

CURRICULUM VITAE

Michael Boehnke

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PERSONAL INFORMATION

Born: May 16, 1956, Eugene, Oregon
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EDUCATION

B.A. Honors College in Mathematics with Distinction, University of Oregon, 1977

Coursework in Mathematics and Biology, Albert-Ludwigs-Universität,
Freiburg, West Germany, 1977-1978

Ph.D. in Biomathematics, University of California, Los Angeles, 1983
Dissertation: Advances in Pedigree Analysis: Ascertainment, Goodness of Fit, and
Optimization. Advisor: Kenneth Lange.

PROFESSIONAL EXPERIENCE

Research Associate, Cedars-Sinai Medical Center, 1979-1980

Teaching Assistant, Department of Biology, UCLA, 1979-1981

Research Assistant, Department of Biomathematics, UCLA, 1980-1983

Assistant Professor, Department of Biostatistics, University of Michigan, 1984-1989

Associate Professor, Department of Biostatistics, University of Michigan, 1989-1993

Professor, Department of Biostatistics, University of Michigan, 1993-present

Director, University of Michigan Genome Science Training Program, 1995-present

Director, University of Michigan Center for Statistical Genetics, 1999-present

Visiting Scholar, Department of Human Genetics, UCLA, 2007-2008

Visiting Scholar, Department of Biostatistics, Bioinformatics, and Epidemiology,
Medical University of South Carolina, 2008

HONORS

Phi Beta Kappa, 1976

DeCou Prize Winner as Outstanding Mathematics Undergraduate at the University of Oregon, 1977

Fulbright Scholar in Freiburg, West Germany, 1977-1978

National Institutes of Health Pre-Doctoral Trainee, 1978-1983

Snedecor Award for Outstanding Statistical Applications Paper, American Statistical Association, 1993, joint with Kenneth Lange

Myrto Lefkopolou Distinguished Lecturer, Harvard University School of Public Health, 1994

University of Michigan School of Public Health Excellence in Research Award, 1999

Pharmacia Research Professor of Biostatistics, 1999-2005

Bernard Greenberg Lecturer, Department of Biostatistics, University of North Carolina School of Public Health, 2002

Fellow, American Statistical Association, 2002-present

Richard G. Cornell Collegiate Professor of Biostatistics, 2005-2008

Member, Institute of Medicine of the National Academies, 2006-present

Benjamin Stapleton Lecturer, University of Colorado at Denver and Health Sciences Center, Denver, Colorado, 2007

Richard G. Cornell Distinguished University Professor of Biostatistics, 2008-present

Fellow, American Association for the Advancement of Science, 2010-present

Prize for outstanding paper in *Genetic Epidemiology*, 2013

Precision Medicine World Conference (PMWC) Pioneer Award, 2018

PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science

American Society of Human Genetics

International Genetic Epidemiology Society

PUBLICATIONS

Publications which have received peer review

1. **Boehnke M**, Guzman M, Hehmann R, Leibold W, and Gatti RA (1980) HLA-D typing with lymphoblastoid cell lines. VIII. Cut points and gene frequency estimates by multiple testing analysis. *Tissue Antigens* 16:161-168.
2. Lange K, **Boehnke M**, and Carson R (1981) Moment computations for subcritical branching processes. *Journal of Applied Probability* 18:52-64.
3. Lange K and **Boehnke M** (1982) How many polymorphic genes will it take to span the human genome? *American Journal of Human Genetics* 34:842-845.
4. Lange K and **Boehnke M** (1983) Extensions to pedigree analysis. IV. Covariance components models for multivariate traits. *American Journal of Medical Genetics* 14:513-524.
5. Lange K and **Boehnke M** (1983) Some combinatorial problems of DNA restriction fragment length polymorphisms. *American Journal of Human Genetics* 35:177-192.
6. **Boehnke M**, Conneally PM, and Lange K (1983) Two models for a maternal factor in the inheritance of Huntington disease. *American Journal of Human Genetics* 35:845-860.
7. Lange K and **Boehnke M** (1983) Extensions to pedigree analysis. V. Optimal calculation of Mendelian likelihoods. *Human Heredity* 33:291-301.
8. **Boehnke M** and Greenberg DA (1984) The effects of conditioning on probands to correct for multiple ascertainment. *American Journal of Human Genetics* 36:1298-1308.
9. **Boehnke M** and Lange K (1984) Ascertainment and goodness of fit of variance component models for pedigree data. *Progress in Clinical and Biological Research* 147:173-192.
10. Gatti RA, **Boehnke M**, Crist M, and Sparkes RS (1985) Genetic linkage studies in ataxia-telangiectasia: Gm markers. *Kroc Foundation Series* 19:163-172.
11. **Boehnke M**, Moll PP, Lange K, Weidman WH, and Kottke BA (1986) Univariate and bivariate analyses of cholesterol and triglyceride levels in pedigrees. *American Journal of Medical Genetics* 23:775-792.
12. Hodge SE and **Boehnke M** (1986) A note on Cannings and Thompson's sequential sampling scheme for pedigrees. *American Journal of Human Genetics* 39:274-281.
13. **Boehnke M** (1986) Estimating the power of a proposed linkage study: a practical computer simulation approach. *American Journal of Human Genetics* 39:513-527.
14. **Boehnke M**, Moll P, Kottke B, and Weidman W (1987) Partitioning the variability of fasting plasma glucose levels in pedigrees. Genetic and environmental factors. *American Journal of Epidemiology* 125:679-689.

15. Bird TD, **Boehnke M**, Schellenberg GD, Deeb SS, and Lipe HP (1987) The use of apolipoprotein CII as a genetic marker for myotonic dystrophy. *Archives of Neurology* 44:273-275.
16. Schellenberg GD, Deeb SS, **Boehnke M**, Bryant EM, Martin GM, Lampe TH, and Bird TD (1987) Association of an apolipoprotein CII allele with familial dementia of the Alzheimer type. *Journal of Neurogenetics* 4:97-108.
17. Diehl SR, **Boehnke M**, Collins FS, Erickson RP, Karolyi IJ, Ploughman LM, Pericak-Vance MA, Aylsworth AS, and Roses AD (1987) Linkage analysis of peripheral neurofibromatosis to DNA markers on chromosome 8. *Journal of Medical Genetics* 24:532-534.
18. Bird TD, **Boehnke M**, Anderson J, Lampe TH, Schellenberg GD, and Larson EB (1987) The frequency of C4B variants of complement in familial and sporadic Alzheimer disease. *Alzheimer Disease and Associated Disorders* 1:251-255.
19. Diehl SR, **Boehnke M**, Erickson RP, Baxter AB, Bruce MA, Lieberman JL, Platt DJ, Ploughman LM, Seiler KA, Sweet AM, and Collins FS (1987) Linkage analysis of von Recklinghausen neurofibromatosis to DNA markers on chromosome 17. *Genomics* 1:361-363.
20. Hanash SM, **Boehnke M**, Chu EH, Neel JV, and Kuick RD (1988) Non-random distribution of structural mutants in ethylnitrosourea-treated cultured human lymphoblastoid cells. *Proceedings of the National Academy of Sciences USA* 85:165-169.
21. Chu EH, **Boehnke M**, Hanash SM, Kuick RD, Lamb BJ, Neel JV, Niezgodka W, Pivrotto S, and Sundling G (1988) Estimation of mutation rates based on the analysis of polypeptide constituents of cultured human lymphoblastoid cells. *Genetics* 119:693-703.
22. Schwartz AG, **Boehnke M**, and Moll PP (1988) Family risk index as a measure of familial heterogeneity of cancer risk. A population-based study in metropolitan Detroit. *American Journal of Epidemiology* 128:524-535.
23. **Boehnke M**, Young MR, and Moll PP (1988) Comparison of sequential and fixed-structure sampling of pedigrees in complex segregation analysis of a quantitative trait. *American Journal of Human Genetics* 43:336-343.
24. Schellenberg GD, Bird TD, Wijsman EM, Moore DK, **Boehnke M**, Bryant EM, Lampe TH, Nochlin D, Sumi SM, Deeb SS, Beyreuther K, and Martin GM (1988) Absence of linkage of chromosome 21q21 markers to familial Alzheimer's disease. *Science* 241:1507-1510.
25. Tarlo KS, **Boehnke M**, and Chin B (1988) Synergism of mutant frequencies in the mouse lymphoma cell mutagenicity assay by binary mixtures of methyl methanesulfonate and ethyl methanesulfonate. *Mutation Research* 206:239-246.
26. Lange K, Weeks D, and **Boehnke M** (1988) Programs for Pedigree Analysis: MENDEL, FISHER, and dGENE. *Genetic Epidemiology* 5:471-472.

27. Young MR, **Boehnke M**, and Moll PP (1988) Correcting for single ascertainment by truncation for a quantitative trait. *American Journal of Human Genetics* 43:705-708.
28. Diehl SR, **Boehnke M**, Erickson RP, Ploughman LM, Seiler KA, Lieberman JL, Clarke HB, Bruce MA, Schorry EK, Pericak-Vance MA, O'Connell P, and Collins FS (1989) A refined genetic map of the region of chromosome 17 surrounding the von Recklinghausen neurofibromatosis (NF1) gene. *American Journal of Human Genetics* 44:33-37.
29. **Boehnke M** and Moll PP (1989) Identifying pedigrees segregating at a major locus for a quantitative trait: an efficient strategy for linkage analysis. *American Journal of Human Genetics* 44:216-224.
30. Ploughman LM and **Boehnke M** (1989) Estimating the power of a proposed linkage study for a complex genetic trait. *American Journal of Human Genetics* 44:543-551.
31. Olson JM, **Boehnke M**, Neiswanger K, Roche AF, and Siervogel RM (1989) Alternative genetic models for the inheritance of the phenylthiocarbamide taste deficiency. *Genetic Epidemiology* 6:423-434.
32. **Boehnke M**, Arnheim N, Li H, and Collins FS (1989) Fine-structure genetic mapping of human chromosomes using the polymerase chain reaction on single sperm: experimental design considerations. *American Journal of Human Genetics* 45:21-32.
33. Ping AJ, Reeve AE, Law DJ, Young MR, **Boehnke M**, and Feinberg AP (1989) Genetic linkage of Beckwith-Wiedemann syndrome to 11p15. *American Journal of Human Genetics* 44:720-723.
34. **Boehnke M**, Omoto KH, and Arduino JM (1990) Selecting pedigrees for linkage analysis of a quantitative trait: the expected number of informative meioses. *American Journal of Human Genetics* 46:581-586.
35. Kwon JM, **Boehnke M**, Burns TL, and Moll PP (1990) Commingling and segregation analyses: comparison of results from a simulation study of a quantitative trait. *Genetic Epidemiology* 7:57-68.
36. Roth MS, Weiner GJ, Allen EA, Terry VH, Harnden CE, **Boehnke M**, Kaminski MS, and Ginsburg D (1990) Molecular characterization of anti-idiotypic antibody-resistant variants of a murine β -cell lymphoma. *Journal of Immunology* 145:768-777.
37. **Boehnke M** (1990) Sample-size guidelines for linkage analysis of a dominant locus for a quantitative trait by the method of lod scores. *American Journal of Human Genetics* 47:218-227.
38. Olson JM and **Boehnke M** (1990) Monte Carlo comparison of preliminary methods for ordering multiple genetic loci. *American Journal of Human Genetics* 47:470-482.
39. Eto K, Sumi SM, Bird TD, McEvoy-Bush T, **Boehnke M**, and Schellenberg G (1990) Family with dominantly inherited ataxia, amyotrophy, and peripheral sensory loss: Spinopontine atrophy or Machado-Joseph Azorean disease in another non-Portuguese family? *Archives of Neurology* 47:968-974.

40. Sieving PA, Bingham EL, Roth MS, Young MR, **Boehnke M**, Kuo CY, and Ginsburg D (1990) Linkage relationship of X-linked juvenile retinoschisis with Xp22.1-p22.3 probes. *American Journal of Human Genetics* 47:616-621.
41. Iannuzzi MC, Hidaka N, **Boehnke M**, Bruck ME, Hanna WT, Collins FS, and Ginsburg D (1991) Analysis of the relationship of von Willebrand disease (vWD) and hereditary hemorrhagic telangiectasia and identification of a potential type IIA vWD mutation. *American Journal of Human Genetics* 48:757-763.
42. **Boehnke M** (1991) Allele frequency estimation from data on relatives. *American Journal of Human Genetics* 48:22-25.
43. **Boehnke M**, Lange K, and Cox DR (1991) Statistical methods for multipoint radiation hybrid mapping. *American Journal of Human Genetics* 49:1174-1188.
44. Richards JE, Kuo C, **Boehnke M**, and Sieving PA (1991) Rhodopsin Thr58Arg mutation in a family with autosomal dominant retinitis pigmentosa. *Ophthalmology* 98:1797-1805.
45. Sowers MR, **Boehnke M**, Jannausch ML, Crutchfield M, Corton G, and Burns TL (1992) Familiality and partitioning the variability of femoral bone mineral density in women of child-bearing age. *Calcified Tissue International* 50:110-114.
46. **Boehnke M** (1992) Genetic Analysis Workshop 7: radiation hybrid and somatic cell hybrid mapping of chromosome 21. *Cytogenetics and Cell Genetics* 59:74-76.
47. **Boehnke M** (1992) Radiation hybrid mapping by minimization of the number of obligate chromosome breaks. *Cytogenetics and Cell Genetics* 59:96-98.
48. Schellenberg GD, **Boehnke M**, Wijsman EM, Moore DK, Martin GM, and Bird TD (1992) Genetic association and linkage analysis of the apolipoprotein CII locus and familial Alzheimer's disease. *Annals of Neurology* 31:223-227.
49. Lange K and **Boehnke M** (1992) Bayesian methods and optimal experimental design for gene mapping by radiation hybrids. *Annals of Human Genetics* 56:119-144.
50. Altherr MR, Plummer S, Bates G, MacDonald M, Taylor S, Lehrach H, Frischauf AM, Gusella J, **Boehnke M**, and Wasmuth JJ (1992) Radiation hybrid map spanning the Huntington disease gene region of chromosome 4. *Genomics* 13:1040-1046.
51. **Boehnke M** (1992) Multipoint analysis for radiation hybrid mapping. *Annals of Medicine* 24:383-386.
52. Frazer KA, **Boehnke M**, Budarf ML, Wolff RK, Emanuel BS, Myers RM, and Cox DR (1992) A radiation hybrid map of the region on human chromosome 22 containing the neurofibromatosis type 2 locus. *Genomics* 14:574-584.
53. Gorski JL, **Boehnke M**, Reyner EL, and Burright EN (1992) A radiation hybrid map of the proximal short arm of the human X chromosome spanning incontinentia pigmenti 1 (IP1) translocation breakpoints. *Genomics* 14:657-665.

54. Spence MA, Bishop DT, **Boehnke M**, Elston RC, Falk C, Hodge SE, Ott J, Rice J, Merikangas K, and Kupfer D (1993) Methodological issues in linkage analyses for psychiatric disorders: secular trends, assortative mating, bilineal pedigrees. *Human Heredity* 43:166-172.
55. Richard CW III, **Boehnke M**, Berg DJ, Lichy JH, Meeker TC, Hauser E, Myers RM, and Cox DR (1993) A radiation hybrid map of the distal short arm of human chromosome 11, containing the Beckwith-Wiedemann and associated embryonal tumor disease loci. *American Journal of Human Genetics* 52:915-921.
56. Chamberlain JS, **Boehnke M**, Frank TS, Kiouisis S, Xu J, Guo SW, Hauser ER, Norum RA, Helmbold EA, Markel DS, Keshavarzi SM, Jackson CE, Calzone K, Garber J, Collins FS, and Weber BL (1993) *BRCA1* maps proximal to D17S579 on chromosome 17q21 by genetic analysis. *American Journal of Human Genetics* 52:792-798.
57. Biesecker BB, **Boehnke M**, Calzone K, Markel DS, Garber JE, Collins FS, and Weber BL (1993) Genetic counseling for families with inherited susceptibility to breast and ovarian cancer. *Journal of the American Medical Association* 269:1970-1974.
58. Abel KJ, **Boehnke M**, Prahalad M, Ho P, Flejter WL, Watkins M, VanderStoep J, Chandrasekharappa SC, Collins FS, Glover TW, and Weber BL (1993) A radiation hybrid map of the *BRCA1* region of chromosome 17q12-21. *Genomics* 17:632-641.
59. Flejter WL, Barcroft CL, Guo SW, Lynch ED, **Boehnke M**, Chandrasekharappa S, Hayes S, Collins FS, Weber BL, and Glover TW (1993) Multicolor FISH mapping with Alu-PCR amplified YAC clone DNA determines the order of markers in the *BRCA1* region on chromosome 17q12-q21. *Genomics* 17:624-631.
60. Schork NJ, **Boehnke M**, Terwilliger JD, and Ott J (1993) Two-trait-locus linkage analysis: a powerful strategy for mapping complex genetic traits. *American Journal of Human Genetics* 53:1127-1136.
61. Richards JE, Lichter PR, **Boehnke M**, Uro JL, Torrez D, Wong D, and Johnson AT (1994) Mapping of a gene for autosomal dominant juvenile-onset open-angle glaucoma to chromosome 1q. *American Journal of Human Genetics* 54:62-70.
62. McDonald MT, Papenberg KA, Ghosh S, Glatfelter AA, Biesecker BB, Helmbold EA, Markel DS, Zolotor A, McKinnon WC, Vanderstoep JL, Jackson CE, Iannuzzi M, Collins FS, **Boehnke M**, Porteous ME, Gutmacher AE, and Marchuk DA (1994) A disease locus for hereditary haemorrhagic telangiectasia maps to chromosome 9q33-34. *Nature Genetics* 6:197-204.
63. Yu CE, Payami H, Olson JM, **Boehnke M**, Wijsman EM, Orr HT, Kukull WA, Goddard KA, Nemens E, White JA, Alonso ME, Taylor TD, Ball MJ, Kaye J, Morris J, Chui H, Sadovnick AD, Martin GM, Larson EB, Heston LL, Bird TD, and Schellenberg GD (1994) The apolipoprotein E/CI/CII gene cluster and late-onset Alzheimer disease. *American Journal of Human Genetics* 54:631-642.

64. Lunetta KL and **Boehnke M** (1994) Multipoint radiation hybrid mapping: comparison of methods, sample size requirements, and optimal study characteristics. *Genomics* 21:92-103.
65. **Boehnke M** (1994) Limits of resolution of genetic linkage studies: implications for the positional cloning of human disease genes. *American Journal of Human Genetics* 55:379-390.
66. Couch FJ, Abel KJ, Brody LC, **Boehnke M**, Collins FS, and Weber BL (1994) Localization of the gene for ATP citrate lyase (ACLY) distal to gastrin (GAS) and proximal to D17S856 on chromosome 17q12-q21. *Genomics* 21:444-446.
67. Oshima J, Yu CE, **Boehnke M**, Weber JL, Edelhoff S, Wagner MJ, Wells DE, Wood S, Distèche CM, Martin GM, and Schellenberg GD (1994) Integrated mapping analysis of the Werner Syndrome region of chromosome 8. *Genomics* 23:100-113.
68. Maliarik M, Kost J, Harrington D, Major M, Popovich J, **Boehnke M**, and Iannuzzi MC (1994) Linkage analysis of major histocompatibility genes in familial sarcoidosis. *Sarcoidosis* 11:236-239.
69. Ford D, Easton DF, Bishop DT, Narod SA, Goldgar DE, Haites N, Milner B, Allan L, Ponder BAJ, Peto J, Smith S, Stratton M, Lenoir GM, Feunteun J, Lynch H, Arason A, Barkardottir R, Egilsson V, Black DM, Kelsell D, Spurr N, Devilee P, Cornelisse CJ, Varsen H, Birch JM, Skolnick M, Santibanezkoref MS, Teare D, Steel M, Porter D, Cohen BB, Carothers A, Smyth EM, Weber B, Newbold B, **Boehnke M**, Collins FS, Cannon-Albright LA, and Goldgar D (1994) Risks of cancer in *BRCA1*-mutation carriers. *Lancet* 343:692-695.
70. Lange K, **Boehnke M**, Cox DR, and Lunetta KL (1995) Statistical methods for polyploid radiation hybrid mapping. *Genome Research* 5:136-150.
71. Lunetta KL, **Boehnke M**, Lange K, and Cox DR (1995) Experimental design and error detection for polyploid radiation hybrid mapping. *Genome Research* 5:151-163.
72. Pawar H, Bingham EL, Lunetta KL, Segal M, Richards JE, **Boehnke M**, and Sieving PA (1995) Refined genetic mapping of juvenile X-linked retinoschisis. *Human Heredity* 45:206-210.
73. Couch FJ, Garber J, Kiouisis S, Calzone K, Hauser ER, Merajver SD, Frank TS, **Boehnke M**, Chamberlain JS, Collins FS, and Weber BL (1995) Genetic analysis of eight breast-ovarian cancer families with suspected *BRCA1* mutations. *Journal of the National Cancer Institute* 17:9-14.
74. **Boehnke M** and Hulbert-Shearon T (1995) Recombination fraction estimate of zero in the presence of apparent recombinants: effects of incomplete penetrance and sporadic cases. *Genetic Epidemiology* 12:509-513.
75. Easton DF, Ford D, Bishop DT, Haites N, Milner B, Allan L, Easton DF, Ponder BAJ, Peto J, Smith S, Ford D, Stratton M, Narod SA, Lenoir GM, Feunteun J, Lynch H, Arason A, Barkardottir R, Egilsson DV, Bishop DT, Black DM, Kelsell D, Spurr NK,

- Devilee P, Cornelisse CJ, Varsen H, Birch JM, Santibanezkoref MS, Teare MD, Steel M, Porter D, Cohen BB, Carothers A, Smyth E, Weber B, **Boehnke M**, Collins FS, Cannon-Albright LA, Goldgar D, and Skolnick M (1995) Breast and ovarian-cancer incidence in *BRCA1*-mutation carriers. *American Journal of Human Genetics* 56:265-271.
76. Narod SA, Ford D, Devilee P, Barkardottir RB, Lynch HT, Smith SA, Ponder BAJ, Weber BL, Garber JE, Birch JM, Cornelis RS, Kelsell DP, Spurr NK, Smyth E, Haites N, Sobol H, Bignon YJ, Chang-claude J, Hamann U, Lindblom A, Borg A, Piver MS, Gallion HH, Struewing JP, Whittimore A, Tonin P, Goldgar DE, Easton DF, Milner B, Allan L, Simard J, Rommens J, McGillivray B, Green R, Ives E, Boyd N, Rosen B, Cole D, Morgan K, Moslehi R, Ponder B, Peto J, Smith S, Stratton M, Dicioccio RA, Gallion H, Santibanezkoref MS, Teare MD, Evans DG, Stoppalyonnet D, Lalle P, Bonaiti C, Essioux L, Girodet C, Maugardlouboutin C, Nicolleau G, Longy M, Toulouse C, Horstein I, Birnbaum D, Eisinger F, Karengueven F, Noguchi T, Hardouin A, Rio P, Machelardroumagnac M, Nogues C, Cohenhaguenaer O, Lortholary A, Bay Jo, Arason A, Barkardottir RB, Egilsson V, Bishop DT, Kelsell D, Murday VA, Solomon E, Spurr N, Turner G, Lenoir G, Feunteun J, Lynch H, Lynch J, Watson P, Conway T, Bonnardel C, Serova O, Torchard D, Larsson C, Vasen H, Vanleeuwen I, Cornelisse CJ, Steel M, Porter D, Cohen BB, Carothers A, Cannon-Albright LA, Goldgar D, Skolnick M, Becher H, Johannsson O, Weber B, Collins FS, **Boehnke M**, Garber J, and Li F (1995) An evaluation of genetic-heterogeneity in 145 breast-ovarian-cancer families. *American Journal of Human Genetics* 56:254-264.
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78. Hulbert-Shearon T, **Boehnke M**, and Lange K (1996) Lod score curves for phase-unknown matings. *Human Heredity* 46:55-57.
79. Hauser ER, **Boehnke M**, Guo SW, and Risch N (1996) Affected-sib-pair interval mapping and exclusion for complex genetic traits: sampling considerations. *Genetic Epidemiology* 13:117-137.
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81. Hou YC, Richards JE, Bingham EL, Pawar H, Scott K, Segal M, Lunetta KL, **Boehnke M**, and Sieving PA (1996) Linkage study of Best's vitelliform macular dystrophy (*VMD2*) in a large North American family. *Human Heredity* 46:211-220.
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83. Johnson AT, Richards JE, **Boehnke M**, Stringham HM, Herman SB, Wong DJ, and Lichter PR (1996) Clinical phenotype of juvenile-onset primary open-angle glaucoma linked to chromosome 1q. *Ophthalmology* 103:808-814.
84. Lunetta KL, **Boehnke M**, Lange K, and Cox DR (1996) Selected locus and multiple mapping panel models for radiation hybrid mapping. *American Journal of Human Genetics* 59:717-725.
85. Stringham HM and **Boehnke M** (1996) Identifying marker typing incompatibilities in linkage analysis. *American Journal of Human Genetics* 59:946-950.
86. Nichols WC, Antin JH, Lunetta KL, Terry VH, Hertel CE, Wheatley MA, Arnold ND, Siemieniak DR, **Boehnke M**, and Ginsburg D (1996) Polymorphism of adhesion molecule CD31 is not a significant risk factor for graft-versus-host disease. *Blood* 88:4429-4434.
87. Lichter PR, Richards JE, **Boehnke M**, Othman M, Cameron BD, Stringham HM, Downs CA, Lewis SB, and Boyd BF (1996) Juvenile glaucoma linked to *GLC1A* in a Panamanian family. *Transactions of the American Ophthalmology Society* 94:335-346.
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91. Lichter PR, Richards JE, Downs CA, Stringham HM, **Boehnke M**, and Farley FA (1997) Cosegregation of open-angle glaucoma and the nail-patella syndrome. *American Journal of Ophthalmology* 124:506-515.
92. **Boehnke M** and Langefeld CD (1998) Genetic association mapping based on discordant sib pairs: the discordant alleles test (DAT). *American Journal of Human Genetics* 62:950-961.
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3. **Boehnke M** (2015) Introduction to the 2014 Curt Stern Award: Gonçalo Abecasis. *American Journal of Human Genetics* 96:361-362. PMID: PMC4375418.

Book reviews/Letters to the editor

1. **Boehnke M** (1990) (Book Review) Multipoint mapping and linkage analysis based upon affected pedigree members: Genetic Analysis Workshop 6 in *Progress in Clinical and Biological Research*, edited by Elston RC, Spence MA, Hodge SE, and MacCluer JW *American Journal of Human Genetics* 47:1031-1032.
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4. Schork NJ, **Boehnke M**, Terwilliger JD, Ott J (1994) Letter to the Editor: reply to Sham. *American Journal of Human Genetics* 55:856-858.
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PRESENTATIONS

Talks delivered at professional meetings (2001-present)

New developments in statistical methods for human gene mapping. Invited presentation: US-Japan Symposium in the Cardiovascular Area, Honolulu, Hawaii, January 9, 2001.

Strategies to identify genetic variants responsible for a linkage signal for a complex genetic trait. Invited presentation: AACR Oncogenomics, Phoenix, Arizona, January 31, 2003.

Mapping type 2 diabetes genes on chromosome 20: FUSION and beyond. Invited presentation: American Society of Human Genetics, Toronto, Ontario, Canada, October 28, 2004.

Design considerations in large-scale genetic association studies. Invited presentation: American Society of Human Genetics, Salt Lake City, Utah, October 27, 2005.

Efficient designs for genome-wide association studies. Invited presentation: Genome-Wide Association Studies: Design and Analysis. Yale University, New Haven, Connecticut, October 27, 2006.

Efficient study designs for two-stage genome-wide association studies and application to bipolar disorder. Invited plenary presentation: World Congress of Psychiatric Genetics, Cagliari, Sardinia, Italy, October 30, 2006.

Efficient design of genome-wide association studies with application to type 2 diabetes. Invited plenary presentation: International Genetic Epidemiology Society, Tampa, Florida, November 24, 2006.

Design and analysis of genome-wide association studies: application to type 2 diabetes. Invited presentation: Kenneth Lange Symposium, University of California at Los Angeles, Los Angeles, California, February 9, 2007.

Efficient design and analysis of genome-wide association studies. Invited presentation: Joint Statistical Meetings, Salt Lake City, Utah, July 30, 2007.

A genome-wide association study of type 2 diabetes. GAIN Analysis Workshop II, Bethesda, Maryland, October 18, 2007.

Efficient statistical analysis of genome-wide case-control association data. Joint Statistical Meetings, Denver, Colorado, August 5, 2008.

Genome wide association studies of type 2 diabetes and associated traits. American College of Epidemiology, Tucson, Arizona, September 14, 2008.

Advantages and challenges of large samples and meta-analyses in GWAS of type 2 diabetes. American Society of Human Genetics, Philadelphia, Pennsylvania, November 15, 2008.

Differences in approaches to examining low-frequency (0.5-5%) and really-rare (<0.5%) variants. The dark matter of human genome wide association studies, Bethesda, Maryland, February 3, 2009.

Which GWAS signals should be followed up: choosing regions. The Challenge of Mapping GWAS Signals. Bethesda, Maryland, March 24, 2009.

Genome wide association studies of type 2 diabetes and related traits. Indiana Regional Bioinformatics Conference. Indianapolis, Indiana, July 7, 2009.

Genome wide association studies of type 2 diabetes and related traits. PQG Conference, Boston, November 12, 2009.

The genetics of type 2 diabetes. American Society of Human Genetics, Washington, D.C., November 4, 2010.

Design of GWAS and resequencing-based genetic association studies. International Biometric Society Meeting, Florianopolis, Brazil, December 10, 2010.

Identifying genes for type 2 diabetes and related traits. Diabetes Research Symposium. Chuncheon, Korea, September 9, 2010.

Identifying type 2 diabetes associated variants by exome and genome resequencing: progress report. Genomics of Common Diseases. Sanger Institute, Hinxton, UK, August 30, 2011.

Identifying genes for type 2 diabetes and related traits by genome-wide association and sequencing studies. Institute of Psychiatry, King's College, London, United Kingdom, June 21, 2012.

Genetics of type 2 diabetes in diverse populations. 1000 Genomes Project Community Meeting. Ann Arbor, Michigan, July 13, 2012.

Identifying genes for type 2 diabetes and related traits by genome-wide association and sequencing studies. University of Copenhagen, Copenhagen, Denmark, August 21, 2012.

Statistical genetics: opportunities and challenges in human gene mapping. University of Southern Denmark, Odense, Denmark, December 6, 2012.

Identifying genes for type 2 diabetes by genome-wide association and sequencing studies. University of Michigan Health System, Metabolism, Endocrinology, & Diabetes (MEND), Ann Arbor, Michigan, November 15, 2013.

Identifying and correcting for sample contamination in DNA sequencing studies. Department of Biostatistics, Harvard University, Boston, Massachusetts, December 12, 2013.

Identifying and correcting for sample contamination in DNA sequencing studies. Mt. Sinai School of Medicine, New York, New York, April 16, 2014.

Identifying genes for type 2 diabetes and related traits by GWA and sequencing studies. SISu symposium, Helsinki, Finland, August 26, 2014.

Type 2 diabetes knowledge portal: A call to action, community participation, and future directions. American Diabetes Association, Boston, Massachusetts, June 7, 2015.

AMP and the type 2 diabetes knowledge portal. American Society of Human Genetics, Baltimore, Maryland, October 7, 2015.

Gene discovery and genotype-based callback phenotyping in type 2 diabetes. Jebsen Center Symposium, NTNU, Trondheim, Norway, June 21, 2016.

Gene discovery and genotype-based callback phenotyping in type 2 diabetes. FIMM, Helsinki, Finland, August 30, 2016.

Seminars (2001-present)

Science Research Club, University of Michigan, Ann Arbor, Michigan, April 3, 2001.

Center for Human Genetics, Duke University, Durham, North Carolina, May 24, 2001.

Department of Biostatistics and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, March 25, 2002.

Rubicon Genomics, Ann Arbor, Michigan, April 12, 2002.

Department of Biostatistics, University of North Carolina, Chapel Hill, North Carolina, Greenberg Lecturer, May 22-24, 2002. Four seminars.

Biogen, Boston, Massachusetts, July 9, 2002.

Department of Human Genetics, University of California at Los Angeles, Los Angeles, California, May 12, 2003.

Wayne State University, Detroit, Michigan, September 8, 2003.

Department of Statistics, Michigan State University, East Lansing, Michigan, November 18, 2003.

McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University, Baltimore, Maryland, February 2, 2004.

Department of Human Genetics, Emory University, Atlanta, Georgia, December 2, 2004.

Universidad Metropolitana, San Juan, Puerto Rico, September 17, 2005.

Department of Mathematics, Howard University, Washington, DC, November 4, 2005.

Department of Genetics, Universidade Federal do Paraná, Curitiba, Brazil, January 24, 2006.

National Institute of Mental Health, Bethesda, Maryland, March 14, 2006.

University of Alabama at Birmingham, Birmingham, Alabama, March 24, 2006.

McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University, Baltimore, Maryland, March 30, 2006.

Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, April 21, 2006.

Queensland Institute of Medical Research, Brisbane, Queensland, Australia, August 25, 2006.

Mount Sinai School of Medicine, December 8, 2006.

Department of Mathematics, Hope College, Holland, Michigan, January 18, 2007.

University of Trondheim, Trondheim, Norway, January 22, 2007.

Department of Genetics, Rutgers University, January 29, 2007.

GlaxoSmithKline, Research Triangle Park, May 30, 2007.

University of California at San Francisco, San Francisco, California, May 2-4, 2007, 2 seminars.

University of Colorado at Denver and Health Sciences Center, Denver, Colorado, Benjamin Stapleton Lecturer, October 11, 2007.

University of Southern California, Los Angeles, California, November 8, 2007.

University of California at Los Angeles, Los Angeles, California, January 10, 2008; January 11, 2008; January 28, 2008.

Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, April 11, 2008.

Department of Genetics, Michigan State University, January 22, 2009.

CIDR Board of Governor's Meeting, Rockville, Maryland, February 13, 2009.

Fred Hutchinson Cancer Research Center, Seattle, Washington, May 13, 2009.

University of Michigan Diabetes Research and Training Center Winter Symposium, March 7, 2009.

National University of Singapore, July 16, 2009.

Department of Mathematics, Central Michigan University, Mount Pleasant, Michigan, September 10, 2009.

Center for Statistical Genetics, University of Michigan, Ann Arbor, Michigan, September 29, 2009.

Distinguished University Professor Lecture, University of Michigan, Ann Arbor, Michigan, February 15, 2010.

University Program in Genetics and Genomics, Duke University, March 22, 2010.

Center for Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, Michigan, March 24, 2010.

Department of Medicine, Wayne State University, September 1, 2010.

Department of Bioinformatics, Seoul National University, September 6, 2010.

Department of Statistics, Seoul National University, September 7, 2010.

Korea National Institute of Health, September 8, 2010.

Department of Mathematics, Howard University, Washington DC, October 29, 2010.

Department of Mathematics, Spelman College, Atlanta, Georgia, November 8, 2010.

Department of Mathematics, Morehouse College, Atlanta, Georgia, November 9, 2011.

CIHR Strategic Training for Advanced Genetic Epidemiology, University of Toronto, Toronto, Ontario, Canada, January 14, 2011.

Department of Biostatistics, University of Texas Health Sciences Center, Houston, Texas, January 31, 2011.

Department of Human Genetics, University of Pittsburgh, Pittsburgh, Pennsylvania, February 4, 2011.

HudsonAlpha Institute, Huntsville, Alabama, February 16, 2011.

Center for Human Genetics, Vanderbilt University, Nashville, Tennessee, March 30, 2011.

Sanger Institute, Hinxton, UK, June 3, 2011.

Washington University, Saint Louis, Missouri, February 17, 2012.

Institute of Psychiatry, Kings College, London, United Kingdom, June 21, 2012.

University of Copenhagen, Copenhagen, Denmark, August 21, 2012.

University of Southern Denmark, Odense, Denmark, December 6, 2012.

University of Michigan Health System, Metabolism, Endocrinology & Diabetes (MEND), November 15, 2013.

Department of Biostatistics, Harvard University School of Public Health, December 12, 2013.

Department of Genetics and Genomic Sciences, Mount Sinai School of Medicine, New York City, New York, April 16, 2014.

National Institute of Aging, Baltimore, Maryland, May 6, 2014.

Department of Genome Sciences, University of Washington, Seattle, Washington, May 22, 2014.

Meru University of Science and Technology, Meru, Kenya, June 18, 2014.

Department of Genetics and Genome Sciences, Case Western Reserve University, Cleveland, Ohio, September 10, 2014.

Interdisciplinary Group Seminar, University of Michigan, Ann Arbor, Michigan, September 16, 2014.

Society of Biology Students, University of Michigan, Ann Arbor, Michigan, October 9, 2014.

Institute of Genetics, University of Florida, Gainesville, Florida, January 20, 2015.

Department of Mathematics, Howard University, Washington, DC, January 23, 2015.

Department of Biomathematics, University of California at Los Angeles, Los Angeles, California, March 9, 2015.

Department of Biostatistics, Columbia University, New York City, New York, April 2, 2015.

Department of Public Health Sciences, University of Chicago, Chicago, Illinois, April 15, 2015.

Big Data Summer Institute Journey Lecture, University of Michigan, Ann Arbor, Michigan, June 3, 2015.

American Diabetes Association, Boston, Massachusetts, June 7, 2015.

Center for Biomedicine, European Academy, Bolzano, Italy, June 23 and 25, 2015.

Michigan R Camp 2015, University of Michigan, Ann Arbor, Michigan, August 13, 2015.

Department of Human Genetics, Emory University, Atlanta, Georgia, November 17, 2015.

Precision Medicine Conference, University of Utah, Salt Lake City, Utah, December 3, 2015.

Duke University, Durham, North Carolina, February 16, 2016.

NHGRI Training and Career Development Meeting, Bethesda, Maryland, April 7, 2016.

Life Sciences Institute, University of Michigan, Ann Arbor, Michigan, April 11, 2016.

Big Data Summer Institute Journey Lecture, University of Michigan, Ann Arbor, Michigan, June 17, 2016.

Computational Biology Camp for High School Students, Ann Arbor, Michigan, July 15, 2016.

Michigan R Camp 2016, University of Michigan, Ann Arbor, Michigan, July 15, 2016.

Big Data Summer Institute Symposium, University of Michigan, Ann Arbor, Michigan, July 21, 2016.

Introduction to Public Health, University of Michigan, Ann Arbor, Michigan, September 27, 2016.

miRcore Volunteer Meeting, Ann Arbor, Michigan, November 12, 2016.

Big Data Summer Institute, University of Michigan, Ann Arbor, Michigan, June 23, 2017.

Computational Biology Camp for High School Students, Ann Arbor, Michigan, July 26, 2017.

Department of Nephrology, Michigan Medicine, Ann Arbor, Michigan, February 6, 2018.

Plenary Lecture, Johns Hopkins University Genetic Research Day, Baltimore, Maryland, February 9, 2018.

Plenary Lecture, Ohio Biostatistics Symposium 2018, Ohio State University, Columbus, Ohio, April 19, 2018.

CURRENT SPONSORED RESEARCH (as Principal Investigator)

Accelerating Medicines Partnership: Enhancement of the Type 2 Diabetes Knowledge Portal, 1/1/18-8/31/20, FNIH, P.I. Michael Boehnke (joint with Gonçalo Abecasis), \$2,567,844.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 9/1/17-9/31/18, P.I. Michael Boehnke, \$404,818.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 6/1/14-5/31/18, P.I. Michael Boehnke, \$2,844,816.

Whole Genome Sequencing for Schizophrenia and Bipolar Disorder in the GPC, NIH U01 MH105653, 9/19/14-5/31/18, P.I. Michael Boehnke, \$2,280,989.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/15-6/30/20, P.I. Michael Boehnke, \$3,293,625.

CURRENT SPONSORED RESEARCH (as Subcontract Principal Investigator)

AMP T2D-GENES Data Coordination Center and Web Portal, NIH/Broad, 5/1/15-4/30/18, Subcontract P.I. Michael Boehnke \$410,565.

The Bipolar Sequencing Consortium: Combined Analyses and Follow-Up, NIH/Johns Hopkins R01 MH110437, 8/1/16-5/31/19, Subcontract P.I. Michael Boehnke, \$362,184.

CURRENT SPONSORED RESEARCH (not as Principal Investigator)

Computational and Statistical Models for Human Genetics, NIH R01 HG007002, 7/18/12-4/30/18, P.I. Gonçalo Abecasis.

Studies of Rare Genetic Variation in the Isolated Population of Sardinia, NIH R01 HL117626, 1/15/13-12/31/18, P.I. Cristen Willer.

Using Genetic Variation to Study Biology of Blood Lipids and Coronary Heart Disease, NIH R01 HL127564, 4/1/15-2/28/19, P.I. Cristen Willer.

Targeted Genetic Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 6/15/15-5/31/19, P.I. Karen Mohlke.

Statistical Methods for Modeling Polygenic Architecture in Association and Re-sequencing Studies, NIH R01 HG0009124-01A1, 6/14/17-4/30/22, P.I. Xiang Zhou.

Genetic Epidemiology of Rare and Regulatory Variants for Metabolic Traits, NIH NIDDK R01 DK093757, 8/1/17-7/31/22, P.I. Karen Mohlke.

Center for Common Disease Genetics, NIH/Broad NHGRI UM1HG008895, 1/14/16-11/30/18, P.I. Gonçalo Abecasis.

PREVIOUS SPONSORED RESEARCH

Linkage Studies in Neurofibromatosis, NIH NINDS R01 NS23410, 4/1/86-3/31/89, P.I. Robert Erickson.

Comparison of Fixed and Sequential Sampling for Family Studies, Rackham Faculty Research Grant, 1/5/87-12/31/87, P.I. Michael Boehnke, \$9,927.

Alzheimer Disease Research Center, subcontract from the University of Washington, Seattle, Michigan, 5/1/87-12/31/87, P.I. Michigan subcontract Michael Boehnke.

Program Project: The Study of Human Mutation, NIH NCI P01 CA26803, 4/6/88-3/31/89, P.I. Samir Hanash.

Design Issues in Genetic Linkage and Segregation Studies, NIH NCHGR R29 HG00376, 9/28/88-8/31/93, P.I. Michael Boehnke, \$276,185.

Macular Genetic Studies of Human X-Chromosomal Retinal Dystrophies, Retinitis Pigmentosa Foundation, 10/1/88-6/30/91, P.I. Paul Sieving.

Michigan Diabetes Research and Training Center, 12/1/88-11/30/90, P.I. Douglas Greene.

Linkage Studies in Neurofibromatosis, NIH NINDS R01 NS23410, 4/1/89-3/31/92, P.I. Francis Collins.

The Effects of Bilineal Pedigrees in Linkage Analysis, MacArthur Foundation, 3/1/90-2/28/91, P.I. Michael Boehnke, \$11,369.

Genomic Technology and Genetic Disease, Statistical Genetics Core, NIH NCHGR P30 HG00209, 9/30/90-7/31/95, P.I. (Core) Michael Boehnke, P.I. (Center) Francis Collins and Miriam Meisler.

Two-Trait Locus Models for Linkage Analysis of Complex Traits, MacArthur Foundation, 5/1/91-12/31/91, P.I. Michael Boehnke, \$7,024.

Retinitis Pigmentosa Research Center, National Retinitis Pigmentosa Foundation, 7/1/91-6/30/94, P.I. Paul Sieving.

Efficient Use of Two-Trait Linkage Analysis, MacArthur Foundation, 6/1/92-5/31/93, P.I. Michael Boehnke, \$12,800.

Molecular Genetics of Juvenile Onset Glaucoma, NIH NEI R01 EY09580, 9/30/92-9/29/96, P.I. Julia Richards.

Mapping Genes for Type 2 Diabetes, supplement to Genomic Technology and Genetic Disease, NIH NCHGR P30 HG00209, 6/1/94-7/31/95, P.I. (Supplement) Michael Boehnke, P.I. (Center) Miriam Meisler.

Institutional Training Grant in Genomic Science, NIH NCHGR T32 HG00040, 7/1/95-6/30/00, P.I. Michael Boehnke, \$1,128,818.

Design and Analysis of Human Gene Mapping Studies, NIH NCHGR R01 HG00376, supplement, 9/1/95-8/31/98, P.I. Michael Boehnke, \$310,535.

Molecular Genetics of Juvenile Onset Glaucoma, NIH NEI R01 EY09580, 12/8/95-3/31/01, P.I. Julia Richards.

Public Health Genetics: An Education Model, NIH NCHGR R01 HG01511, 12/09/96-11/30/01, P.I. Susan Caumartin.

Isolation of the Gene(s) for Ataxia-Telangiectasia, NIH NCI R01 CA57569, 4/1/97-3/31/99, P.I. Patrick Concannon, Virginia Mason Research Center.

FUSION: Statistical Analysis and Database Support, NIH, 5/1/97-9/30/00, P.I. Michael Boehnke, \$390,066.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH NEI EY11671, 12/1/97-11/30/03, P.I. Julia Richards.

Design and Analysis of Human Gene Mapping Studies, NIH NCHGR R01 HG00376, 9/1/98-8/31/01, P.I. Michael Boehnke, \$396,610.

Molecular Epidemiology of Colorectal Cancer, NIH NCI R01 CA81488, 4/1/99-2/28/09, P.I. Stephen Gruber.

Consortium Linkage Studies of Type 2 Diabetes, NIH NIDDK U01 DK58026, 8/1/99-1/31/05, P.I. Nancy Cox, University of Chicago.

Mental Illness Research, Education, and Clinical Center (MIRECC), United States Department of Veterans Affairs, 10/1/99-9/30/05, P.I. Murray Raskind, University of Washington.

Software for Integrated Linkage and Association Analysis, NIH NIMH R01 MH59528, 4/1/00-6/30/03, P.I. Elizabeth Hauser, Duke University.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/00-6/30/05, P.I. Michael Boehnke, \$1,975,854.

Pritzker Neuropsychiatric Disorders Research Consortium, Pritzker Foundation, 12/1/00-11/30/09, P.I. Stan Watson, Huda Akil.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG00376, 9/1/01-8/31/05, P.I. Michael Boehnke, \$814,020.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 6/1/03-5/31/08, P.I. Michael Boehnke, \$3,408,131.

Genomic Analysis of Schizophrenia, Veterans Administration Seattle Institute of Biomedical and Clinical Research, 4/1/04-3/31/07, P.I. Gerard Schellenberg.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH NEI R01 EY11671, 4/1/04-3/31/09, P.I. Julia Richards.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/05-6/30/10, P.I. Michael Boehnke, \$2,425,302.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 9/1/05-6/30/10, P.I. Michael Boehnke, \$1,161,770.

Targeted Genetics Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 9/1/05-6/30/10, P.I. Karen Mohlke.

National Center for Integrative Biomedical Informatics, NIH NIDA U54 DA021519, 9/25/05-7/31/10, P.I. Brian Athey.

Integrated Parametric and Non-Parametric Mapping for Genome-Wide Association Data, NIH NHLBI U01 HL084729, 6/15/06-5/31/09, P.I. Gonçalo Abecasis.

Postdoctoral Training Award, American Diabetes Association, 7/1/06-6/30/10, P.I. Michael Boehnke, \$180,000.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R56 DK062370, 6/1/08-5/31/09, P.I. Michael Boehnke, \$328,948.

EpiGen Var Coordinating Center, NIH NHGRI Subaward 3548, 7/01/08-5/31/09, P.I. Tara Matise.

Identifying Genes for Type 2 Diabetes: FUSION, NIH NIDDK R01 DK062370, 6/1/09-5/31/14, P.I. Michael Boehnke, \$6,139,683.

Molecular Genetics of Primary Open-Angle Glaucoma, NIH/NEI R01 EY1167109 A2, 7/1/09-6/30/12, P.I. Julia Richards, \$8,325.

Quality Control, Genotype Calling and Study Design for 1000 Genomes Project, NIH U01 HG005214, 9/11/09-6/30/11, P.I. Michael Boehnke, \$94,305.

Identifying T2D Variants by DNA Sequencing in Multiethnic Samples, NIH NIDDK U01 DK085584, 9/20/09-7/31/14, P.I. Michael Boehnke, \$3,605,640.

Quality Control, Genotype Calling and Study Design for 1000 Genomes Project, NIH NHGRI U01 HG005214, 9/11/09-6/30/11, P.I. Goncalo Abecasis

Low-Pass Sequencing and High-Density SNP Genotyping for Type 2 Diabetes, NIH NIDDK RC2 DK088389, 9/30/09-8/31/11, P.I. Michael Boehnke, \$17,182,927.

Institutional Training Grant in Genomic Science, NIH NHGRI T32 HG00040, 7/1/10-6/30/15, P.I. Michael Boehnke, \$3,616,237.

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 1/11/11-12/31/15, P.I. Michael Boehnke, \$2,118,261.

Targeted Genetic Analysis of T2D and Quantitative Traits, NIH NIDDK R01 DK72193, 7/1/11-5/31/15, P.I. Karen Mohlke.

HUNTING for Myocardial Infarction Genes by Combined Genome and Exome Sequencing, NIH R01 HL109946, 8/18/11-6/30/16, P.I. Cristen Willer.

Whole Genome and Exome Sequencing for Bipolar Disorder, NIH NIMH R01 MH 094145, 8/30/11-6/30/14, P.I. Michael Boehnke, \$1,843,345.

Genetic Epidemiology of Rare and Regulatory Variants for Metabolic Traits, NIH/NIDDK R01 DK093757, 9/5/11-7/31/16, P.I. Karen Mohlke.

H3Africa Kidney Disease Research Network, NIH/University Ghana Medical School, 8/15/12-7/31/15, P.I. Akinlolu Ojo.

Center for Common Disease Genetics, NIH/Broad UM GH008895, 1/14/16-11/30/16, P.I. Gonçalo Abecasis.

The Impact of Human Gene Knockouts in Type 2 Diabetes and Related Traits, NIH R01 DK098032, 9/15/12-7/31/17, contact P.I. Michael Boehnke (joint with Jason Flannick and Mark McCarthy).

Design and Analysis of Human Gene Mapping Studies, NIH NHGRI R01 HG000376, 1/11/11-8/31/17, P.I. Michael Boehnke.

Accelerating Medicines Partnership: Deposit of METSIM and FUSION data into the Knowledge Portal, 10/1/15-8/31/17, FNIH, P.I. Michael Boehnke (joint with Markku Laakso).

Accelerating Medicines Partnership: Enhancement of the Type 2 Diabetes Knowledge Portal, 6/1/15-12/31/17, FNIH, P.I. Michael Boehnke (joint with Gonçalo Abecasis).

TEACHING

Introduction to Biostatistics: 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1995, 1997, 2000, 2005, 2009, 2012, 2013, 2016, 2017.

Textbook: D.S. Moore et al., *Introduction to the Practice of Statistics*, ninth edition.

Foundations of Biostatistical Inference: 1984, 1985, 1986.

Textbook: B. Lindgren, *Statistical Theory*.

Statistical Models and Numerical Methods in Human Genetics: 1985, 1987, 1989, 1991, 1993, 1995, 1997, 1999, 2007, 2009.

Introduction to Applied Stochastic Processes: 1986.

Textbook: H.M. Taylor and S. Karlin, *Introduction to Stochastic Modeling*.

Introduction to Mathematical Modeling in Clinical Research: 1986, 1988.

Statistical Computer Packages: 1987.

Readings in Statistical Human Genetics: 1992, 1996, 1997, 1998, 2000, 2004.

Advanced Topics in Genetic Modeling: 1999, 2003, 2005.

Textbook: K. Lange, *Mathematical and Statistical Models for Genetic Analysis*.

Readings in Quantitative Genetics: 2004.

Textbook: M. Lynch and B. Walsh, *Genetics and Analysis of Quantitative Traits*.

DOCTORAL COMMITTEE SERVICE: CHAIR OR CO-CHAIR

Lynn M. Ploughman, Department of Biostatistics, 1990. Chair. Linkage Analysis: Power Estimation and Comparison of Methods. Current position: Bristol-Myers Squibb, Princeton, New Jersey.

Nicholas Schork, Department of Epidemiology, 1994. Co-Chair. Advances in the Genetic-Epidemiologic Analysis of Complex Phenotypes. Current position: Professor of Molecular and Experimental Medicine, The Scripps Research Institute, San Diego, California. Professor of Psychiatry and Biostatistics, University of California at San Diego, San Diego, California.

Kathryn Lunetta, Department of Biostatistics, 1996. Chair. Models and Experimental Design for Radiation Hybrid Mapping. Current position: Professor of Biostatistics, Boston University, Boston, Massachusetts.

Elizabeth Hauser, Department of Biostatistics, 1998. Chair. Methods for Linkage Analysis of Complex Genetic Disease. Current position: Professor of Medical Genetics, Duke University, Durham, North Carolina.

Carl Langefeld, Department of Biostatistics, 1999. Chair. The Application of Statistical Methods for Highly Stratified Data to Linkage and Association Analysis of Complex Genetic Traits. Current position: Professor of Biostatistical Sciences, Wake Forest University, Winston-Salem, North Carolina.

Heather Stringham, Department of Biostatistics, 2000. Chair. Bayesian Solutions to Problems of Uncertainty in Genetic Data. Current position: Research Area Specialist Lead, Department of Biostatistics, University of Michigan, Ann Arbor, Michigan.

Ethan M. Lange, Department of Biostatistics, 2001. Chair. Methods for Mapping Disease Susceptibility Genes Using Allele-Sharing Statistics. Current position: Professor, Department of Medicine, University of Colorado, Denver, Colorado.

Julie A. Douglas, Department of Biostatistics, 2001. Chair. Methods for Resolving Genotype and Haplotype Ambiguity in Human Genetic Data. Current position: Professor of Mathematics, Skidmore College, Saratoga Springs, New York.

Michael P. Epstein, Department of Biostatistics, 2002. Co-Chair. Statistical Methods in Gene Mapping of Familial Traits. Current position: Professor of Human Genetics, Biostatistics and Bioinformatics, Emory University, Atlanta, Georgia.

Chun Li, Department of Biostatistics, 2003. Chair. Association Methods for Mapping Genes for Complex Diseases. Current position: Associate Professor of Epidemiology and Biostatistics, Case Western Reserve University.

Tasha E. Fingerlin, Department of Epidemiology, 2003. Co-Chair. Application of Association and Linkage Methods in Studies of Complex Traits. Current position: Director of the Center for Genes, Environment and Health and Director of the Quantitative Genetics Program at National Jewish Health, Denver, Colorado.

Mingyao Li, Department of Biostatistics, 2005. Co-Chair. Statistical Methods in Gene Mapping of Complex Diseases. Current position: Professor of Biostatistics, University of Pennsylvania, Philadelphia, Pennsylvania.

Andrew Skol, Department of Biostatistics, 2006. Chair. Efficient Methods for Gene Mapping of Complex Diseases. Current position: Senior Statistical Geneticist, Institute for Genomics and Systems Biology, University of Chicago, Chicago, Illinois.

Karen N. Conneely, Department of Biostatistics, 2008. Chair. Methods for Large-Scale Genetic Association Studies. Current position: Associate Professor of Human Genetics, Emory University, Atlanta, Georgia.

Yun Li, Department of Biostatistics, 2009. Co-Chair. *In Silico* Haplotyping, Genotyping and Analysis of Resequencing Data Using Markov Models. Current position: Associate Professor of Genetics and Biostatistics, University of North Carolina, Chapel Hill, North Carolina.

Rui Xiao, Department of Biostatistics, 2009. Chair. Statistical Methods in Genetic Association Studies. Current position: Assistant Professor of Biostatistics, University of Pennsylvania, Philadelphia, Pennsylvania.

Weihua Guan, Department of Biostatistics, 2010. Co-Chair. Models and Methods for Genome-Wide Association Studies. Current position: Associate Professor of Biostatistics, University of Minnesota, Minneapolis, Minnesota.

Ryan Welch, Program in Bioinformatics, 2013. Co-Chair. Bioinformatics Software and Methods for Genome-Wide Association and Chip-Seq Studies. Current position: Research Area Specialist Lead, Department of Biostatistics, University of Michigan, Ann Arbor, Michigan.

Clement Ma, Department of Biostatistics, 2014. Chair. Statistical methods for low-frequency and rare genetic variants. Current position: Lead Biostatistician, Division of Pediatric Oncology and Hematology, Dana-Farber/Boston Children's Cancer Center, Boston, Massachusetts.

Matthew Flickinger, Department of Biostatistics, 2015. Chair. Detecting and Correcting Contamination in Genetic Data. Applications Programmer/Analyst Senior, Department of Biostatistics, University of Michigan, Ann Arbor, Michigan.

DOCTORAL COMMITTEE SERVICE: MEMBER

Daniel J. Odenheimer, Department of Epidemiology, 1985. An Evaluation of the Validity of Complex Segregation Analysis in Identifying an Individual's Genotype at a Major Locus.

Ann R. G. Schwartz, Department of Epidemiology, 1986. A New Method for Detecting Familial Heterogeneity of Cancer Risk: A Population-Based Study in Metropolitan Detroit.

Mark Graves, Department of Electrical Engineering and Computer Science, 1994. Theories and Tools for Designing Application-Specific Knowledge Base Data Models.

Kim Papenberg, Department of Human Genetics, 1995. Hereditary Hemorrhagic Telangiectasia: From Linkage to Mutation Analysis.

Benjamin Rybicki, Department of Epidemiology, 1997. Genetic Epidemiology of Sarcoidosis.

Ruzong Fan, Department of Biostatistics, 1998. Mathematical and Statistical Models for Mutant Genes in Nonstationary Populations.

George J. Papanicolaou, Department of Human Genetics, 1999. Genotypic and Phenotypic Analysis of Malignant Melanoma: Analysis of Gene Expression Patterns.

Leslie Lange, Department of Epidemiology, 2000. Identification and Analysis of Candidate Genes for Coronary Artery Calcification.

Anne V. Jackson, Department of Human Genetics, 2000. A Mouse Model System for Quantitative Genetics of Age-Sensitive Traits.

Mohammad Khoshnevisan, Department of Epidemiology, 2001. Selected Genetic and Environmental Risk Factors in the Etiology of Human Oral Clefting.

Cathryn H. Bock, Department of Epidemiology, 2003. Early Detection Practices, Decreasing Age at Diagnosis, and a Linkage Analysis in Prostate Cancer Families.

Erik Ferragut, Department of Mathematics, 2003. Detection of Epistatic Effects in Genetic Data.

Bethany L. Niell, Department of Epidemiology, 2003. Colorectal Cancer Epidemiology: Genes, Environment, and History.

Laura Rozek, Department of Epidemiology, 2003. Candidate Genes for Colorectal Cancer in Structured Populations.

Michelle Cote, Department of Epidemiology, 2003. Early Onset Lung Cancer: Racial Differences in Familial Aggregation, Genetic Polymorphisms and Survival.

Charles Krafchak, Department of Epidemiology, 2004. Genetic Characterization of Posterior Polymorphous Corneal Dystrophy.

Richard McEachin, Department of Human Genetics, 2004. An Integrated Experimental and Computational Approach to Understanding Complex Disease: Differential Gene Expression in Type 2 Diabetes Mellitus.

Jennifer Poynter, Department of Epidemiology, 2005. Molecular Epidemiology of Colorectal Cancer: Mechanisms of Risk and Clues Towards Chemoprevention.

Liming Liang, Department of Biostatistics, 2009. Efficient Methods for Analysis of Genome Scale Data.

Kristen Stevens, Department of Epidemiology, 2010. Epidemiologic Approaches to Understanding Complex Diseases: Applications in Congenital Heart Disease and Cancer.

Jun Ding, Department of Biostatistics, 2010. Statistical Methods for Genome-wide Association Studies of Gene Expression, with Applications to the Genetic Study of Psoriasis.

Alex Tsoi, Department of Biochemistry and Molecular Biology, 2010. Using Ontology Fingerprint to Enhance Analysis of High Throughput Experimental Results.

Jin Zheng, Department of Biostatistics, 2010. Models and Methods for Genetic Linkage and Association Analyses.

Lucy Huang, Department of Bioinformatics, 2011. Genotype Imputation in Diverse Populations: Empirical and Theoretical Approaches.

Wei Chen, Department of Biostatistics, 2011. Statistical Methods and Analysis in Genome Wide Association Studies and Next-Generation Sequencing.

Michael DeGiorgio, Program in Bioinformatics, 2011. Genetic Variation and Modern Human Origins.

Matthew Zawistowski, Department of Biostatistics, 2011. Statistical Methods and Models for Modern Genetic Analysis.

Shyam Gopalakrishnan, Department of Biostatistics, 2011. Methods for Statistical and Population Genetics Analyses.

Chaolong Wang, Program in Bioinformatics, 2012. Statistical Methods for Analyzing Human Genetic Variation in Diverse Populations.

Peng Zhang, Program in Bioinformatics, 2013. The Road to Identifying Disease-Causing Genes: Association Tests, Genotype Imputations, and Sampling Strategies for Sequencing Studies.

Zachary Szpiech, Program in Bioinformatics, 2013. Human Migration, Population Divergence, and the Accumulation of Deleterious Alleles: Insights from Private Genetic Variation and Whole-Exome Sequencing.

Mark Reppell, Department of Biostatistics, 2014. Using Rare Genetic Variation to Understand Human Demography and the Etiology of Complex Traits.

Xiaowei Zhan, Department of Biostatistics, 2014. Statistical Methods and Analysis in Next Generation Sequencing.

Sayantana Das, Department of Biostatistics, 2017. Next Generation Genotype Imputation Methods.

Jingchunzi Shi, Department of Biostatistics, 2017. Statistical Methods for Modeling Heterogeneous Effects in Genetic Association Studies.

POST-DOCTORAL MENTOR

Soumitra Ghosh, 1992-1994. Current position: Executive Director of Immuno-Inflammatory Genetics, GlaxoSmithKline.

Richard M. Watanabe, 1995-1998. Current position: Professor of Preventive Medicine (Biostatistics) and Physiology and Biophysics, University of Southern California.

Laura J. Scott, 2000-2002. Current position: Research Associate Professor, University of Michigan.

Cristen J. Willer, 2004-2010. Current position: Associate Professor of Computational Medicine and Bioinformatics, Internal Medicine, and Human Genetics, University of Michigan.

Christian Fuchsberger, 2010-2014. Current position: Senior Researcher, Center for Biomedicine, Bozen, Italy.

Xueling Sim, 2011-2014. Current position: Assistant Professor, Saw Swee Hock School of Public Health, National University of Singapore, Singapore.

Jeroen Huyghe, 2011-2015. Current position: Staff Scientist, Cancer Prevention Program, Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, Washington.

Adam E. Locke, 2011-2015. Current position: Assistant Professor, Washington University School of Medicine, St. Louis, Missouri.

Tanya Teslovich, 2008-2016. Current position: Associate Director of Statistical Genetics, Regeneron Pharmaceuticals, Eastview, New York.

Daniel Taliun, 2014-present.

Debashree Ray, 2015-2017. Current Position: Assistant Professor, Genetic Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland.

Sarah Gagliano, 2016-present.

Xianyong Yin, 2017-present.

PROFESSIONAL SERVICE

Associate Editor:

<i>American Journal of Human Genetics</i>	1989-1991
<i>Journal of the American Statistical Association</i>	1993-2003
<i>Human Heredity</i>	1992-present

Editorial Advisory Board:

Genome Research
Genetic Epidemiology

1995-1999, 2010-2014
1997-2010

Referee for:

American Journal of Human Genetics
Annals of Statistics
Annals of Thoracic Surgery
Bioinformatics
Biotechniques
Biological Psychiatry
Biometrics
BMC Medical Genetics
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Cephalalgia
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Diabetes
Diabetologia
European Journal of Human Genetics
Genetic Epidemiology
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Human Genetics
Human Genomics
Human Heredity
Human Molecular Genetics
Journal of Clinical Endocrinology and Metabolism
Journal of Clinical Investigation
Journal of Heredity
Journal of the American Statistical Association
Molecular Biology and Evolution
Molecular Medicine
Nature
Nature Genetics
Nature Reviews Genetics
Nature Medicine
New England Journal of Medicine
Pharmacogenomics
PLoS Genetics
PLoS Medicine
Proceedings of the National Academy of Sciences USA
Science
Scientific Reports
Theoretical and Applied Genetics
Trends in Pharmacological Sciences

Major Grant Review Service

Member, Mammalian Genetics Study Section, 1994-1997.

Member, Center for Inherited Disease Research (CIDR) Access Committee, 1997-2002.

Member, NIGMS Human Mutant Cell Repository Advisory Committee, 1998-2001.

Chair, Genome Research Review Committee (GNOM G) Study Section, 2014-present.

Other:

Co-Organizer (with Nancy Cox), International Type 2 Diabetes Linkage Analysis Consortium. Chair, Steering Committee. Member, Analysis and Mapping Committee.

Member, Genetics Steering Committee, NIMH, 2003-present.

Member, External Advisory Board, International Type 1 Diabetes Genetics Consortium, NIDDK, 2003-2010.

Member, External Advisory Board, European Academy Bolzano Institute for Genetic Medicine, Bolzano, Italy, 2004-present.

Member, Awards Committee, American Society of Human Genetics, 2005-2008.

Member, Board of Directors, American Society of Human Genetics, 2006-2008.

Co-Organizer (with Mark McCarthy), DIAGRAM Consortium.

Steering Committee Member of the MAGIC, GIANT, and Global Lipids Genetics Genome-Wide Association Study Consortia.

Member, Council, National Human Genome Research Institute, 2009-2012.

Nominating Committee, American Society of Human Genetics, 2009-2010. Member, 2009. Chair, 2010.

Chair, Steering Committee, T2D-GENES, 2009-present.