CURRICULUM VITAE

Karl W. Broman

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EDUCATION

1997 – 1999   Postdoctoral Fellow, Center for Medical Genetics, Marshfield Medical Research Foundation, Marshfield, Wisconsin (Advisor: James L. Weber)

1997   PhD, Statistics, University of California, Berkeley (Advisor: Terry Speed; thesis: *Identifying quantitative trait loci in experimental crosses*)

1991   BS, *Summa Cum Laude*, Mathematics, University of Wisconsin–Milwaukee

PROFESSIONAL POSITIONS

2009 – present   Professor, Department of Biostatistics and Medical Informatics, School of Medicine and Public Health, University of Wisconsin–Madison

2007 – 2009   Associate Professor, Department of Biostatistics and Medical Informatics, School of Medicine and Public Health, University of Wisconsin–Madison

2002 – 2007   Associate Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University, Baltimore, Maryland

1999 – 2002   Assistant Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University, Baltimore, Maryland

1999   Associate Research Scientist, Center for Medical Genetics, Marshfield Medical Research Foundation, Marshfield, Wisconsin

ADDITIONAL PROFESSIONAL APPOINTMENTS

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

RESEARCH INTERESTS

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

SCIENTIFIC ADVISORY BOARDS

2009 – present   Nature Source Genetics, Ithaca, New York

2010 – 2011   Wisconsin Genomics Initiative

HONORS AND AWARDS

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

2004 – 2010   Associate Editor, *Genetics*

2006 – 2009   Associate Editor, *Journal of the American Statistical Association*, Applications and Case Studies
2004 – 2007   Associate Editor, *Biostatistics*

Peer Review Activities

Referee for American Journal of Epidemiology; American Journal of Human Genetics; Annals of Applied Statistics; Annals of Human Genetics; Annals of Statistics; Arteriosclerosis, Thrombosis, and Vascular Biology; Bioinformatics; Biometrics; Biostatistics; BMC Bioinformatics; BMC Biology; BMC Genetics; BMC Genomics; BMC Proceedings; BMC Research Notes; Cancer Research; Circulation Research; Computational Statistics & Data Analysis; Crop Science; European Journal of Human Genetics; Evolution; Gene; Genes, Brain, and Behavior; Genes & Immunity; Genetic Epidemiology; Genetica; Genetical Research; Genetics; Genetics Research; Genetics Selection Evolution; Genome; Genome Research; Genomics; Growth, Development, & Aging; Heredity; Human Genetics; Human Heredity; Human Molecular Genetics; IEEE/ACM Transactions on Computational Biology and Bioinformatics; Journal of Agricultural, Biological, and Environmental Statistics; Journal of the American Society of Nephrology; Journal of the American Statistical Association; Journal of Applied Genetics; Journal of Bioinformatics and Computational Biology; Journal of Computational and Graphical Statistics; Journal of Fish Biology; Journal of Heredity; Journal of Immunology; Journal of Neuroscience; Journal of Statistical Planning and Inference; Journal of Statistical Software; Mammalian Genome; Molecular Biology and Evolution; Molecular Genetics and Genomics; Nature Communications; Nature Genetics; Nature Methods; Nature

Protocols; Nature Reviews–Genetics; Nucleic Acids Research; Ophthalmic Epidemiology; Pacific Symposium on Biocomputing; Physiological Genomics; PLoS Biology; PLoS Computational Biology; PLoS Genetics; PLoS ONE; Proceedings of the National Academy of Sciences USA; Scandinavian Journal of Immunology; Science; Statistical Applications in Genetics and Molecular Biology; Statistics; Theoretical Population Biology; and Trends in Genetics

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

Review Panels

2010 – present   Center for Inherited Disease Research (CIDR) Access Committee, National Human Genome Research Institute, National Institutes of Heath (*Chair*, 2014 – present)

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 Institute of Environmental Health Sciences Special Emphasis Panel (NIH); National Institute on Aging Special Emphasis Panel (NIH); National Science Council (Republic of China); National Science Foundation; National Sciences and Engineering Research Council (Canada); Council for Earth and Life Sciences, Netherlands Organization for Scientific Research; Neurological Sciences and Disorders A Study Section (NIH); and Telethon (Italy)

PUBLICATIONS

Books

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

Journal Articles

Whitney KD, **Broman KW**, Kane NC, Hovick SM, Randell RA, Rieseberg LH. QTL mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. *Mol Ecol*, to appear

2015   **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. *Amer 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 Genetics* 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, Kendziorski CM, **Broman KW**, Yandell BS, Schadt EE, Attie ED (2012) *Tsc2*, a positional candidate gene underlying a quantitative trait locus for hepatic steatosis. *J Lipid Res* 53:1493–1501

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

Amlin-Van Schaick JC, Kim S, **Broman KW**, Reilly KM (2012) *Scram1* is a modifier of spinal cord resistance for astrocytoma on mouse chromosome 5. *Mamm Genome* 23:277–285

Broman KW (2012) Genotype probabilities at intermediate generations in the construction of recombinant inbred lines. *Genetics* 190:403–412

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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**, Lutty GA, Zigler JS Jr (2008) βA3/A1-crystallin in astroglial cells regulates retinal vascular remodeling during development. *Mol Cell Neurosci* 37:85–95

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

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

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

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

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

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

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

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

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

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

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

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

Sundin OH, **Broman KW**, Chang HH, Vito ECL, Stark WJ, Gottsch JD (2006) A common locus for 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 GG, 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

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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

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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 (with discussion). *J Roy Stat Soc* B 64:641–656, 737–775

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

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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

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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

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Suarez BK, Lin J, Burmester JK, **Broman KW**, Weber JL, Banerfee 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, Gray IC (eds) *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-Moiseiwitsch F (ed) *Statistics in Molecular Biology and Genetics. IMS Lecture Notes–Monograph Series*, Vol. 33, pp. 114–142

Technical Reports

Broman KW (2013) Thirteen years of R/qtl: Just barely sustainable. Contribution to *First Workshop on Sustainable Software for Science: Practice and Experiences.* arXiv:1309.1192

Broman KW (2011) Haplotype probabilities in advanced intercross populations. Technical report #223, Department of Biostatistics & Medical Informatics, University of Wisconsin-Madison

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

Manichaikul A, Moon JY, Sen Ś, Yandell BS, **Broman KW** (2008) A model selection approach for the identification of quantitative trait loci in experimental crosses, allowing epistasis. Technical report #205, 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

Broman KW (2004) The genomes of recombinant inbred lines: The gory details. Working paper 47, 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

Broman KW, Boyartchuk VL, Dietrich WF (2000) Mapping time-to-death quantitative trait loci in a mouse cross with high survival rates. Technical Report MS00-04, Department of Biostatistics, Johns Hopkins University, Baltimore, MD

Broman K, Speed T, Tigges M (1996) Estimation of antigen-responsive T cell frequencies in PBMC from human subjects. Technical Report #454, Department of Statistics, University of California, Berkeley

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 (`www.rqtl.org`).
R/qtlcharts	An R package to create interactive data visualizations for quantitative trait locus mapping data (`kbroman.org/qtlcharts`).
aRxiv	An R package for searching arXiv, a repository of electronic preprints for computer science, mathematics, physics, quantitative biology, quantitative financy, and statistics. (`github.com/ropensci/aRxiv`).
git/GitHub guide	Online tutorial on the git version control system and its use with `GitHub.com` (`kbroman.org/github_tutorial`).
knitr in a knutshell	Online tutorial on knitr, a tool for creating documents that mix code and text (`kbroman.org/knitr_knutshell`).

minimal make	Online tutorial on GNU Make, for automating computational tasks (`kbroman.org/minimal_make`).
R package primer	Online tutorial on writing packages for the R statistical software (`kbroman.org/pkg_primer`).
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

Jianan Tian, PhD student, Statistics, University of Wisconsin–Madison

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

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

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

Master's Advisees

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

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

Undergraduate Advisees

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

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

Academic Advisees, Johns Hopkins University

2006 – 2007	Sheng-Chih Jin	ScM candidate, Biostatistics
2005 – 2007	Ani Manichaikul	PhD candidate, Biostatistics
2005 – 2006	Alex Phan	candidate for MHS in Bioinformatics
2005 – 2006	Jichao Chen	candidate for MHS in Bioinformatics
2004 – 2006	Snaebjorn Gunnsteinsson	PhD candidate, Biostatistics
2003 – 2007	Benilton Carvalho	PhD candidate, Biostatistics
2003 – 2005	Wenyi Wang	PhD candidate, Biostatistics
2000 – 2004	Wei-Min Chen	PhD candidate, Biostatistics
2000 – 2003	Michelle Shardell	PhD candidate, Biostatistics
1999 – 2001	Sora Kim	ScM candidate, Biostatistics

Doctoral Thesis Committees, University of Wisconsin–Madison

2014 – present	Alessandra Torno	Genetics
2013 – present	Shuang Huang	Statistics
2013 – present	Richard Wang	Genetics
2012 – present	Michelle Parmenter	Genetics
2012 – present	Molly McDevitt	Biochemistry
2011 – 2013	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics
2010 – present	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

2014	Shuyun Ye	Statistics
	Michelle Parmenter	Genetics
	Jeea Choi	Statistics
2013	Jianan Tian	Statistics
	Richard Wang	Genetics
	Shuang Huang	Statistics
	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics
	Molly McDevitt	Biochemistry
2012	Katie Clowers	Genetics
2011	Il Youp Kwak	Statistics
2010	Jee Young Moon	Statistics
	John Dawson	Statistics
	Elias Chaibub Neto	Statistics
	Qinglin Pei	Statistics
	Jingfang Zhang	Oncology
2008	Beth Dumont	Genetics

Oral Exams, Johns Hopkins University

2006	Lindsey Garver	Molecular Microbiology and Immunology
	Benilton Carvalho	Biostatistics
	Yen-Yi Ho	Biostatistics
	Lindsey Enewold	Epidemiology

	Renee Gardner	Environmental Health Sciences
2005	Ani Manichaikul	Biostatistics
	Wenyi Wang	Biostatistics
	Meera Venkatesan	Molecular Microbiology and Immunology
	Audrey Grant	Epidemiology
2004	Katherine Swanson	Molecular Microbiology and Immunology
2003	Sadeep Shrestha	Epidemiology
	Wei-Min Chen	Biostatistics
2002	Marie-Hélène Roy-Gagnon	Epidemiology
2001	Leslie Cope	Mathematical Sciences (School of Engineering)
	Vivian Yuan	Mathematical Sciences (School of Engineering)
	Jean-Paul Chretien	Epidemiology
2000	Xin Liu	Epidemiology
	Tsuo-Hung Lan	Epidemiology
	Halcyon Skinner	Epidemiology
1999	David Kaufman	Epidemiology

Doctoral Thesis Defenses, University of Wisconsin–Madison

2014	Il-Youp Kwak	Statistics
2013	Qinglin Pei	Statistics
2012	John Dawson	Statistics
2011	Michael White	Genetics
2010	Beth Dumont	Genetics
	Elias Chaibub Neto	Statistics
2009	YounJeong Choi	Statistics

Doctoral Thesis Defenses, Johns Hopkins University

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

Master's Thesis Defenses, University of Wisconsin–Madison

2013	Raja Farhana Raja Mohd Anuar	Plant Breeding and Plant Genetics

Master's Thesis Reading, Johns Hopkins University

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

Classroom Instruction, University of Wisconsin–Madison

Spring, 2015	BMI 826-003	Tools for Reproducible Research
Spring, 2014	BMI 826-003	Tools for Reproducible Research (*new*)
	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
Fall, 2012	BMI 826-001	Statistical Methods for QTL Mapping
Spring, 2012	Statistics 877	Statistical Methods in Molecular Biology (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, Wang, and Keles)
Spring, 2011	Statistics 992-001	Statistical Methods for QTL Mapping (*new*)
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, Kendziorski, 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 (*new*) (jointly with Drs. Newton, Kendziorski, Larget, Ané, Yandell, and Keles)

Classroom Instruction, Johns Hopkins University

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

	Biostatistics 140.615–616	Statistics for Laboratory Scientists
2002 – 2003	Biostatistics 140.668	Special Topics in Genetics and Genomics (*new*) (jointly with Dr. Parmigiani)
	Biostatistics 140.615–616	Statistics for Laboratory Scientists
2001 – 2002	Biostatistics 140.615	Statistics for Laboratory Scientists (*new*)
2000 – 2001	Biostatistics 140.778	Advanced Statistical Computing (*new*)
	Biostatistics 140.667	Genetics for Statisticians
	Biostatistics 140.668	Statistical Genetics
1999 – 2000	Biostatistics 140.846	Genetics for Statisticians (*new*)
	Biostatistics 140.668	Statistical Genetics (*new*)

Classroom Instruction, University of California, Berkeley

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

Classroom Instruction, University of Wisconsin–Milwaukee

1991 – 1992	Mathematics 095	Basic Algebra

Other teaching

2008 – 2014	Instructor and co-organizer, Short Course on Systems Genetics, The Jackson Laboratory, Bar Harbor, Maine
2014	Instuctor, Software Carpentry Bootcamp, Advanced Computing Infrastructure, 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
2014	Lecture on "Creating effective figures and tables" to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison
2008 – 2013	Lecture on my consulting experiences in Statistical Consulting (Stat 998), Department of Statistics, University of Wisconsin–Madison
2013	Lecture on "How to display data badly" to MD/PhD students, School of Medicine and Public Health, University of Wisconsin–Madison
2013	Lecture on "A brief introduction to git and GitHub" to graduate students, Department of Statistics, University of Wisconsin–Madison
2013	Lecture on "Why aren't all of our graphs interactive?" to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison
2012	Instructor, Training Course on Field Trials & QTL Analysis using R and R/qtl, ICRISAT, Hyderabad, India
2012	Lecture on "Programming style" to graduate students in the Biostatistics Training Program, Department of Biostatistics & Medical Informatics, University of Wisconsin–Madison

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

ACADEMIC LEADERSHIP AND PROGRAM DEVELOPMENT

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

SERVICE ACTIVITIES

International and National

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

2012 – present	Steering Committee, Medical Scientist Training Program, School of Medicine and Public Health, University of Wisconsin–Madison
2012 – 2015	Faculty Advisory Committee, School of Medicine and Public Health, University of Wisconsin–Madison
2011 – 2015	University Library Committee, University of Wisconsin–Madison (*Chair*, 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

2010 – present	Chair, Education and Curriculum Committee, Department of 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

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

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

A Program of Research in Population Cytogenetics   NIH/NICHD
Terry Hassold (Washington State), PI   12/01/10 – 7/31/15   (8%)
Study meiosis in human oocytes and spermatocytes to examine the way in which homologous chromosomes find and synapse with each other and how these processes relate to the formation of crossovers, and to compare the recombination processes between human males and females, including the contribution of chromatin structure and interference to sex-specific differences in recombination rates.
Role: Co-investigator

Systems Genetic Analysis of Methamphetamine's Motivational Effects in Mouse AIL   NIH/NIDA
Abraham Palmer (U Chicago), PI   07/01/11 – 03/31/16   (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 for Analysis and Integration in Genomic Studies of Disease   NIH/NIGMS
Christina Kendziorski, PI   08/01/12 – 04/30/16   (7%)
This project aims to develop and disseminate statistical methods to address challenges that arise in genomic based studies of disease, with particular focus on methods that integrate data across multiple platforms and scales to both identify as well as comprehensively characterize genomic features affecting an individual's disease course and/or likelihood of response to treatment.
Role: Co-investigator

The Genetics and Evolution of Extreme Body Size in Mice From Gough Island   NIH/NIGMS
Bret Payseur, PI   09/10/12 – 06/30/16   (10%)
This project aims to integrate genetic mapping, comparative morphometrics, and population genetics to provide the first detailed genetic portrait of rapid body size evolution in an island mammal, using the Gough Island wild house mice, which have evolved extreme body size in just hundreds of generations.
Role: Co-investigator

NIAID Centers of Excellence for Influenza Research and Surveillance   NIH/NIAID
Yoshihiro Kawaoka, PI   04/01/14 – 03/31/15   (8%)
In a genetics study with Diversity Outbred (DO) mice, identify host genes that, in the context of a functional Mx1 *gene, affect the outcome of H5N1 influenza virus infections.*
Role: Co-investigator

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

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

Previous Grant Support

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Center for Craniofacial Development and Disorders   NIH/NIDR
Terri Beaty, PI   08/01/01 – 08/01/04   (5%)
Biostatistical Core for program project on the genetics of craniofacial disorders.
Role: Co-Investigator
Mouse QTL in Endotoxic Shock   NIH
Roger Reeves, PI   08/01/01 – 07/30/05   (10%)
Identify genomic regions contributing to susceptibility to endotoxic shock in mice.
Role: Co-Investigator

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

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

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

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

INVITED PRESENTATIONS

Scientific Meetings

2015   American Association for the Advancement of Science (AAAS) annual meeting, San Jose, California

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

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

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

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

2010   Fourteenth QTL-MAS Workshop, Poznań, Poland

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

2007   Systems Medicine Workshop, NHLBI, Bethesda, Maryland

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

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

2002   Royal Statistical Society, London, England

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

1996   WNAR/IMS Western Regional Conference, Pullman, Washington

Seminars

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

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

2012   Department of Pathology and Laboratory Medicine, University of Wisconsin–Madison

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 Pathology and Laboratory Medicine, 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
Department of Pathology and Laboratory Medicine, University of Wisconsin–Madison

2007   Department of Human Genetics, University of Chicago
Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland
Statistics Program, St. Olaf College, Northfield, Minnesota
Center for Interdisciplinary Research, St. Olaf College, Northfield, Minnesota
Annual Retreat, Laboratory of Genetics, University of Wisconsin–Madison
Division of Statistics, Northern Illinois University, DeKalb, Illinois
Department of Biostatistics and Medical Informatics, University of Wisconsin–Madison
Department of Human Genetics, University of California, Los Angeles
Department of Statistics, University of California, Berkeley
The Jackson Laboratory, Bar Harbor, Maine
Department of Biostatistics, University of Michigan, Ann Arbor

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

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

2004   Department of Biostatistics, Yale University, New Haven, Connecticut
Marshfield Clinic Research Foundation, Marshfield, Wisconsin
Genetics and Genomic Biology, Hospital for Sick Children, Toronto, Canada
Genetic Interest Group, Center for Human Genetic Research, Vanderbilt University, Nashville, Tennessee
Department of Biostatistics, University of Buffalo

Immunogenetics, Universität Rostock, Germany
Department of Epidemiology and Biostatistics, Memorial Sloan–Kettering Cancer Center, New York

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

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

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

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

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

1998   Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
Queensland Institute for Medical Research, Brisbane, Australia
Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia
deCODE Genetics, Reykjávik, Iceland
Biostatistics Department, University of Michigan, Ann Arbor
Department of Statistics, University of California, Berkeley
Department of Mathematical Sciences, University of Wisconsin–Milwaukee

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