 102:9553–9558
- Gottsch JD, Sundin OH, Liu SH, Jun AS, **Broman KW**, Stark WJ, Vito EC, Narang AK, Thompson JM, Magovern M (2005) Inheritance of a novel *COL8A2* mutation defines a distinct early-onset subtype of Fuchs corneal dystrophy. *Invest Ophthalmol Vis Sci* 46:1934–1939
- Owens SE, **Broman KW**, Wiltshire T, Elmore JB, Bradley KM, Smith JR, Southard-Smith EM (2005) Genome-wide linkage identifies novel modifier loci of aganglionosis in the *Sox10^{Dom}* model of Hirschsprung disease. *Hum Mol Genet* 14:1549–1558
- Broman KW** (2005) The genomes of recombinant inbred lines. *Genetics* 169:1133–1146
[Erratum: *Genetics* 173:2419, 2006]
- Guler ML, Ligons DL, Wang Y, Bianco M, **Broman KW**, Rose NR (2005) Two autoimmune diabetes loci influencing T cell apoptosis control susceptibility to experimental autoimmune myocarditis. *J Immunol* 174:2167–2173
- Congdon N, **Broman KW**, Lai H, Munoz B, Bowie H, Gilbert D, Wojciechowski R, West SK (2005) Cortical, but not posterior subcapsular, cataract shows significant familial aggregation in an older population after adjustment for possible shared environmental factors. *Ophthalmology* 112:73–77
- Chen WM, **Broman KW**, Liang KY (2005) Power and robustness of linkage tests for quantitative traits in general pedigrees. *Genet Epidemiol* 28:11–23
- 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
- The Complex Trait Consortium [113 authors] (2004) The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nat Genet* 36:1133–1137
- Chen S, Wang W, **Broman KW**, Katki HA, Parmigiani G (2004) BayesMendel: an R environment for Mendelian risk prediction. *Stat Appl Genet Mol Biol* 3(1): article 21

- Neff MW, Robertson KR, Wong AK, Safra N, **Broman KW**, Slatkin M, Mealey KL, Pedersen NC (2004) Breed distribution and history of canine *mdr1-1Δ*, a pharmacogenetic mutation that marks the emergence of breeds from the collie lineage. *Proc Natl Acad Sci USA* 101:11725–11730
- Tankersley CG, **Broman KW** (2004) Interactions in hypoxic and hypercapnic breathing are genetically linked to mouse chromosomes 1 and 5. *J Appl Physiol* 97:77–84
- Congdon N, **Broman KW**, Lai H, Munoz B, Bowie H, Gilbert D, Wojciechowski R, Alston C, West SK (2004) Nuclear cataract shows significant familial aggregation in an older population after adjustment for possible shared environmental factors. *Invest Ophthalmol Vis Sci* 45:2182–2186
- Tankersley CG, Campen M, Bierman A, Flanders SE, **Broman KW**, Rabold R (2004) Particle effects on heart-rate regulation in senescent mice. *Inhal Toxicol* 16:381–390
- Sivagnanasundaram S, **Broman KW**, Liu M, Petronis A (2004) Quasi-linkage: a confounding factor in linkage analysis of complex disease? *Hum Genet* 114:588–593
- Chen WM, **Broman KW**, Liang KY (2004) Quantitative trait linkage analysis by generalized estimating equations: Unification of variance components and Haseman-Elston regression. *Genet Epidemiol* 26:265–272
- Kieffer TL, Finucane MM, Nettles RE, Quinn TC, **Broman KW**, Ray SC, Persaud D, Siliciano RF (2004) Genotypic analysis of HIV-1 drug resistance at the limit of detection: Virus production without evolution in treated adults with undetectable HIV loads. *J Infect Dis* 189:1452–1456
- 2003 Lidman O, Swanberg M, Horvath L, **Broman KW**, Olsson T, Piehl F (2003) Discrete gene loci regulate neurodegeneration, lymphocyte infiltration and major histocompatibility complex class II expression in the CNS. *J Neurosci* 23:9817–9823
- Glaser RL, **Broman KW**, Schulman RL, Eskenzai B, Wyrobek AJ, Jabs EW (2003) The paternal age effect in Apert syndrome is due in part to the increased frequency of mutations in sperm. *Am J Hum Genet* 73:939–947
- Denny P, Hopes E, Gingles N, **Broman KW**, McPheat W, Morten J, Alexander J, Andrew PW, Brown SDM (2003) A major locus conferring susceptibility to infection by *Streptococcus pneumoniae* in mice. *Mamm Genome* 14:448–453
- Lamichhane G, Zignol M, Blades NJ, Geiman DE, Dougherty A, **Broman KW**, Bishai WR (2003) A post-genomic method for predicting essential genes at subsaturation levels of mutagenesis: Application to *Mycobacterium tuberculosis*. *Proc Natl Acad Sci USA* 100:7213–7218
- Broman KW**, Wu H, Sen Ś, Churchill GA (2003) R/qtl: QTL mapping in experimental crosses. *Bioinformatics* 19:889–890
- Broman KW** (2003) Mapping quantitative trait loci in the case of a spike in the phenotype distribution. *Genetics* 163:1165–1175
- Becanovic K, Wallstrom E, Kornek B, Glaser A, **Broman KW**, Dahlman I, Olofsson P, Holmdahl R, Luthman H, Lassmann H, Olsson T (2003) New loci regulating rat myelin oligodendrocyte glycoprotein-induced experimental autoimmune encephalomyelitis. *J Immunol* 170:1062–1069
- 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
- Jun AS, **Broman KW**, Do DV, Akpek EK, Stark WJ, Gottsch JD (2002) Endothelial dystrophy, iris hypoplasia, congenital cataract, and stromal thinning (EDICT) syndrome maps to chromosome 15q22.1-q25.3. *Am J Ophthalmol* 134:172–176
- Broman KW**, Rowe LB, Churchill GA, Paigen K (2002) Crossover interference in the mouse. *Genetics* 160:1123–1131
- 2001 Hunter KW, **Broman KW**, Le Voyer T, Lukes L, Cozma D, Debies MT, Rouse J, Welch DR (2001) Predisposition to efficient mammary tumor metastatic progression is linked to the breast cancer metastasis suppressor gene *Brms1*. *Cancer Res* 61:8866–8872

Ravenel JD, **Broman KW**, Perlman EJ, Niemitz EL, Jayawardena TM, Bell DW, Haber DA, Uejima H, Feinberg AP (2001) Loss of imprinting of Insulin-Like Growth Factor-II (IGF2) and specific biological subtypes of Wilms' tumor. *J Natl Cancer Inst* 93:1698–1703

Broman KW (2001) Review of statistical methods for QTL mapping in experimental crosses. *Lab Animal* 30(7):44–52

Broman KW (2001) Estimation of allele frequencies with data on sibships. *Genet Epidemiol* 20:307–315 [Erratum: *Genet Epidemiol* 23:465–466, 2002]

Giglio S, **Broman KW**, Matsumoto N, Calvari V, Gimelli G, Neumann T, Ohashi H, Voullaire L, Larizza D, Giorda R, Weber JL, Ledbetter DH, Zuffardi O (2001) Olfactory receptor-gene clusters, genomic-inversion polymorphisms, and common chromosome rearrangements. *Am J Hum Genet* 68:874–883

Boyartchuk VL, **Broman KW**, Mosher RE, D'Orazio SEF, Starnbach MN, Dietrich WF (2001) Multigenic control of *Listeria monocytogenes* susceptibility in mice. *Nat Genet* 27:259–260

Yu A, Zhao C, Fan Y, Jang W, Mungall AJ, Deloukas P, Olsen A, Doggett NA, Ghebranious N, **Broman KW**, Weber JL (2001) Comparison of human genetic and sequence-based physical maps. *Nature* 409:951–953

Lichter-Konecki U, **Broman KW**, Blau EB, Konecki DS (2001) Genetic and physical mapping of the locus for autosomal dominant renal Fanconi syndrome, on chromosome 15q15.3. *Am J Hum Genet* 68:264–268

2000 Kissebah AH, Sonnenberg GE, Myklebust J, Goldstein M, **Broman K**, James RG, Marks JA, Krakower GR, Jacob HJ, Weber J, Martin L, Blangero J, Comuzzie AG (2000) Quantitative trait loci on chromosomes 3 and 17 influence phenotypes of the metabolic syndrome. *Proc Natl Acad Sci USA* 97:14478–14483

Witte JS, Goddard KAB, Conti DV, Elston RC, Lin J, Suarez BK, **Broman KW**, Burmester JK, Weber JL, Catalona WJ (2000) Genomewide scan for prostate cancer-aggressiveness loci. *Am J Hum Genet* 67:92–99

Broman KW, Weber JL (2000) Characterization of human crossover interference. *Am J Hum Genet* 66:1911–1926

Suarez BK, Lin J, Burmester JK, **Broman KW**, Weber JL, Banerjee TK, Goddard KAB, Witte JS, Elston RC, Catalona WJ (2000) A genome screen of multiplex prostate cancer sibships. *Am J Hum Genet* 66:933–944

Brown AS, Feingold E, **Broman KW**, Sherman SL (2000) Genome-wide variation in recombination in female meiosis: A risk factor for non-disjunction of chromosome 21. *Hum Mol Genet* 9:515–523

1999 **Broman KW**, Weber JL (1999) Long homozygous chromosomal segments in reference families from the Centre d'Étude du Polymorphisme Humain. *Am J Hum Genet* 65:1493–1500

Broman KW, Weber JL (1999) Method for constructing confidently ordered linkage maps. *Genet Epidemiol* 16:337–343

Neff MW, **Broman KW**, Mellersh CS, Ray K, Acland GM, Aguirre GD, Ziegle JS, Ostrander EA, Rine J (1999) A second-generation linkage map of the domestic dog, *Canis familiaris*. *Genetics* 151:803–820

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

Broman K, Speed T, Tigges M (1998) Estimation of antigen-responsive T cell frequencies in PBMC from human subjects. *Stat Sci* 13:4–8

1996 **Broman K**, Speed T, Tigges M (1996) Estimation of antigen-responsive T cell frequencies in PBMC from human subjects. *J Immunol Meth* 198:119–132

Dernburg AF, **Broman KW**, Fung JC, Marshall WF, Philips J, Agard DA, Sedat JW (1996) Perturbation of nuclear architecture by long-distance chromosome interactions. *Cell* 85:745–759

Editorials

Broman KW (2005) Mapping expression in randomized rodent genomes. *Nat Genet* 37:209–210

Broman KW, Feingold E (2004) SNPs made routine. *Nat Methods* 1:104–105

Letters

Sieberts SK, **Broman KW**, Gudbjartsson DF (2004) “Biased towards the null” means reduced power. *Am J Hum Genet* 75:720–722

Broman KW, Caffo BS (2003) Simulation-based *P* values: Response to North et al. *Am J Hum Genet* 72:496

Ravenel JD, Perlman EJ, **Broman KW**, Feinberg AP (2002) Response: Re: Loss of imprinting of Insulin-Like Growth Factor-II (IGF2) gene in distinguishing specific biologic subtypes of Wilms tumor. *J Natl Cancer Inst* 94:1809–1810

Broman KW, Weber JL (1998) Estimation of pairwise relationships in the presence of genotyping errors. *Am J Hum Genet* 63:1563–1564

Proceedings and Book Chapters

Broman KW (2012) Applied statistics and exposition (commentary). In: Dudoit S (ed) *Selected Works of Terry Speed*, Springer, pp. 353–355

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

Broman KW, Heath SC (2007) Managing and manipulating genetic data. In: Barnes MR (ed) *Bioinformatics for Geneticists*, 2nd edition, Wiley, pp. 17–31

Broman KW, Matsumoto N, Giglio S, Martin CL, Roseberry JA, Zuffardi O, Ledbetter DH, Weber JL (2003) Common long human inversion polymorphism on chromosome 8p. In: Goldstein DR (ed) *Science and Statistics: A Festschrift for Terry Speed*. IMS Lecture Notes-Monograph Series, Vol 40, pp. 237–245

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

Broman KW, Speed TP (1999) A review of methods for identifying QTLs in experimental crosses. In: Seillier-Moisewitsch F (ed) *Statistics in Molecular Biology and Genetics*. IMS Lecture Notes-Monograph Series, Vol. 33, pp. 114–142

Technical Reports and Preprints

Lobo AK, Traeger LL, Keller MP, Attie AD, Rey FE, **Broman KW** (2019) Identification of sample mix-ups and mixtures in microbiome data in Diversity Outbred mice. *bioRxiv* doi:10.1101/529040

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

| | |
|-------------------------|---|
| 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/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 finance, 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). |
| 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 – present | 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

| | | |
|----------------|------------------------------|-----------------------------------|
| 2019 – present | Athena Golfinos | Cellular and Molecular Pathology |
| 2018 – present | Theeva Chandereng | Statistics |
| 2018 – present | Michael Kartje | Genetics |
| 2017 – present | Jeremy Lange | Genetics |
| 2017 – present | Christopher McAllester | Genetics |
| 2016 – present | April Peterson | Genetics |
| 2015 – present | Quentin Sprengelmeyer | Genetics |
| 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

| | | |
|------|---|---|
| 2019 | Michael Kartje | Genetics |
| 2018 | Christopher McAllester Thevaa Chandereng | Genetics Statistics |
| 2017 | Constanza Rojo Quentin Sprengelmeyer Jeremy Lange Kyubin Lee Fred Boehm | Statistics Genetics Genetics 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 Hopkins University

| | | |
|------|--|--|
| 2006 | Lindsey Garver Benilton Carvalho Yen-Yi Ho Lindsey Enewold Renee Gardner | Molecular Microbiology and Immunology Biostatistics Biostatistics Epidemiology Environmental Health Sciences |
| 2005 | Ani Manichaikul Wenyi Wang Meera Venkatesan Audrey Grant | Biostatistics Biostatistics 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 |

Doctoral Thesis Defenses, University of Wisconsin–Madison

| | | |
|------|------------------------------------|---------------------------------|
| 2019 | Fred Boehm Molly McDevitt | Statistics Biochemistry |
| 2018 | Kyubin Lee René Welch | Computer Sciences Statistics |
| 2017 | Richard Wang Michelle Parmenter | Genetics 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

| | | |
|--------------|-------------------------------|--|
| Fall, 2019 | BMI 881 | Biomedical Data Science Scholarly Literature (<i>new</i>) |
| Spring, 2019 | Statistics 877 | Statistical Methods in Molecular Biology (jointly with Drs. Kendzierski, Lu, Dewey, Newton, Keles, Roy, Ané, and Tang) |
| Spring, 2018 | Agronomy 957 | Plant Breeding and Plant Genetics seminar (jointly with Brian Yandell) |
| Spring, 2017 | Statistics 877 | Statistical Methods in Molecular Biology (jointly with Drs. Kendzierski, Larget, Ané, Newton, Roy, Keles, Wang, and Craven) |
| Spring, 2016 | BMI 826-003 | Tools for Reproducible Research |
| Spring, 2015 | BMI 826-003 | Tools for Reproducible Research |
| Spring, 2014 | BMI 826-003 Statistics 877 | Tools for Reproducible Research (<i>new</i>) Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendzierski, Larget, Ané, Yandell, Wang, and Keles) |
| Fall, 2012 | BMI 826-001 | Statistical Methods for QTL Mapping |
| Spring, 2012 | Statistics 877 | Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendzierski, Larget, Ané, Yandell, Wang, and Keles) |
| Spring, 2011 | Statistics 992-001 | Statistical Methods for QTL Mapping (<i>new</i>) |
| Summer, 2010 | Population Health 904-003 | Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Meyers) |
| Spring, 2010 | Statistics 877 | Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendzierski, Larget, Ané, Yandell, Wang, and Keles) |
| Fall, 2008 | Statistics 371-003 | Introductory Applied Statistics for the Life Sciences |
| Summer, 2008 | Population Health 904-003 | Analytic Methods in Genetic Epidemiology (jointly with Drs. Engelman, Payseur, and Skinner) |
| Spring, 2008 | Statistics 992-002 | Statistical Methods in Molecular Biology (<i>new</i>) (jointly with Drs. Newton, Kendzierski, Larget, Ané, Yandell, and Keles) |

Classroom Instruction, Johns Hopkins University

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| 2006 – 2007 | Biostatistics 140.668 | Special Topics in Genetics and Genomics |
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| 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. Ruczinski) 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 (<i>new</i>) |
| 2000 – 2001 | Biostatistics 140.667 Biostatistics 140.667 Biostatistics 140.668 | Advanced Statistical Computing (<i>new</i>) Genetics for Statisticians Statistical Genetics |
| 1999 – 2000 | Biostatistics 140.846 Biostatistics 140.668 | Genetics for Statisticians (<i>new</i>) Statistical Genetics (<i>new</i>) |

Classroom Instruction, University of California, Berkeley

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| Summer, 1994 | Statistics 131A | Introductory Statistics for Social and Life Scientists |
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Classroom Instruction, University of Wisconsin–Milwaukee

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|-------------|-----------------|---------------|
| 1991 – 1992 | Mathematics 095 | Basic Algebra |
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Other teaching

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| 2016 – 2018 | Instructor, Data Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison | |
| 2017 – 2018 | Workshop on Reproducible Research, Summer Institute in Statistics for Big Data, Seattle, Washington | |
| 2013 – 2018 | Lecture on “Creating effective figures and tables” to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison | |
| 2018 | Instructor, Workshop on Advanced R and R/qlt, ICRISAT, Hyderabad, India | |
| 2018 | Lecture on “Steps toward reproducible research” for the Cellular and Molecular Pathology Graduate Program, 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/qlt and R/qlt2 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
- 2008 – 2017 Periodic seminars on “Creating effective figures and tables” in the Department of Pathology and Laboratory Medicine, University of Wisconsin–Madison
- 2008 – 2017 Lecture on my consulting experiences in Statistical Consulting (Stat 998), Department of Statistics, University of Wisconsin–Madison
- 2008 – 2016 Instructor and co-organizer, Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, Maine
- 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 R/qlt 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/qlt, 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

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| 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 – present | 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 15 th 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 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) |

University

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|----------------|---|
| 2017 – present | Faculty Senator, University of Wisconsin–Madison |
| 2012 – present | Steering Committee, Medical Scientist Training Program, School of Medicine and Public Health, 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 |

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| 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 |

Departmental

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|----------------|---|
| 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 – present | 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
co-PI with Gary Churchill (Jackson Laboratory)

07/01/15 – 07/31/23 (25%)

NIH/NIGMS R01GM070683

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

Yoshihiro Kawaoka, PI

04/01/14 – 03/31/20 (8%)

NIH/NIAID HHSN272201400008C

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

Terry Hassold (Washington State), PI

12/01/10 – 07/31/20 (8%)

NIH/NICHD R37HD021341

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

Collaborative Cross of the Microbiome and Metabolic Disease

Federico Rey (UW–Madison), PI

09/23/15 – 08/31/20 (5%)

NIH/NIDDK R01DK018259

Identify genes and pathways that modulate gut microbial composition and abundance, and their association to disease, in the mouse Diversity Outcross.

Role: Co-investigator

Genetics of the Island Rule

Bret Payseur (UW–Madison), PI

09/10/12 – 02/28/21 (5%)

NIH/NIGMS R01GM100426

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

Evolution of the Genome-wide Recombination Rate in Mice

Bret Payseur (UW–Madison), PI

05/15/17 – 03/31/21 (5%)

NIH/NIGMS R01GM100426

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

A Unified High-Performance Web Service for Systems Genetics and Precision Medicine

Robert W. Williams and Saunak Sen (U Tennessee), PIs

04/15/17 – 03/31/21 (10%)

NIH/NIGMS R01GM1238489

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

Alexander Disease: Mechanisms, Modifiers, and Therapeutics

Albee Messing (UW–Madison), PI

09/20/14 – 07/31/19

(5%)

NIH/NIHD P01HD076892

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

Alan Attie (UW–Madison), PI

04/01/14 – 01/31/19

(5%)

NIH/NIDDK R01DK101573

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

Gary Churchill (Jackson Laboratory), PI

04/01/06 – 06/30/16

(9%)

NIH/NIGMS P50GM076468

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

Christina Kendzierski (UW–Madison), PI

08/01/12 – 04/30/16

(7%)

NIH/NIGMS R01GM102756

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

Abraham Palmer (U Chicago), PI

07/01/11 – 12/31/15

(10%)

NIH/NIDA R01DA021336

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

Karl Broman, PI

06/01/05 – 05/31/15

(30%)

NIH/NIGMS R01GM074244

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

Alan Attie (UW–Madison), PI

12/01/09 – 11/30/14

(5%)

NIH/NIDDK R01DK66369

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

Michelle Southard-Smith (Vanderbilt University), PI

07/01/07 – 06/30/12

(8%)

NIH/NIDDK R01DK060047

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

Saunak Sen (UCSF), PI

07/01/07 – 06/30/12

(10%)

NIH/NIGMS R01GM078338

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*

Jason Rasgon (Johns Hopkins University), PI

07/01/07 – 10/31/11

(2%)

NIH/NIAID R01AI067371

*Identify genetic loci contributing to variation in West Nile virus vector competence in susceptible and refractory colonies of *Culex tarsalis*.*

Role: Co-Investigator

Genetic Basis of Nanophthalmos and Axial Hyperopia

Olof Sundin (Texas Tech), PI

09/01/09 – 08/31/11

(10%)

NIH/NEI R01EY013610

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

Wayne Mitzner (Johns Hopkins University), PI

12/01/04 – 6/30/07

(3%)

NIH/NHLBI P01HL010342

Identify genetic loci contributing to variation in inflammation-induced airway hyperactivity in mice.

Role: Co-Investigator

Center for Epigenetics of Common Human Diseases

Andrew Feinberg (Johns Hopkins University), PI

04/01/04 – 06/30/07

(10%)

NIH/NHGRI P50HG003233

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

James Potash (Johns Hopkins University), PI

04/01/05 – 06/30/07

(10%)

NIH/NIMH R01MH074131

Establish the connection between genetic, environmental, and epigenetic factors and susceptibility to depression.

Role: Co-Investigator

Genetic Mechanisms of Autoimmune Myocarditis

Noel Rose (Johns Hopkins University), PI

07/01/04 – 06/30/07

(4%)

NIH/NHLBI R01HL077611

Identify genetic loci contributing to susceptibility to autoimmune myocarditis in mice.

Role: Co-Investigator

Catechol-O-methyltransferase and Breast Cancer

James Yager (Johns Hopkins University), PI

09/21/04 – 06/30/07

(2.5%)

NIH/NCI R01CA77550

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

Sheila West (Johns Hopkins University), PI

07/01/04 – 06/30/07

(5%)

NIH/NEI EY01765

Provide biostatistics support for epidemiological research in ophthalmology.

Role: Senior Biostatistician

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| Older Americans Independence Center Linda Fried (Johns Hopkins University), PI NIH/NIA P50AG21334 <i>The Center is dedicated to developing the next generation of research to determine the causes and treatments for frailty in older adults.</i> Role: Advisory Board Member | 06/01/03 – 06/30/07 | (1.5%) |
| Statistical Methods for Genetic Epidemiology Kung-Yee Liang, PI; Karl Broman, acting PI NIH/NIGMS R01GM049909 <i>Develop and implement new statistical methodology useful for genetic epidemiologic studies of complex chronic diseases.</i> Role: Co-Investigator | 12/01/00 – 11/30/05 | (25%) |
| Portable Software for Mapping Quantitative Traits Ken Manly (Rosewell Park Cancer Institute, PI NIH/NHGRI P41HG001656 <i>Design and test a graphical user interface for software R/qtl and ensure that the GUI makes the proper connections with the core program.</i> Role: Co-Investigator | 09/24/04 – 08/31/05 | (5%) |
| Center for Craniofacial Development and Disorders Terri Beaty (Johns Hopkins University), PI NIH/NIDR P60DE013078 <i>Biostatistical Core for program project on the genetics of craniofacial disorders.</i> Role: Co-Investigator | 08/01/01 – 08/01/04 | (5%) |
| Mouse QTL in Endotoxic Shock Roger Reeves (Johns Hopkins University), PI NIH/NIGMS R01GM062599 <i>Identify genomic regions contributing to susceptibility to endotoxic shock in mice.</i> Role: Co-Investigator | 08/01/01 – 07/30/05 | (10%) |
| Genetic Basis of Nanophthalmos Olof Sundin (Johns Hopkins University), PI NIH/NEI R01EY010813 <i>Identify the gene responsible for nanophthalmos in a single large pedigree.</i> Role: Co-Investigator | 08/15/01 – 06/30/04 | (10%) |
| Center for Craniofacial Development and Disorders Ethylin Jabs (Johns Hopkins University), PI NIH/NIDR P50DE011131 <i>Map and identify genes contributing to susceptibility to craniofacial disorders by linkage in multiplex families.</i> Role: Co-Investigator | 08/01/99 – 04/30/04 | (10%) |
| The Genetics of Age Related Cataract in Salisbury Nathan Congdon (Johns Hopkins University), PI NIH/NIA R01AG018730 <i>Identify genes contributing to susceptibility to cataract</i> Role: Co-Investigator | 09/30/00 – 08/31/03 | (10%) |
| JHSPH Faculty Innovation Fund grant Karl Broman, PI Johns Hopkins School of Public Health <i>Applications of tree-based models to identify epistatic interactions between QTLs in model organisms.</i> Role: Principal Investigator | 05/01/01 – 04/30/02 | (30%) |

INVITED PRESENTATIONS

Scientific Meetings

- 2019 RStudio Conference, Austin, Texas
American Association for the Advancement of Science (AAAS) annual meeting, Washington, DC

- 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 Australasian 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

- 2019 Providence/Boston Center for AIDS Research Biostatistics Core, Boston University
- 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, Reykjavik, 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