

CURRICULUM VITAE

Karl W. Broman

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

EDITORIAL ACTIVITIES

Editorial Board Membership

2016 – 2021 Senior Editor, *Genetics*

2016 – 2021 Editorial Board, *BMC Biology*

2017 – 2019 Academic Editor, *PeerJ*

2004 – 2010 Associate Editor, *Genetics*

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

2004 – 2007 Associate Editor, *Biostatistics*

Peer Review Activities

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

Statistician; Annals of Applied Statistics; Annals of Human Genetics; Annals of Statistics; Arteriosclerosis, Thrombosis, and Vascular Biology; Bioinformatics; Biometrics; Biostatistics; BMC Bioinformatics; BMC Biology; BMC Genetics; BMC Genomics; BMC Medical Research Methodology; BMC Proceedings; BMC Research Notes; Cancer Research; Circulation Research; Computational Statistics & Data Analysis; Crop Science; eLife; European Journal of Human Genetics; Evolution; G3 (Bethesda); Gene; Genes, Brain, and Behavior; Genes & Immunity; Genetic Epidemiology; Genetica; Genetical Research; Genetics; Genetics Research; Genetics Selection Evolution; Genome; Genome Research; Genomics; Growth, Development, & Aging; Harvard Data Science Review; Heredity; Human Genetics; Human Heredity; Human Molecular Genetics; IEEE/ACM Transactions on Computational Biology and Bioinformatics; Journal of Agricultural, Biological, and Environmental Statistics; Journal of the American Society of Nephrology; Journal of the American Statistical Association; Journal of Applied Genetics; Journal of Bioinformatics and Computational Biology; Journal of Computational and Graphical Statistics; Journal of Fish Biology; Journal of Heredity; Journal of Immunology; Journal of Neuroscience; Journal of Open Source Software; Journal of Statistical Distributions and Applications; Journal of Statistical Planning and Inference; Journal of Statistical Software; Lab Animal; 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; New Phytologist; Nucleic Acids Research; Ophthalmic Epidemiology; Pacific Symposium on Biocomputing; Physical Review Letters; Physiological Genomics; Plant Cell; Plant Physiology; PLoS Biology; PLoS Computational Biology; PLoS Genetics; PLoS ONE; Proceedings of the National Academy of Sciences USA; Proceedings of the Royal Society B: Biological Sciences; 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); NWO Talent Programme (Netherlands); and Telethon (Italy)

PUBLICATIONS

Books

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

Journal Articles

- 2023 Zhang Q, Linke V, Overmyer KA, Traeger LL, Kasahara K, Miller IJ, Manson DE, Polaske TJ, Kerby RL, Kemis JH, Trujillo EA, Reddy TR, Russell JD, Schueler KL, Stapleton DS, Rabaglia ME, Seldin M, Gatti DM, Keele GR, Pham DT, Gerdt JP, Vivas EI, Lusi AJ, Keller MP, Churchill GA, Blackwell HE, **Broman KW**, Attie AD, Coon JJ, Rey FE (2023) Genetic mapping of microbial and host traits reveals production of immunomodulatory lipids by *Akkermansia muciniphila* in the murine gut. *Nat Microbiol* 8:424–440 doi:10/jz3m
- 2022 Yoshihara T, Miller ND, Rabanal FA, Myles H, Kwak I-Y, **Broman KW**, Sadkhin B, Baxter I, Dilkes BP, Hudson ME, Spalding EP (2022) Leveraging orthology within maize and Arabidopsis QTL to identify genes affecting natural variation in gravitropism. *Proc Natl Acad Sci USA* 119: e2212199119 doi:10.1073/pnas.2212199119
- Vincent M, Gyuricza IG, Keele GR, Gatti DM, Keller MP, **Broman KW**, Churchill GA (2022) QTLViewer: An interactive webtool for genetic analysis in the Collaborative Cross and Diversity Outbred mouse populations. *G3 (Bethesda)* 12:jkac146 doi:10.1093/g3journal/jkac146
- Michel KJ, Lima DC, Hudley H, Singan V, Yoshinaga Y, Daum C, Barry K, **Broman KW**, Buell CR, de Leon N, Kaeppler SM (2022) Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. *Genetics* 221:iyac063 doi:10.1093/genetics/iyac063
- Broman KW** (2022) A generic hidden Markov model for multi-parent populations. *G3 (Bethesda)* 12:jkab396 doi:10.1093/g3journal/jkab396
- 2021 Trotter C, Kim H, Farage G, Prins P, Williams RW, **Broman KW**, Sen S (2021) Speeding up eQTL scans in the BXD population using GPUs. *G3 (Bethesda)* 11:jkab254 doi:10.1093/g3journal/jkab254
- Lobo AK, Traeger LL, Keller MP, Attie AD, Rey FE, **Broman KW** (2021) Identification of sample mix-ups and mixtures in microbiome data in Diversity Outbred mice. *G3 (Bethesda)* 11:jkab308 doi:10.1093/g3journal/jkab308
- Tran Q, **Broman KW** (2021) Treatment of the X chromosome in mapping multiple quantitative trait loci. *G3 (Bethesda)* 11:jkab005 doi:10.1093/g3journal/jkab005
- Hassold T, Maylor-Hagen H, Wood A, Gruhn J, Hoffmann E, **Broman KW**, Hunt P (2021) Failure to recombine is a common feature of human oogenesis. *Am J Hum Genet* 108:16–24 doi:10/gm56
- 2020 Linke V, Overmyer KA, Miller IJ, Brademan DR, Hutchins PD, Trujillo EA, Reddy TR, Russell JD, Cushing EM, Schueler DL, Stapleton DS, Rabaglia ME, Keller MP, Gatti DM, Keele GR, Pham D, **Broman KW**, Churchill GA, Attie AD, Coon JJ (2020) A large-scale genome-lipid association map guides lipid identification. *Nat Metab* 2:1149–1162 doi:10/gk5cn6
- Schwerbel K, Kamitz A, Krahmer N, Hallahan N, Jähnert M, Gottmann P, Lebek S, Schallschmidt T, Arends D, Schumacher F, Kleuser B, Haltenhof T, Heyd F, Gancheva S, **Broman KW**, Roden M, Joost HG, Chadt A, Al-Hasani H, Vogel H, Jonas W, Schürmann A (2020) Immunity-related GTPase induces lipophagy to prevent excess hepatic lipid accumulation. *J Hepatol* 73:771–782 doi:10/gjpnzk
- Broman KW** (2020) Reproducibility report: Identifying essential genes by mutagenesis. *ReScience C* 6(1): #12 doi:10.5281/zenodo.3959516

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

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

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

Boehm FJ, Chesler EJ, Yandell BS, **Broman KW** (2019) Testing pleiotropy vs. separate QTL in multiparental populations. *G3 (Bethesda)* 9:2317–2324 doi:10.1534/g3.119.400098

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

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

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

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

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

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

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

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

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

- 2016 Keller MP, Paul PK, Rabaglia ME, Stapleton DS, Schueler KL, Broman AT, Ye SI, Leng N, Brandon CJ, Neto EC, Plaisier CL, Simonett SP, Kebede MA, Sheynkman GM, Klein MA, Baliga NS, Smith LM, **Broman KW**, Yandell BS, 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 doi:10.1371/journal.pgen.1006466
- Parmenter MD, Gray MM, Hogan CA, Ford IN, **Broman KW**, Vinyard CJ, Payseur BA (2016) Genetics of skeletal evolution in unusually large mice from Gough Island. *Genetics* 204:1559–1572 doi:10.1534/genetics.116.193805
- Zigler JS Jr, Hodgkinson CA, Wright M, Klise A, Sundin O, **Broman KW**, Hejtmancik F, Huang H, Patek B, Sergeev Y, Hose S, Brayton C, Xiaodong J, Vasquez D, Maragakis N, Mori S, Goldman D, Hoke A, Sinha D (2016) A spontaneous missense mutation in branched chain keto acid dehydrogenase kinase in the rat affects both the central and peripheral nervous systems. *PLoS ONE* 11:e0160447 doi:10.1371/journal.pone.0160447
- Sloan Z, Arends D, **Broman KW**, Centeno A, Furlotte N, Nijveen H, Yan L, Zhou X, Williams RW, Prins P (2016) GeneNetwork: framework for web-based genetics. *J Open Source Software* 1(2):25 doi:10.21105/joss.00025
- De Simone M, Spagnuolo L, Lorè NI, Cigana C, De Fino I, **Broman KW**, Iraqi FA, Bragonzi A (2016) Mapping genetic determinants of host susceptibility to *Pseudomonas aeruginosa* lung infection in mice. *BMC Genomics* 17:351 doi:10/gdsf9t
- Tian J, Keller MP, Broman AT, Kendzierski C, Yandell BS, Attie AD, **Broman KW** (2016) The dissection of expression quantitative trait locus hotspots. *Genetics* 202:1563–1574 doi:10.1534/genetics.115.183624
- Gruhn JR, Al-Asmar N, Fasnacht R, Maylor-Hagen H, Peinado V, Rubio C, **Broman KW**, Hunt PA, Hassold T (2016) Correlations between synaptic initiation and meiotic recombination: A study of humans and mice. *Am J Hum Genet* 98:102–115 doi:10.1016/j.ajhg.2015.11.019
- Kwak I-L, Moore CR, Spalding EP, **Broman KW** (2016) Mapping quantitative trait loci underlying function-valued traits using functional principal component analysis and multi-trait mapping. *G3 (Bethesda)* 6:79–86 doi:10.1534/g3.115.024133
- 2015 Tian J, Keller MP, Oler AT, Rabaglia ME, Schueler KL, Stapleton DS, Broman AT, Zhao W, 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 doi:10.1534/genetics.115.179432
- 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 (Bethesda)* 5:2177–2186 doi:10.1534/g3.115.019778
- Gray MM, Parmenter M, Hogan C, Ford I, Cuthbert RJ, Ryan PG, **Broman KW**, Payseur BA (2015) Genetics of rapid and extreme size evolution in island mice. *Genetics* 201:213–228 doi:10.1534/genetics.115.177790
- Whitney KD, **Broman KW**, Kane NC, Hovick SM, Randell RA, Rieseberg LH (2015) Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. *Mol Ecol* 24:2194–2211 doi:10.1111/mec.13044
- Broman KW** (2015) R/qtcharts: Interactive graphics for quantitative trait locus mapping. *Genetics* 199:359–361 doi:10.1534/genetics.114.172742

- 2014 Florek NW, Weinfurter JT, Jegaskanda S, Brewoo JN, Powell TD, Young GR, Das SC, Hatta M, **Broman KW**, Hungnes O, Dudman SG, Kawaoka Y, Kent SJ, Stinchcomb DT, Osorio JE, Friedrich TC (2014) Modified vaccinia Ankara encoding influenza virus hemagglutinin induces heterosubtypic immunity in macaques. *J Virol* 88:13418–13428 doi:10.1128/JVI.01219-14
- Gatti DM, Svenson KL, Shabalin A, Wu L-Y, Valdar W, Simecek P, Goodwin N, Cheng R, Pomp D, Palmer A, Chesler EJ, **Broman KW**, Churchill GA (2014) Quantitative trait locus mapping methods for Diversity Outbred mice. *G3 (Bethesda)* 4:1623–1633 doi:10.1534/g3.114.013748
- Street VA, Kujawa SG, Manichaikul A, **Broman KW**, Kallman JC, Shilling DJ, Iwata AJ, Robinson LC, Robbins CA, Li J, Liberman MC, Tempel BL (2014) Resistance to noise-induced hearing loss in 129S6 and MOLF mice: Identification of independent, overlapping, and interacting chromosomal regions. *J Assoc Res Otolaryngol* 15:721–738 doi:10/f6hwgk
- Kwak I-Y, Moore CR, Spalding EP, **Broman KW** (2014) A simple regression-based method to map quantitative trait loci underlying function-valued phenotypes. *Genetics* 197: 1409–1416 doi:10.1534/genetics.114.166306
- Broman KW** (2014) Fourteen years of R/qtl: Just barely sustainable. *J Open Res Softw* 2(1):e11 doi:10.5334/jors.at
- Rowsey R, Gruhn J, **Broman KW**, Hunt PA, Hassold T (2014) Examining variation in recombination levels in the human female: A test of the production line hypothesis. *Am J Hum Genet* 95:108–112 doi:10.1016/j.ajhg.2014.06.008
- Huang BE, Raghavan C, Mauleon R, **Broman KW**, Leung H (2014) Efficient imputation of missing markers in low-coverage genotyping-by-sequencing data from multi-parent crosses. *Genetics* 197:401–404 doi:10.1534/genetics.113.158014
- Baier B, Hunt P, **Broman KW**, Hassold T (2014) Variation in genome-wide levels of meiotic recombination is established at the onset of prophase in mammalian males. *PLoS Genet* 10:e1004125 doi:10.1371/journal.pgen.1004125
- 2013 Gruhn JR, Rubio C, **Broman KW**, Hunt PA, Hassold T (2013) Cytological studies of human meiosis: sex-specific differences in recombination originate at, or prior to, establishment of double-strand breaks. *PLoS ONE* 8:e85075 doi:10.1371/journal.pone.0085075
- Moore CR, Johnson LS, Kwak IY, Livny M, **Broman KW**, Spalding EP (2013) High-throughput computer vision introduces the time axis to a quantitative trait map of a plant growth response. *Genetics* 195:1077–1086 doi:10.1534/genetics.113.153346
- Bautz DJ, **Broman KW**, Threadgill DW (2013) Identification of a novel polymorphism in X-linked sterol-4-alpha-carboxylate 3-dehydrogenase (Nsdhl) associated with reduced HDL cholesterol levels in I/LnJ mice. *G3 (Bethesda)* 3:1819–1825 doi:10.1534/g3.113.007567
- Harris M, Burns CM, Becker EA, Braasch AT, Gostick E, Johnson RC, **Broman KW**, Price DA, Friedrich TC, O'Connor SL (2013) Acute-phase CD8 T cell responses that select for escape variants are needed to control live attenuated simian immunodeficiency virus. *J Virol* 87:9353–9364 doi:10.1128/JVI.00909-13
- Maenner MJ, Baker MW, **Broman KW**, Tian J, Barnes JK, Atkins A, McPherson E, Hong J, Brilliant MH, Mailick MR (2013) *FMR1* CGG expansions: Prevalence and sex ratios. *Am J Med Genet B Neuropsychiatr Genet* 162:466–473 doi:10.1002/ajmg.b.32176

- 2012 **Broman KW**, Kim S, Sen S, Ané C, Payseur BA (2012) Mapping quantitative trait loci onto a phylogenetic tree. *Genetics* 192:167–179 doi:10.1534/genetics.112.142448
- Rice CA, Riehl J, **Broman K**, Soukup JW, Gengler WR (2012) Comparing the degree of exothermic polymerization in commonly used acrylic and provisional composite resins for intraoral appliances. *J Vet Dent* 29: 78–83 doi:10/gm58
- Galvan A, Colombo F, Noci S, Pazzaglia S, Mancuso M, Manenti G, **Broman KW**, Saran A, Dragani TA (2012) The *Lsktm1* locus modulates lung and skin tumorigenesis in the mouse. *G3 (Bethesda)* 2:1041–1046 doi:10.1534/g3.112.003525
- Greene JM, Chin EN, Budde ML, Lhost JJ, Hines PJ, Burwitz BJ, **Broman KW**, Nelson JE, Friedrich TC, O'Connor DH (2012) *Ex vivo* SIV-specific CD8 T cell responses in heterozygous animals are primarily directed against peptides presented by a single MHC haplotype. *PLoS ONE* 7:e43690 doi:10.1371/journal.pone.0043690
- Neto EC, Keller MP, Broman AF, Attie AD, Jansen RC, **Broman KW**, Yandell BS (2012) Quantile-based permutation thresholds for quantitative trait loci hotspots. *Genetics* 191:1355–1365 doi:10.1534/genetics.112.139451
- King EG, Merkes CM, McNeil CL, Hoofer SR, Sen S, **Broman KW**, Long AD, Macdonald SJ (2012) Genetic dissection of a model complex trait using the *Drosophila* Synthetic Population Resource. *Genome Res* 22:1558–1566 doi:10.1101/gr.134031.111
- Wang CY, Stapleton DS, Schueler KL, Rabaglia ME, Oler AT, Keller MP, 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 doi:10.1194/jlr.M025239
- Arends D, van der Velde KJ, Prins P, **Broman KW**, Möller S, Jansen RC, Swertz MA (2012) xQTL workbench: a web based environment for xQTL analysis. *Bioinformatics* 28:1042–1044 doi:10.1093/bioinformatics/bts049
- Amlin-Van Schaick JC, Kim S, **Broman KW**, Reilly KM (2012) *Scram1* is a modifier of spinal cord resistance for astrocytoma on mouse chromosome 5. *Mamm Genome* 23:277–285 doi:10/fwbzj7
- Broman KW** (2012) Genotype probabilities at intermediate generations in the construction of recombinant inbred lines. *Genetics* 190:403–412 doi:10.1534/genetics.111.132647
- Broman KW** (2012) Haplotype probabilities in advanced intercross populations. *G3 (Bethesda)* 2:199–202 doi:10.1534/g3.111.001818
- Collaborative Cross Consortium [97 authors] (2012) The genome architecture of the Collaborative Cross mouse genetic reference population. *Genetics* 190:389–401 doi:10.1534/genetics.111.132639
- Amlin-Van Schaick JC, Kim S, DiFabio C, Lee M-H, **Broman KW**, Reilly KM (2012) *Arlm1* is a male-specific modifier of astrocytoma resistance on mouse chr 12. *Neuro Oncol* 14:160–174 doi:10.1093/neuonc/nor206
- Davis RC, Van Nas A, Castellani LW, Zhao Y, Zhou Z, Wen P, Yu S, Qi H, Rosales M, Schadt EE, **Broman KW**, Peterfy M, Lusis AJ (2012) Systems genetics of susceptibility to obesity-induced diabetes in mice. *Physiol Genomics* 44:1–13 doi:10/djfhjh

- 2011 Weinfurter JT, Brunner K, Capuano SV III, Li C, **Broman KW**, Kawaoka Y, Friedrich T (2011) Cross-reactive T cells are involved in rapid clearance of 2009 pandemic H1N1 influenza virus in nonhuman primates. *PLoS Pathog* 7:e1002381 doi:10.1371/journal.ppat.1002381
- Aylor DL, Valdar W, Foulds-Mathes W, Buus RJ, Verdugo RA, Baric RS, Ferris MT, Frelinger JA, Heise M, Frieman MB, Gralinski LE, Bell TA, Didion JD, Hua K, Nehrenberg DL, Powell CL, Steigerwalt J, Xie Y, Kelada SNP, Collins F, Yang IV, Schwartz DA, Branstetter LA, Chesler EJ, Miller DR, Spence J, Liu EY, McMillan L, Sarkar A, Wang J, Wang W, Zhang Q, **Broman KW**, Korstanje R, Durrant C, Mott R, Iraqi FA, Pomp D, Threadgill D, Pardo-Manuel de Villena F, Churchill GA (2011) Genetic analysis of complex traits in the emerging Collaborative Cross. *Genome Res* 21:1213–1222 doi:10.1101/gr.111310.110
- Greene JM, Wiseman RW, Lank SM, Bimber BN, Karl JA, Burwitz BJ, Lhost JJ, Hawkins OE, Kunstman KJ, **Broman KW**, Wolinsky SM, Hildebrand WH, O'Connor DH (2011) Differential MHC class I expression in distinct leukocyte subsets. *BMC Immunol* 12:39 doi:10/bg6j8r
- Bradley KM, Breyer JP, Melville DB, **Broman KW**, Knapik EW, Smith JR (2011) A SNP-based linkage map for zebrafish reveals sex determination loci. *G3 (Bethesda)* 1:3–9 doi:10.1534/g3.111.000190
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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 doi:10.1002/gepi.1370170714

Broman KW, Speed TP (1999) A review of methods for identifying QTLs in experimental crosses. In: Seillier-Moiseiwitsch F (ed) *Statistics in Molecular Biology and Genetics. IMS Lecture Notes-Monograph Series*, Vol. 33, pp. 114–142 doi:10/cxnmgv

Technical Reports and Preprints

Yu Z, Farage G, Williams RW, **Broman KW**, Sen Ś (2023) BulkLMM: Real-time genome scans for multiple quantitative traits using linear mixed models. bioRxiv doi:10.1101/2023.12.20.572698

Litichevskiy L, Considine M, Gill J, Shandar V, Cox TO, Descamps HC, Wright KM, Amses KR, Dohnalová L, Liou MJ, Tetlak M, Galindo-Fiallos MR, Wong AC, Lundgren P, Kim J, Uhr GT, Rahman RJ, Mason S, Merenstein C, Bushman FD, Raj A, Harding F, Chen Z, Prateek GV, Mullis M, Deighan AG, Robinson L, Tanes C, Bittinger K, Chakraborty M, Bhatt AS, Li H, Barnett I, Davenport ER, **Broman KW**, Cohen RL, Botstein D, Freund A, Di Francesco A, Churchill GA, Li M, Thaïs CA (2023) Interactions between the gut microbiome, dietary restriction, and aging in genetically diverse mice. bioRxiv doi:10.1101/2023.11.28.568137

Broman KW (2010) Genetic map construction with R/qlt. 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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| R/qlt | An R package for mapping genes contributing to variation in quantitative traits in experimental crosses (rqtl.org). |
| R/qlt2 | A reimplement of the R package R/qlt, to better handle high-dimensional data and complex cross designs (kbroman.org/qlt2). |
| R/qlt2convert | An R package for converting QTL data (cran.r-project.org/package=qlt2convert). |
| R/qlt2fst | An R package for storing genotype probabilities (cran.r-project.org/package=qlt2fst). |
| R/qltcharts | An R package to create interactive data visualizations for quantitative trait locus mapping data (kbroman.org/qltcharts). |
| d3panels | A CoffeeScript library of interactive graphics panels (kbroman.org/d3panels). |
| R/simcross | An R package for simulating general experimental crosses (kbroman.org/simcross). |
| R/lineup | An R packages for identifying sample mixups in QTL data (cran.r-project.org/package=lineup). |
| R/lineup2 | An R packages for identifying sample mixups in QTL data, rewritten to not be tied to the R/qlt package (cran.r-project.org/package=lineup2). |
| R/negenes | An R package for estimating the number of essential genes by random transposon mutagenesis (cran.r-project.org/package=negenes). |
| R/xoi | An R package for the analysis of crossover interference (cran.r-project.org/package=xoi). |
| R/broman | An R package with miscellaneous tools for graphics, statistics, and data analysis (cran.r-project.org/package=broman). |

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| R/mbmixture | An R package for assessing mixtures in microbiome samples (cran.r-project.org/package=mbmixture). |
| aRxiv | An R package for searching arXiv, a repository of electronic preprints for computer science, mathematics, physics, quantitative biology, quantitative finance, and statistics (github.com/ropensci/aRxiv). |
| R/mmconvert | An R package for converting mouse genome positions between physical and genetic maps. (cran.r-project.org/package=mmconvert). |
| git/GitHub guide | Online tutorial on the git version control system and its use with GitHub (kbroman.org/github_tutorial). |
| knitr in a knutshell | Online tutorial on knitr, a tool for creating documents that mix code and text (kbroman.org/knitr_knutshell). |
| minimal make | Online tutorial on GNU Make, for automating computational tasks (kbroman.org/minimal_make). |
| R package primer | Online tutorial on writing packages for the R statistical software (kbroman.org/pkg_primer). |
| simple site | Online tutorial on constructing simple websites with GitHub Pages (kbroman.org/simple_site). |
| RelCheck | Software for the verification of relationships between individuals with use of autosomal genotype data. |
| Marshfield genetic maps | Genetic maps of the human genome, with internet-based tools for the search for genetic markers and semi-automated map construction. |

EDUCATIONAL ACTIVITIES

PhD Advisees

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

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

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

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

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

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

Master's Advisees

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

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

Undergraduate Advisees

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

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

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

Academic Advisees, University of Wisconsin–Madison

| | | |
|-------------|-------------------------|---------------------------------------|
| 2022 | Francesca Nimityongskul | MS candidate, Biomedical Data Science |
| 2021 – 2022 | Tim Gruenloh | MS candidate, Biomedical Data Science |
| 2021 – 2022 | Huan Liang | MS candidate, Biomedical Data Science |
| 2018 – 2020 | Alexandra Spicer | MS candidate, Biomedical Data Science |

Academic Advisees, Johns Hopkins University

| | | |
|-------------|-------------------------|-------------------------------|
| 2006 – 2007 | Sheng-Chih Jin | ScM candidate, Biostatistics |
| 2005 – 2007 | Ani Manichaikul | PhD candidate, Biostatistics |
| 2005 – 2006 | Alex Phan | MHS candidate, Bioinformatics |
| 2005 – 2006 | Jichao Chen | MHS candidate, 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

| | | |
|----------------|------------------------|----------------------------------|
| 2017 – present | Christopher McAllester | Genetics |
| 2022 – 2023 | Ashley Henry | Botany |
| 2018 – 2023 | Qijun Zhang | Cellular and Molecular Pathology |
| 2022 | Jie Song | Statistics |
| 2021 – 2022 | Zihao Zheng | Statistics |
| 2021 – 2022 | Chenyang Dong | Statistics |
| 2021 – 2022 | Joseph Lalli | Genetics |
| 2000 – 2021 | Nathan Wally Anderson | Integrative Biology |
| 2019 – 2021 | Athena Golfinos | Cellular and Molecular Pathology |
| 2018 – 2021 | Michael Kartje | Genetics |
| 2017 – 2021 | Jeremy Lange | Genetics |
| 2016 – 2021 | April Peterson | Genetics |
| 2015 – 2021 | Quentin Sprengelmeyer | Genetics |
| 2018 – 2020 | Theeva Chandereng | Statistics |

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|-------------|------------------------------|-----------------------------------|
| 2012 – 2019 | Molly McDevitt | Biochemistry |
| 2017 – 2018 | Kyubin Lee | Computer Sciences |
| 2015 – 2018 | René Welch | Statistics |
| 2012 – 2017 | Michelle Parmenter | Genetics |
| 2014 – 2017 | Alessandra York | Genetics |
| 2013 – 2017 | Richard Wang | Genetics |
| 2013 – 2016 | Shuang Huang | Statistics |
| 2011 – 2013 | Raja Farhana Raja Mohd Anuar | Plant Breeding and Plant Genetics |
| 2010 – 2015 | Katie Clowers | Genetics |
| 2010 | Jingfang Zhang | Oncology |
| 2010 – 2011 | Michael White | Genetics |
| 2010 | Elias Chaibub Neto | Statistics |
| 2007 – 2010 | Beth Dumont | Genetics |

Doctoral Thesis Committees, Johns Hopkins University

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

Oral Exams, University of Wisconsin–Madison

| | | |
|------|------------------------|----------------------------------|
| 2021 | Zihao Zheng | Statistics |
| | Quoc Tran | Statistics |
| | Chenyang Dong | Statistics |
| 2020 | Qijun Zhang | Cellular and Molecular Pathology |
| | Athena Golfinos | Cellular and Molecular Pathology |
| 2019 | Michael Kartje | Genetics |
| 2018 | Christopher McAllester | Genetics |
| | Thevaa Chandereng | Statistics |
| 2017 | Constanza Rojo | Statistics |
| | Quentin Sprengelmeyer | Genetics |
| | Jeremy Lange | Genetics |
| | Kyubin Lee | Computer Sciences |
| | Fred Boehm | Statistics |
| 2016 | April Peterson | Genetics |
| | Alessandra York | Genetics |
| 2015 | René Welch | Statistics |

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|------|---|---|
| 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

| | | |
|------|---|--|
| 2023 | Ashley Henry Qijun Zhang | Botany Cellular and Molecular Pathology |
| 2022 | Zihao Zheng Chenyang Dong Jie Song | Statistics Statistics Statistics |
| 2021 | Jeremy Lange Quentin Sprengelmeyer April Peterson | Genetics Genetics Genetics |
| 2020 | Thevaa Chandereng | Statistics |
| 2019 | Constanza Rojo Fred Boehm Molly McDevitt | Statistics 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 |

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| 2001 | Alison Klein Tsuo-Hung Lan | Epidemiology Epidemiology |
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Master's Thesis Defenses, University of Wisconsin–Madison

| | | |
|------|------------------------------|-----------------------------------|
| 2013 | Raja Farhana Raja Mohd Anuar | Plant Breeding and Plant Genetics |
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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

| | | |
|-------------|--|--|
| 2023 – 2024 | BMI 881 BMI 883 BMI 884 | Biomedical Data Science Scholarly Literature 1 Biomedical Data Science Professional Skills 1 Biomedical Data Science Professional Skills 2 |
| 2022 – 2023 | BMI 881 BMI 882 BMI 883 BMI 884 | Biomedical Data Science Scholarly Literature 1 Biomedical Data Science Scholarly Literature 2 Biomedical Data Science Professional Skills 1 Biomedical Data Science Professional Skills 2 |
| 2021 – 2022 | BMI 881 BMI 882 BMI 883 BMI 884 | Biomedical Data Science Scholarly Literature 1 Biomedical Data Science Scholarly Literature 2 Biomedical Data Science Professional Skills 1 Biomedical Data Science Professional Skills 2 |
| 2020 – 2021 | BMI 881 BMI 882 BMI 883 BMI 884 | Biomedical Data Science Scholarly Literature 1 Biomedical Data Science Scholarly Literature 2 Biomedical Data Science Professional Skills 1 (<i>new</i>) Biomedical Data Science Professional Skills 2 (<i>new</i>) |
| 2019 – 2020 | BMI 881 BMI 882 BMI 826-001 | Biomedical Data Science Scholarly Literature 1 (<i>new</i>) Biomedical Data Science Scholarly Literature 2 (<i>new</i>) Advanced Data Analysis (<i>new</i>) |
| 2018 – 2019 | Statistics 877 | Statistical Methods in Molecular Biology (<i>jointly</i>) |
| 2017 – 2018 | Agronomy 957 | Plant Breeding and Plant Genetics seminar (<i>jointly</i>) |
| 2016 – 2017 | Statistics 877 | Statistical Methods in Molecular Biology (<i>jointly</i>) |
| 2015 – 2016 | BMI 826-003 | Tools for Reproducible Research |
| 2014 – 2015 | BMI 826-003 | Tools for Reproducible Research |
| 2013 – 2014 | BMI 826-003 Statistics 877 | Tools for Reproducible Research (<i>new</i>) Statistical Methods in Molecular Biology (<i>jointly</i>) |
| 2012 – 2013 | BMI 826-001 | Statistical Methods for QTL Mapping |

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| 2011 – 2012 | Statistics 877 | Statistical Methods in Molecular Biology (<i>jointly</i>) |
| 2010 – 2011 | Statistics 992-001 | Statistical Methods for QTL Mapping (<i>new</i>) |
| 2009 – 2010 | Statistics 877 Population Health 904-003 | Statistical Methods in Molecular Biology (<i>jointly</i>) Analytic Methods in Genetic Epidemiology (<i>jointly</i>) |
| 2008 – 2009 | Statistics 371-003 | Introductory Applied Statistics for the Life Sciences |
| 2007 – 2008 | Statistics 992-002 Population Health 904-003 | Statistical Methods in Molecular Biology (<i>new, jointly</i>) Analytic Methods in Genetic Epidemiology (<i>jointly</i>) |

Classroom Instruction, Johns Hopkins University

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|-------------|---|--|
| 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 (<i>jointly</i>) |
| 2004 – 2005 | Biostatistics 140.776 Biostatistics 140.668 Biostatistics 140.615–616 Epidemiology 340.631 | Statistical Computing (<i>jointly</i>) Special Topics in Genetics and Genomics (<i>jointly</i>) Statistics for Laboratory Scientists Methods in Genetic Epidemiology I (<i>jointly</i>) |
| 2003 – 2004 | Biostatistics 140.776 Biostatistics 140.615–616 | Statistical Computing (<i>new, jointly</i>) Statistics for Laboratory Scientists |
| 2002 – 2003 | Biostatistics 140.668 Biostatistics 140.615–616 | Special Topics in Genetics and Genomics (<i>new, jointly</i>) Statistics for Laboratory Scientists |
| 2001 – 2002 | Biostatistics 140.615 | Statistics for Laboratory Scientists (<i>new</i>) |
| 2000 – 2001 | Biostatistics 140.778 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

| | | |
|--------------|-----------------|--|
| 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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| 2018 – 2022 | Lecture on “Data management” to KL2 scholars, Institute for Clinical and Translational Research, School of Medicine and Public Health, University of Wisconsin–Madison | |
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| 2022 | Lecture on “QTL mapping in multi-parent populations” in BMI 877 (Statistical Methods for Molecular Biology), Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2021 – 2022 | Lecture on “Steps toward reproducible research” for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2021 | Lectures on “QTL mapping in MAGIC populations with R/qt12” in Horticulture 615 (Genetic Mapping), University of Wisconsin–Madison |
| 2008 – 2021 | Lecture on my consulting experiences in Statistical Consulting (Stat 998), Department of Statistics, University of Wisconsin–Madison |
| 2020 | Lecture on “Steps toward reproducible research” in BMI 877 (Statistical Methods for Molecular Biology), Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2020 | Lectures on “Steps toward reproducible research” and “Exploratory data analysis” in BMI 773 (Clinical Research Informatics), Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2019 – 2020 | Lecture on “Steps toward reproducible research” to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison |
| 2018 | Instructor, Workshop on Advanced R and R/qt1, ICRISAT, Hyderabad, India |
| 2018 | Lecture on “Steps toward reproducible research” for the Cellular and Molecular Pathology Graduate Program, University of Wisconsin–Madison |
| 2017 – 2018 | Workshop on Reproducible Research, Summer Institute in Statistics for Big Data, Seattle, Washington |
| 2017 – 2018 | Lecture on “Steps toward reproducible research” for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2016 – 2018 | Instructor, Data Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison |
| 2013 – 2018 | Lecture on “Creating effective figures and tables” to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison |
| 2017 | Instructor, Data Carpentry workshop, National Society of Black Engineers Professional Development Conference, Chicago, Illinois |
| 2017 | Workshop on Systems Genetics of Neurodegeneration, Frauenchiemsee, Germany |
| 2017 | Workshop on R/qt1 and R/qt12 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 |

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| 2017 | Lecture to AP Statistics students, Madison East High School, Madison, Wisconsin |
| 2017 | Lecture on “Genetics of extreme body size evolution in mice from Gough Island” for the Summer Research Program in Biomedical Data Science, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2008 – 2017 | Periodic seminars on “Creating effective figures and tables” in the Department of Pathology and Laboratory Medicine, University of Wisconsin–Madison |
| 2016 | Lecture on “Creating effective figures and tables” at the Demography Training Seminar, Center for Demography of Health and Aging, University of Wisconsin–Madison |
| 2008 – 2016 | Instructor and co-organizer, Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, Maine |
| 2015 | R/qtl workshop, Texas A&M, College Station, Texas |
| 2015 | Lecture on “Reproducible Research” for undergraduate researchers in the Summer Institute for Training in Biostatistics (SIBS), University of Wisconsin–Madison |
| 2015 | Instructor, Software Carpentry workshop, Washington State University, Pullman, Washington |
| 2014 – 2015 | Instructor, Software Carpentry workshops, Advanced Computing Initiative, University of Wisconsin–Madison |
| 2014 | Lecture on “Creating effective figures and tables” in a manuscript writing workshop, Institute for Clinical and Translational Research, University of Wisconsin–Madison |
| 2013 | Lecture on “A brief introduction to git and GitHub” to graduate students, Department of Statistics, University of Wisconsin–Madison |
| 2013 | Lecture on “Why aren’t all of our graphs interactive?” to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison |
| 2012 | Instructor, Training Course on Field Trials & QTL Analysis using R and R/qtl, ICRI SAT, 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 |

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

ACADEMIC LEADERSHIP AND PROGRAM DEVELOPMENT

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

SERVICE ACTIVITIES

International and National

| | |
|----------------|---|
| 2023 – present | GeneNetwork Leadership Team, University of Tennessee Health Sciences Center (Memphis, Tennessee) |
| 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 12th Annual Meeting (Madison, Wisconsin)
- 2003 – 2004 ENAR Distinguished Student Paper Awards Committee
- 2003 IMS Contributed Papers Chair, ENAR/IMS Annual Meeting (Tampa, Florida)

University

- 2023 – present Space Planning Committee, School of Computer, Data & Information Sciences
- 2022 – present Scholarly Communication Advisory Group, University of Wisconsin–Madison
- 2020 – present Executive Committee, Plant Breeding and Plant Genetics PhD Program, University of Wisconsin–Madison
- 2017 – present Faculty Senator, University of Wisconsin–Madison
- 2018 Review Committee for Biometry Master of Science Program, College of Agricultural and Life Sciences, University of Wisconsin–Madison
- 2016 Genomics Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison
- 2012 – 2015 Faculty Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison
- 2011 – 2015 University Library Committee, University of Wisconsin–Madison (*Chair*, 2014 – 2015)
- 2012 – 2014 Steering Committee, Medical Scientist Training Program, School of Medicine and Public Health, University of Wisconsin–Madison
- 2009 – 2012 Master of Public Health Program Curriculum Committee, School of Medicine and Public Health, University of Wisconsin–Madison
- 2009 – 2012 Curriculum Planning Committee, Biological Sciences Division, University of Wisconsin–Madison
- 2008 – 2012 Faculty Senator, University of Wisconsin–Madison
- 2002 – 2007 Maintainer of the Faculty Senate web site, Johns Hopkins Bloomberg School of Public Health
- 2001 – 2004 Faculty Senate representative to the Committee on Information Technology, Johns Hopkins Bloomberg School of Public Health
- 2001 – 2003 Organizer of a monthly discussion forum for junior faculty, Johns Hopkins Bloomberg School of Public Health
- 2001 – 2002 Secretary of the Faculty Senate, Johns Hopkins Bloomberg School of Public Health
- 2000 – 2002 Faculty Senator, Johns Hopkins Bloomberg School of Public Health
- 2000 – 2001 Biochemistry and Molecular Biology Strategic Plan Committee, Johns Hopkins Bloomberg School of Public Health

Departmental

| | |
|----------------|--|
| 2015 – present | Steering Committee, Biostatistics Computing Group, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2014 – 2022 | Steering Committee, Biomedical Data Science MS Program, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2010 – 2020 | Chair, Education and Curriculum Committee, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2015 – 2016 | Co-chair, Faculty Search Committee, Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2010 – 2013 | Seminar organizer, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2010 – 2012 | Steering Committee, Biomedical Computing Group, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2008 | Committee for Information Technology Assessment, Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison |
| 2004 – 2007 | Intellectual and Social Environment Committee, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health |
| 2000 – 2002 | Biostatistics Information Technology Committee, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health |
| 2000 – 2001 | Seminar organizer, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health |

GRANT SUPPORT

Current Grant Support

| | | |
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| System Genetic Analysis of Multi-Parent Crosses co-PI with Gary Churchill (Jackson Laboratory) <i>Develop statistical methods and software for the analysis of multi-parent crosses, such as the mouse Diversity Outcross population and the Collaborative Cross.</i> Role: Co-Principal investigator | 07/01/15 – 07/31/23 | NIH/NIGMS (25%) |
| A Unified High-Performance Web Service for Systems Genetics and Precision Medicine Robert W. Williams and Saunak Sen, PIs <i>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.</i> Role: Co-investigator | 04/15/17 – 07/31/25 | NIH/NIGMS (10%) |
| A Resource for the Genetic Dissection of Complex Traits Stuart Macdonald and Tony Long, PIs <i>Enhance the usability of the Drosophila Synthetic Population Resource by integrating analysis software into R/qt12, enable extreme QTL mapping, and explore the nature of expression regulation with developing dynamic eQTL mapping methods.</i> Role: Co-investigator | 01/01/23 – 12/31/26 | NIH (10%) |

Previous Grant Support

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| NIAID Centers of Excellence for Influenza Research and Surveillance Yoshihiro Kawaoka, PI | 04/01/14 – 08/31/21 | NIH/NIAID (8%) |
| <i>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.</i> | | |
| Role: Co-investigator | | |
| A Program of Research in Population Cytogenetics Terry Hassold (Washington State), PI | 12/01/10 – 07/31/21 | NIH/NICHD (8%) |
| <i>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.</i> | | |
| Role: Co-investigator | | |
| Evolution of the Genome-wide Recombination Rate in Mice Bret Payseur, PI | 05/15/17 – 03/31/21 | NIH/NIGMS (5%) |
| <i>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.</i> | | |
| Role: Co-investigator | | |
| Genetics of the Island Rule Bret Payseur, PI | 09/10/12 – 02/28/21 | NIH/NIGMS (5%) |
| <i>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.</i> | | |
| Role: Co-investigator | | |
| Collaborative Cross of the Microbiome and Metabolic Disease Federico Rey, PI | 09/23/15 – 08/31/20 | NIH/NIDDK (5%) |
| <i>Identify genes and pathways that modulate gut microbial composition and abundance, and their association to disease, in the mouse Diversity Outcross.</i> | | |
| Role: Co-investigator | | |
| Alexander Disease: Mechanisms, Modifiers, and Therapeutics Albee Messing, PI | 09/20/14 – 07/31/19 | NIH/NIHD (5%) |
| <i>Identify genomic regions, and ultimately specific genes, that contribute to GFAP accumulation and toxicity in a mouse model of Alexander disease.</i> | | |
| Role: Co-investigator | | |
| The Collaborative Cross Project of Diabetes Alan Attie, PI | 04/01/14 – 01/31/19 | NIH/NIDDK (5%) |
| <i>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.</i> | | |
| Role: Co-investigator | | |
| Genome Dynamics: Evolution, Organization, and Function Gary Churchill (Jackson Laboratory), PI | 04/01/06 – 06/30/16 | NIH/NIGMS (9%) |
| <i>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.</i> | | |
| Role: Co-Investigator | | |

- Statistical Methods for Analysis and Integration in Genomic Studies of Disease
Christina Kendzierski, PI 08/01/12 – 04/30/16 NIH/NIGMS (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
Abraham Palmer (U Chicago), PI 07/01/11 – 12/31/15 NIH/NIDA (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
Karl Broman, PI 06/01/05 – 05/31/15 NIH/NIGMS (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
Alan Attie (UW-Madison), PI 12/01/09 – 11/30/14 NIH/NIDDK (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
Michelle Southard-Smith (Vanderbilt University), PI 07/01/07 – 06/30/12 NIH/NIDDK (8%)
The goal of the proposed studies is to identify additional genes and gene interactions that impact aganglionosis in the Sox10^{Dom} model.
Role: Co-Investigator
- Statistical Methods for Experimental Genome Populations
Saunak Sen (UCSF), PI 07/01/07 – 06/30/12 NIH/NIGMS (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*
Jason Rasgon (Johns Hopkins University), PI 07/01/07 – 10/31/11 NIH/NIAID (2%)
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 NIH/NEI (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

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| Mechanism of Inflammation-Induced Airway Hyperactivity Wayne Mitzner (Johns Hopkins University), PI <i>Identify genetic loci contributing to variation in inflammation-induced airway hyperactivity in mice.</i> Role: Co-Investigator | 12/01/04 – 6/30/07 | NIH/NHLBI (3%) |
| Center for Epigenetics of Common Human Diseases Andrew Feinberg, PI <i>Develop tools for medical epigenetics, including epigenome discovery, its quantitative analysis, and its application to medicine.</i> Role: Co-Investigator | 04/01/04 – 06/30/07 | NIH/NHGRI (10%) |
| Epigenetic Variation and its Determinants in Depression James Potash, PI <i>Establish the connection between genetic, environmental, and epigenetic factors and susceptibility to depression.</i> Role: Co-Investigator | 04/01/05 – 06/30/07 | NIH/NIMH (10%) |
| Genetic Mechanisms of Autoimmune Myocarditis Noel Rose, PI <i>Identify genetic loci contributing to susceptibility to autoimmune myocarditis in mice.</i> Role: Co-Investigator | 07/01/04 – 06/30/07 | NIH/NHLBI (4%) |
| Catechol-O-methyltransferase and Breast Cancer James Yager, PI <i>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.</i> Role: Co-Investigator | 09/21/04 – 06/30/07 | NIH/NCI (2.5%) |
| Core Center Grant: Biostatistical Center Sheila West, PI <i>Provide biostatistics support for epidemiological research in ophthalmology.</i> Role: Senior Biostatistician | 07/01/04 – 06/30/07 | NIH/NEI (5%) |
| Older Americans Independence Center Linda Fried, PI <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 | NIH/NIA (1.5%) |
| Statistical Methods for Genetic Epidemiology Kung-Yee Liang, PI; Karl Broman, acting PI <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 | NIH/NIGMS (25%) |
| Portable Software for Mapping Quantitative Traits Ken Manly, PI <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 | NIH/NHGRI (5%) |
| Center for Craniofacial Development and Disorders Terri Beaty, PI <i>Biostatistical Core for program project on the genetics of craniofacial disorders.</i> Role: Co-Investigator | 08/01/01 – 08/01/04 | NIH/NIDR (5%) |

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| Mouse QTL in Endotoxic Shock Roger Reeves, PI <i>Identify genomic regions contributing to susceptibility to endotoxic shock in mice.</i> Role: Co-Investigator | 08/01/01 – 07/30/05 | NIH (10%) |
| Genetic Basis of Nanophthalmos Olof Sundin, PI <i>Identify the gene responsible for nanophthalmos in a single large pedigree.</i> Role: Co-Investigator | 08/15/01 – 06/30/04 | NIH/NEI (10%) |
| Center for Craniofacial Development and Disorders Ethylin Jabs, PI <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 | NIH/NIDR (10%) |
| The Genetics of Age Related Cataract in Salisbury Nathan Congdon, PI <i>Identify genes contributing to susceptibility to cataract</i> Role: Co-Investigator | 09/30/00 – 08/31/03 | NIH/NIA (10%) |
| JHSPH Faculty Innovation Fund grant Karl Broman, PI <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 | JHSPH (30%) |

INVITED PRESENTATIONS

Scientific Meetings

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| 2021 | csv,conf (<i>online</i>) Data Mishaps Night (<i>online</i>) |
| 2019 | RStudio Conference, Austin, Texas American Association for the Advancement of Science (AAAS) annual meeting, Washington, DC Michigan State Plant Breeding, Genetics, and Biotechnology (PBGB) Symposium, East Lansing, Michigan |
| 2018 | Complex Trait Community meeting, Glasgow, Scotland Purdue Symposium on Statistics, West Lafayette, Indiana |
| 2017 | Complex Trait Community meeting, Memphis, Tennessee |
| 2016 | Genome and Gene Mapping Satellite, Queenstown Research Week, Nelson, New Zealand Joint Statistical Meetings, Chicago, Illinois Conference on Learning Tools to Promote Reproducible Research and Open Science, Chicago Chapter, American Statistical Association, Chicago, Illinois |
| 2015 | Plant breeding symposium, Texas A&M, College Station, Texas Joint Statistical Meetings, Seattle, Washington BioC 2015 (Bioconductor annual meeting), Seattle, Washington Complex Trait Community annual meeting, Portland, Oregon The Challenge of Inference from Genome to Phenome, CSIRO Chief Executive Cutting Edge Symposium, Brisbane, Australia American Association for the Advancement of Science (AAAS) annual meeting, San Jose, California |

- 2014 Fourth Symposium on Biological Data Visualization, Boston, Massachusetts
Scholarly Publishing Symposium, University of Wisconsin–Madison
- 2013 Open Access, Open Data @ UW, University of Wisconsin–Madison
Workshop on MAGIC-type populations, Cambridge, United Kingdom
Kansas State University Plant Breeding and Genetics Symposium, Manhattan, Kansas
International Biometric Society/ENAR Annual Meeting, Orlando, Florida
- 2012 EvoSysBio meeting, Wisconsin Institutes for Discovery, University of Wisconsin – Madison
EURATRANS annual meeting, Tutzing, Germany
- 2011 Quantitative Biology and Bioinformatics in Modern Medicine, Dublin, Ireland
- 2010 Fourteenth QTL-MAS Workshop, Poznań, Poland
- 2008 Emerging Statistical Challenges in Genome and Translational Research, Banff, Canada
- 2007 Systems Medicine Workshop, NHLBI, Bethesda, Maryland
- 2005 Fifth 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

- 2023 BIG Collection Sequence of Convenings, Big 10 Academic Alliance Libraries (*online*)
Computation and Informatics in Biology and Medicine (CIBM), University of Wisconsin–Madison (*online*)
- 2021 Department of Biomedical Informatics, University of Pittsburgh (*online*)
NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome (*online*)
- 2020 Center for Quantitative Methods and Data Science, Tufts Medical Center (*online*)
- 2019 Providence/Boston Center for AIDS Research Biostatistics Core, Boston University
Department of Mathematics, Statistics, and Computer Science, St. Olaf College, Northfield, Minnesota
- 2018 Department of Statistics, Colorado State University, Fort Collins, Colorado
qBio seminar series, Wisconsin Institute for Discovery, University of Wisconsin–Madison
BBC seminar series, University of California, San Francisco

- 2017 Department of Bioinformatics and Genomics, University of North Carolina at Charlotte
Berkeley Institute for Data Science, University of California, Berkeley
Genetics Program, North Carolina State University, Raleigh, North Carolina
- 2016 Department of Genetics, Genomics, and Informatics, University of Tennessee Health Science Center,
Memphis, Tennessee
Department of Statistics, University of Auckland, Auckland, New Zealand
Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, New York
Graduate Researchers interested in Data (GRiD), University of Massachusetts, Amherst, Massachusetts
Bioinformatics and Computational Biology, Genentech, South San Francisco, California
- 2015 Holz Series in Research Data Management, University of Wisconsin–Madison
Division of Biostatistics, Department of Preventive Medicine, University of Tennessee Health Science
Center, Memphis, Tennessee
Bioinformatics Division, Walter & Eliza Hall Institute for Medical Research, Melbourne, Australia
- 2014 Delta Program, University of Wisconsin–Madison
Department of Biostatistics, Harvard School of Public Health, Boston, Massachusetts
Danforth Plant Science Center, St. Louis, Missouri
- 2013 Graphics Working Group, Department of Statistics, Iowa State University, Ames, Iowa
- 2012 Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
- 2011 Department of Biostatistics, University of Washington, Seattle
Department of Statistics, George Mason University, Fairfax, Virginia
Groningen Bioinformatics Centre, University of Groningen, Groningen, The Netherlands
Department of Biostatistics, Columbia University, New York
- 2010 Institute of Mathematics and Computer Sciences, Wrocław University of Technology, Wrocław, Poland
Department of Genetics and Animal Breeding, Wrocław University of Environmental and Life Sciences,
Wrocław, Poland
Quantitative Biology and Modeling Initiative Program, Michigan State University, East Lansing,
Michigan
Integrative Genomics Seminar Series, Vanderbilt University, Nashville, Tennessee
Evolution Seminar Series, University of Wisconsin–Madison
Curriculum in Genetics and Molecular Biology, University of North Carolina at Chapel Hill
- 2009 Department of Human Genetics, University of California, Los Angeles
Laboratory of Genetics, University of Wisconsin–Madison
Department of Statistics, University of Wisconsin–Madison
Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
Groningen Bioinformatics Centre, University of Groningen, Groningen, The Netherlands
Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom
- 2008 Annual Retreat, Genomic Sciences Training Program, University of Wisconsin–Madison
Division of Human Genetics, Cincinnati Children’s Hospital, Cincinnati, Ohio
Computation and Informatics in Biology and Medicine (CIBM), University of Wisconsin–Madison
Evolution Seminar Series, University of Wisconsin–Madison
Department of Animal Sciences, University of Wisconsin–Madison
- 2007 Department of Human Genetics, University of Chicago
Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
Statistics Program, St. Olaf College, Northfield, Minnesota

- Center for Interdisciplinary Research, St. Olaf College, Northfield, Minnesota
 Annual Retreat, Laboratory of Genetics, University of Wisconsin–Madison
 Division of Statistics, Northern Illinois University, DeKalb, Illinois
 Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison
 Department of Human Genetics, University of California, Los Angeles
 Department of Statistics, University of California, Berkeley
 The Jackson Laboratory, Bar Harbor, Maine
 Department of Biostatistics, University of Michigan, Ann Arbor
- 2006 Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland
 Department of Biostatistics, University of Michigan, Ann Arbor
 Laboratory of Genetics, University of Wisconsin–Madison
 Department of Biostatistics, University of Washington, Seattle
- 2005 Department of Statistics, University of California, Davis
 Department of Genetics, School of Medicine, University of Pennsylvania, Philadelphia
 Department of Mathematics and Statistics, University of Maryland, Baltimore County
 Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
 Section for Medical Inflammation Research, Department of Cell and Molecular Biology, Lund University, Lund, Sweden
- 2004 Department of Biostatistics, Yale University, New Haven, Connecticut
 Marshfield Clinic Research Foundation, Marshfield, Wisconsin
 Genetics and Genomic Biology, Hospital for Sick Children, Toronto, Canada
 Genetic Interest Group, Center for Human Genetic Research, Vanderbilt University, Nashville, Tennessee
 Department of Biostatistics, University of Buffalo
 Immunogenetics, Universität Rostock, Germany
 Department of Epidemiology and Biostatistics, Memorial Sloan–Kettering Cancer Center, New York
- 2003 Departments of Statistics and Biostatistics & Medical Informatics, University of Wisconsin–Madison
 Department of Statistics, University of California, Los Angeles
 Department of Mathematics, Haverford College, Pennsylvania
 Department of Biostatistics, University of North Carolina, Chapel Hill
 Department of Biostatistics, University of California, San Francisco
- 2002 Section on Statistical Genetics, University of Alabama, Birmingham
 Department of Statistics, University of California, Berkeley
 Department of Biostatistics, Johns Hopkins University
 Department of Molecular and Cellular Biology, Roswell Park Cancer Institute, Buffalo, New York
 Department of Mathematics and Statistics, American University, Washington, DC
- 2001 Department of Statistics, Yale University
 Department of Mathematical Sciences, University of Wisconsin–Milwaukee
- 2000 Biometric Research Branch, National Cancer Institute, Bethesda, Maryland
 The Jackson Laboratory, Bar Harbor, Maine
- 1999 Department of Biostatistics, Johns Hopkins University
 Department of Biostatistics, University of Washington, Seattle
 Gemini Research, Cambridge, England
 Department of Biostatistics, Johns Hopkins University
 Department of Statistics, University of California, Berkeley
 Department of Molecular and Cell Biology, University of California, Berkeley

- 1998 Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
Queensland Institute for Medical Research, Brisbane, Australia
Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
deCODE Genetics, 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