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CURRICULUM VITAE
John Muschelli

Part I

PERSONAL DATA

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EDUCATION AND TRAINING

Degrees

- PhD, Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2016).
- ScM, Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2010).
- BS, Biomathematics and Neuroscience, The University of Scranton, Scranton, PA (2008).

PROFESSIONAL EXPERIENCE

- Assistant Scientist, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health (2016–Present)
- Research Associate, Johns Hopkins Biostatistics Consulting Center (2009–2016)
- Trainee, T32AG021334: Epidemiology and Biostatistics of Aging Training Grant, Mentors: Dr. Michelle Carlson, Dr. Ravi Varadhan (2012–2016)
- Data Analyst / Data Manager, Brain Injury Outcomes Division Baltimore, MD (2009–2014)
- Data Analyst, Laboratory for Neurocognitive and Imaging Research at Kennedy Krieger Institute Baltimore, MD (2010–2012)

PROFESSIONAL ACTIVITIES

Professional Memberships

- American Statistical Association.
- International Biometric Society.
- American Heart Association.

Program Development

- Session Chair, Joint Statistical Meetings ().
- Session Chair, Eastern North Atlantic Region Meeting (2019).
- Session Organizer, Joint Statistical Meetings (2002, 2005, 2006).
- Session Organizer, Eastern North Atlantic Region Meeting (2018, 2007).

EDITORIAL ACTIVITIES

Peer Review Activities

Scientific Reports, Human Brain Mapping, NeuroImage, Radiology: Artificial Intelligence, Journal of Neuroimaging, Transactions on Biomedical Engineering, International Journal of Information Technology & Decision Making, Expert Systems With Applications, Data

HONORS AND AWARDS

PUBLICATIONS The white numbers indicate first or senior author manuscripts.

Published Peer-Reviewed Articles

1 Daya M / ⋯ 55 authors ⋯ / Ruczinski I, Mathias RA, and Barnes KC on behalf of CAAPA (2018). Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations. ► Nature Communications (to appear).

2 Sherman T, Fu J, Scharpf RB, Bureau A, Ruczinski I (2018). Detection of rare disease variants in extended pedigrees using RVS. ► Bioinformatics (to appear).

3 Sherman RM / ⋯ 41 authors ⋯ / Ruczinski I, Mathias RA, Barnes KC on behalf of CAAPA, and Steven L. Salzberg SL (2018). Assembly of the pan-genome of humans of African descent reveals nearly 300 megabases of novel DNA. ► Nature Genetics (to appear).

4 Rosenthal EA, Shirts BH, Amendola LM, Horike-Pyne M, Robertson PD, Hisama FM, Bennett RL, Dorschner MO, Nickerson DA, Stanaway IB, Nassir R, Vickers KT, Li C, Grady WM, Peters U, Jarvik GP; NHLBI GO Exome Sequencing Project incl. Ruczinski I (2018). Rare loss of function variants in candidate genes and risk of colorectal cancer. ► Human Genetics (to appear).

5 Natarajan P, Peloso GM, Zekavat SM, Montasser M, Ganna A, Chaffin M, Khera AV, Zhou W, Bloom JM, Engreitz JM, Ernst J, O'Connell JR, Ruotsalainen SE, Alver M, Manichaikul A, Johnson WC, Perry JA, Poterba T, Seed C, Surakka IL, Esko T, Ripatti S, Salomaa V, Correa A, Vasan RS, Kellis M, Neale BM, Lander ES, Abecasis G, Mitchell B, Rich SS, Wilson JG, Cupples LA, Rotter JI, Willer CJ, Kathiresan S; NHLBI TOPMed Lipids Working Group incl. Ruczinski I (2018). Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. ► Nature Communications 9(1): 3391.

6 Fu JM, Leslie EJ, Scott AF, Marazita ML, Beaty TH, Scharpf RB, Ruczinski I (2018). Detection of de novo copy number deletions from targeted sequencing of trios. ► Bioinformatics (to appear).

7 Qiao D, Amel A, Prokopenko D, Chen H, Kho AT, Parker MM, Morrow J, Hobbs BD, Liu Y, Beaty TH, Crapo JD, Barnes KC, Nickerson DA, Bamshad M, Hersh CP, Lomas DA, Agusti A, Make BJ, Calverley PM, Donner CF, Wouters EF, Vestbo J, Pare PD, Levy RD, Rennard SI, Tal-Singer R, Spitz MR, Sharma A, Ruczinski I, Lange C, Silverman E, Cho MH (2018). Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. ► Human Molecular Genetics (to appear).

8 Bureau A, Begum F, Taub MA, Hetmanski J, Parker MM, Albacha-Hejazi H, Scott AF, Murray JC, Marazita ML, Bailey-Wilson JE, Beaty TH, Ruczinski I (2018). Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. ► Genetic Epidemiology (to appear).

9 Zekavat SM, Ruotsalainen S, Handsaker RE, Alver M, Bloom J, Poterba T, Seed C, Ernst J, Chaffin M, Engreitz J, Peloso GM, Manichaikul A, Yang C, Ryan KA, Fu M, Johnson WC, Tsai M, Budoff M, Ramachandran VS, Cupples LA, Rotter JI, Rich SS, Post W, Mitchell BD, Correa A, Metspalu A, Wilson JG, Salomaa V, Kellis M, Daly MJ, Neale BM, McCarroll S, Surakka I, Esko T, Ganna A, Ripatti S, Kathiresan S, Natarajan P; NHLBI TOPMed Lipids Working Group incl. Ruczinski I (2018). Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. ► Nature Communications 9(1): 2606.

10 Sun X, Gao J, Jin P, Eng C, Burchard EG, Beaty TH, Ruczinski I, Mathias RA, Barnes KC, Wang F, Qin Z on behalf of CAAPA consortium (2018). Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. ► Gigascience 7(6): giy052.

11 Obeidat M, Zhou G, Li X, Hansel NN, Rafaels N, Mathias RA, Ruczinski I, Beaty TH, Barnes KC, Pare PD, Sin DD (2018). The genetics of smoking in individuals with chronic obstructive pulmonary disease. ► Respiratory Research 19(1): 59.

12 Reynolds LM, Howard TD, Ruczinski I, Kanchan K, Seeds MC, Mathias RA, Chilton FH (2018). Tissue-specific impact of FADS cluster variants on FADS1 and FADS2 gene expression. ► PLoS One 13(3): e0194610.

13 Parks S, Avramopoulos D, Mulle J, McGrath J, Wang R, Goes FS, Nestadt G, Conneely K, Hopkins M, Ruczinski I, Yolken R, Pulver AE, Pearce BD (2018). HLA typing using genome wide data reveals susceptibility types for infections in a psychiatric disease enriched Ashkenazi Jewish population. ► Brain, Behavior, and Immunity 70: 203-213.

14 Keramati A, Yanek L, Iyer K, Taub MA, Ruczinski I, Becker DM, Becker L, Faraday N, Mathias RA (2018). Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. ► Platelets Mar 19: 1-7.

15 Obeidat M, Li X, Burgess S, Zhou G, Fishbane N, Hansel NN, Bosse Y, Joubert P, Hao K, Nickle DC, Postma DS, Cho MH, Hobbs BD, de Jong K, Boezen HM, Timens W, Hung R, Rafaels N, Mathias RA, Ruczinski I, Beaty TH, Barnes KC, Pare PD, Sin DD (2017). Surfactant protein D is a causal risk factor for chronic obstructive pulmonary disease: results of Mendelian randomization. ► European Respiratory Journal 50(5): 1700657.

16 Rahbar E, Howard TD, Ruczinski I, Mathias RA, Seeds MC, Sergeant S, Langefeld CD, Chilton FH (2017). Uncovering the DNA methylation landscape in key regulatory regions within the FADS cluster. ► PLoS One 12(9): e0180903.

17 Johnston HR, Hu YJ, Gao J, O'Connor TD, Abecasis GR, Wojcik GL, Gignoux CR, Gourraud PA, Lizee A, Hansen M, Genuario R, Bullis D, Lawley C, Kenny EE, Bustamante C, Beaty TH, Mathias RA, Barnes KC, Qin ZS, on behalf of the CAAPA Consortium incl. Ruczinski I (2017). Identifying tagging SNPs for African specific variation from the African Diaspora Genome. ► Scientific Reports 7:46398.

18 Wain LV / ⋯ 65 authors ⋯ / Ruczinski I / ⋯ 40 authors ⋯ / Tobin MD (2017). Genetic associations with lung function and chronic obstructive pulmonary disease implicate novel genes, biological pathways and druggable targets. ► Nature Genetics 49(3): 416-425.

19 Yu Y, Zuo X, He M, Gao J, Fu Y, Qin C, Meng L, Wang W, Song Y, Cheng Y, Zhou F, Chen G, Zheng X, Wang X, Liang B, Zhu Z, Fu X, Sheng Y, Hao J, Liu Z, Yan H, Mangold E, Ruczinski I, Liu X, Marazita ML, Ludwig KU, Beaty TH, Zhang X, Sun L, Bian Z (2017). Genetic studies identified fourteen novel risk loci for NSCLP and highlighted the important roles of FGF signaling pathway with etiology of NSCLP in Chinese Han population. ► Nature Communications 8:14364.

20 Qiao D, Lange C, Laird NM, Won S, Hersh CP, Morrow J, Hobbs B, Lutz SM, Ruczinski I, Crapo JD, Beaty TH, Silverman EK, Cho MH (2017). Gene-based segregation method for identifying rare variants in family-based sequencing studies. ► Genetic Epidemiology 41(4): 309-319.

21 Long X, Daya M, Zhao J, Rafaels N, Liang H, Potee J, Campbell M, Zhang B, Araujo MI, Oliveira RR, Mathias RA, Gao L, Ruczinski I, Georas SN, Vercelli D, Beaty TH, Barnes KC, Chen X, Chen Q (2017). The role of ST2 and ST2 genetic variants in schistosomiasis. ► Journal of Allergy and Clinical Immunology, 140(5): 1416-1422.

22 Kammers K, Leek JT, Ruczinski I, Martin J, Taub MA, Yanek L, Frazee A, Hoyle D, Faraday N, Becker D, Cheng L, Wang ZZ, Becker L, Mathias RA (2017). Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis. ► PLoS One 12(1): e0167794.

23 Xiao Y, Taub MA, Ruczinski I, Begum F, Hetmanski JB, Schwender H, Leslie EJ, Marazita ML, Murray JC, Koboldt DC, Beaty TH (2017). Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. ► Genetic Epidemiology 41(3): 244-250.

24 Fu J, Beaty TH, Scott AF, Hetmanski J, Parker MM, Bailey-Wilson JE, Marazita ML, Mangold E, Albacha-Hejazi H, Murray JC, Bureau A, Carey J, Cristiano S, Ruczinski I, Scharpf RB (2017). Whole exome association of rare deletions in multiplex oral cleft families. ► Genetic Epidemiology 41(1): 61-69.

25 Begum F, Ruczinski I, Hokanson JE, Parker MM, Cho MH, Hetmanski JB, Scharpf RB, Crapo J, Silverman EK, Beaty TH on behalf of the COPDGene investigators (2016). Hemizygous deletion on chromosome 3p26.1 is associated with heavy smoking among African American subjects in the COPDGene study. ► PLoS One 11(10): e0164134.

26 Kessler MD, Yerges-Armstrong L, Taub MA, Shetty A, Maloney K, Bone Jeng LJ, Ruczinski I, Beaty TH, Mathias RA, Barnes KC, Bamshad M, O'Connor TD (2016). Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. ► Nature Communications 7:12521.

27 Mathias RA, Taub MA, O'Connor TD, Fu W / ⋯ 52 authors ⋯ / Ruczinski I, Akey J, CAAPA Consortium, Barnes KC (2016). A continuum of admixture in the western hemisphere revealed by the African diaspora genome. ► Nature Communications 7:12522.

28 Begum F, Ruczinski I, Li S, Silverman EK, Cho MH, Lynch DA, Curran-Everett D, Crapo J, Scharpf RB, Parker MM, Hetmanski JB, Beaty TH, on behalf of the COPDGene investigators (2016). Identifying a deletion affecting total lung capacity among subjects in the COPDGene study cohort. ► Genetic Epidemiology 40(1): 81-8.

29 Sergeant S, Ruczinski I, Ivester P, Lee TC, Parks JS, Morgan TM, Nicklas BJ, Mathias RA, Chilton FH (2016). Impact of methods used to express levels of circulating fatty acids on the degree and direction of associations with blood lipids in humans. ► British Journal of Nutrition 115(2): 251-61.

30 Gao L, Emond MJ, Louie T, Cheadle C, Berger AE, Rafaels N, Kim Y, Taub MA, Ruczinski I, Mathai SC, Rich SS, Nickerson DA, Hummers LK, Bamshad MJ, Mathias RA, Hassoun PM, National Heart, Lung, and Blood Institute (NHLBI) GO Exome Sequencing Project, Lung GO, Barnes KC (2016). Identification of rare variants in ATP8B4 as a risk factor for systemic sclerosis by whole-exome sequencing. ► Arthritis & Rheumatology 68(1): 191-200.

31 Gao L, Bin L, Rafaels NM, Huang L, Potee J, Ruczinski I, Beaty TH, Paller AS, Schneider LC, Gallo R, Hanifin JM, Beck LA, Geha RS, Mathias RA, Barnes KC, Leung DY (2015). Targeted deep sequencing identifies rare loss-of-function variants in IFNGR1 for risk of atopic dermatitis complicated by eczema herpeticum. ► Journal of Allergy and Clinical Immunology 136(6): 1591-600.

32 Lee SE, West KP, Cole RN, Schulze K, Christian P, Wu LS, Yager JD, Groopman J, Ruczinski I (2015). Plasma proteome biomarkers tracking with inflammation in children. ► PLoS One 10(12): e0144279.

33 Goes FS, McGrath J, Avramapolous D, Wolyniec P, Pirooznia M, Ruczinski I, Nestadt G, Kenny E, Vacic V, Peters I, Lencz T, Darvasi A, Mulle JG, Warren ST, Pulver AE (2015). Genome-wide association of schizophrenia in the Ashkenazi Jews. ► American Journal of Medical Genetics Part B: Neuropsychiatric Genetics 168(8): 649-59.

34 Auer PL, Nalls M, Meschia JF, Worrall BB, Longstreth WT Jr, Seshadri S, Kooperberg C, Burger KM, Carlson CS, Carty CL, Chen WM, Cupples LA, DeStefano AL, Fornage M, Hardy J, Hsu L, Jackson RD, Jarvik GP, Kim DS, Lakshminarayan K, Lange LA, Manichaikul A, Quinlan AR, Singleton AB, Thornton TA, Nickerson DA, Peters U, Rich SS; National Heart, Lung, and Blood Institute Exome Sequencing Project incl. Ruczinski I (2015). Rare and coding region genetic variants associated with risk of ischemic stroke: the NHLBI Exome Sequence Project. ► JAMA Neurology 72(7): 781-8.

35 Long X, Chen Q, Zhao J, Rafaels N, Mathias P, Liang H, Potee J, Campbell M, Zhang B, Gao L, Georas SN, Vercelli D, Beaty TH, Ruczinski I, Mathias RA, Barnes KC, Chen X (2015). An IL-13 promoter polymorphism associated with liver fibrosis in patients with schistosoma japonicum. ► PLoS One 10(8): e0135360.

36 Kammers K, Cole RN, Tiengwe C, Ruczinski I (2015). Detecting significant changes in protein abundance. ► EuPA Open Proteomics 7: 11-19.

37 Younkin SG, Scharpf RB, Schwender H, Parker MM, Scott AF, Marazita ML, Beaty TH, Ruczinski (2015). A genome-wide study of inherited deletions identifies two regions associated with non-syndromic isolated oral clefts. ► Birth Defects Research Part A: Clinical and Molecular Teratology 103(4): 276-83.

38 Leslie E, Taub M, Liu H, Steinberg KM, Koboldt D, Zhang Q, Carlson J, Hetmanski J, Wang H, Larson D, Fulton R, Kousa Y, Fahkouri W, Naji A, Ruczinski I, Begum F, Parker M, Busch T, Standley J, Rigdon J, Hecht J, Scott A, Wehby G, Christensen K, Czeizel A, Deleyiannis F, Schutte B, Wilson R, Cornell R, Lidral A, Weinstock G, Beaty TH, Marazita M, Murray J (2015). Identification of functional variants for cleft lip with or without cleft palate in or near PAX7, FGFR2, and NOG by targeted sequencing of GWAS loci. ► American Journal of Human Genetics 96(3): 397-411.

39 Avramopoulos D, Pearce, McGrath J, Wolyniec P, Ruczinski I, Wang R, Hatzimanolis A, Goes F, Mulle J, Coneely K, Hopkins M, Yolken R, Pulver A (2015). Infection and inflammation in schizophrenia and bipolar disorder: a genome wide study for interactions with genetic variation. ► PLoS One 10(3): e0116696.

40 Hansel NN, Pare PD, Rafaels N, Sin D, Sandford A, Daley D, Vergara C, Huang L, Elliott WM, Pascoe CD, Arsenault BA, Postma DS, Boezen HM, Bosse Y, van den Berge M, Hiemstra PS, Cho MH, Litonjua AA, Sparrow D, Ober C, Wise RA, Connett J, Neptune ER, Beaty TH, Ruczinski I, Mathias R, Barnes KC, on behalf of the Lung Health Study (2015). Genome wide association study identifies novel loci associated with airway responsiveness in COPD. ► American Journal of Respiratory Cell and Molecular Biology 53(2): 226-34.

41 Do R, Stitziel NO, Won HH, Jorgensen AB, Duga S, Angelica Merlini P, Kiezun A, Farrall M, Goel A, Zuk O, Guella I, Asselta R, Lange LA, Peloso GM, Auer PL; NHLBI Exome Sequencing Project (incl. Ruczinski I), Girelli D, Martinelli N, Farlow DN, DePristo MA, Roberts R, Stewart AF, Saleheen D, Danesh J, Epstein SE, Sivapalaratnam S, Hovingh GK, Kastelein JJ, Samani NJ, Schunkert H, Erdmann J, Shah SH, Kraus WE, Davies R, Nikpay M, Johansen CT, Wang J, Hegele RA, Hechter E, Marz W, Kleber ME, Huang J, Johnson AD, Li M, Burke GL, Gross M, Liu Y, Assimes TL, Heiss G, Lange EM, Folsom AR, Taylor HA, Olivieri O, Hamsten A, Clarke R, Reilly DF, Yin W, Rivas MA, Donnelly P, Rossouw JE, Psaty BM, Herrington DM, Wilson JG, Rich SS, Bamshad MJ, Tracy RP, Cupples LA, Rader DJ, Reilly MP, Spertus JA, Cresci S, Hartiala J, Tang WH, Hazen SL, Allayee H, Reiner AP, Carlson CS, Kooperberg C, Jackson RD, Boerwinkle E, Lander ES, Schwartz SM, Siscovick DS, McPherson R, Tybjaerg-Hansen A, Abecasis GR, Watkins H, Nickerson DA, Ardissino D, Sunyaev SR, O'Donnell CJ, Altshuler D, Gabriel S, Kathiresan S (2015). Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. ► Nature 518(7537): 102-6.

42 Dluzniewski PJ, Xu J, Ruczinski I, Isaacs WB, Platz EA (2015). Polymorphisms influencing prostate specific antigen concentration may bias genome-wide association studies on prostate cancer. ► Cancer Epidemiology, Biomarkers and Prevention 24(1): 88-93.

43 Neumann C, Taub MA, Younkin SG, Beaty TH, Ruczinski I, Schwender H (2014). Analytic power and sample size calculation for the genotypic transmission disequilibrium test. ► Biometrical Journal 56(6): 1076-92.

44 Golozar A, Beaty TH, Gravitt PE, Ruczinski I, Qiao YL, Fan JH, Ding T, Tang ZZ, Etemadi A, Hu N, Hyland PL, Wang L, Wang C, Dawsey SM, Freedman ND, Abnet CC, Goldstein AM, Taylor PR (2014). Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. ► European Journal Of Cancer 50(16): 2855-65.

45 Tabor HK, Auer PL, Jamal SM, Chong JX, Yu JH, Gordon AS, Graubert TA, O'Donnell CJ, Rich SS, Nickerson DA; NHLBI Exome Sequencing Project (incl. Ruczinski I), Bamshad MJ (2014). Pathogenic variants for Mendelian and complex traits in exomes of 6,517 European and African Americans: implications for the return of incidental results. ► American Journal of Human Genetics 95(2): 183-93.

46 Schwender H, Li Q, Neumann C, Taub MA, Younkin SG, Berger P, Scharpf RB, Beaty TH, Ruczinski I (2014). Detecting disease variants in case-parent trio studies using the Bioconductor software package trio. ► Genetic Epidemiology 38(6): 516-22.

47 Scharpf RB, Mireles L, Yang Q, Koettgen A, Ruczinski I, Susztak K, Halper-Stromberg E, Tin A, Cristiano S, Chakravarti A, Boerwinkle E, Fox C, Coresh J, Kao WH (2014). Copy number polymorphisms near SLC2A9 are associated with serum uric acid concentrations. ► BMC Genetics 15(1): 81.

48 Bureau A, Parker MM, Ruczinski I, Taub MA, Marazita ML, Murray JC, Mangold E, Noethen MM, Ludwig KU, Bailey-Wilson JE, Cropp CD, Li Q, Szymczak S, Hetmanski JB, Albacha-Hejazi H, Field LL, Doheny KF, Ling H, Scott AF, Beaty TH (2014). Whole exome sequencing of distant relatives drawn from multiplex families identifies novel potentially damaging variants for oral clefts. ► Genetics 97(3): 1039-1044.

49 Tang W / ⋯ 7 authors ⋯ / Ruczinski I / ⋯ 71 authors ⋯ / Cassano PA (2014). Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. ► PLoS One 9(7): e100776.

50 Bureau A, Parker MM, Younkin SG, Bailey-Wilson JE, Marazita ML, Murray JC, Albacha-Hejazi H, Beaty TH, Ruczinski I (2014). Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. ► Bioinformatics 30(15): 2189-96.

51 Wu T, Schwender H, Ruczinski I, Murray JC, Marazita ML, Munger RG, Hetmanski JB, Wang P, Murray T, Redett RJ, Fallin MD, Liang KY, Wu-Chou YH, Chong SS, Yeow V, Ye X, Wang H, Huang S, Jabs EW, Shi B, Wilcox AJ, Jee SH, Scott AF, Beaty TH (2014). Evidence of gene-environment interaction for two genes on chromosome 4 and environmental tobacco smoke in controlling the risk of non-syndromic cleft palate. ► PLoS One 9(2): e88088

52 Younkin SG, Scharpf RB, Schwender H, Parker MM, Scott AF, Marazita ML, Beaty TH, Ruczinski (2014). A genome-wide study of de novo deletions identifies a candidate locus for non-syndromic isolated cleft lip/palate risk. ► BMC Genetics 15(1): 24.

53 Lange LA / ⋯ 100 authors ⋯ / Willer CJ; NHLBI Grand Opportunity Exome Sequencing Project incl. Ruczinski I (2014). Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. ► American Journal of Human Genetics 94(2): 233-45.

54 Gordon AS, Tabor HK, Johnson AD, Snively BM, Assimes TL, Auer PL, Ioannidis JP, Peters U, Robinson JG, Sucheston LE, Wang D, Sotoodehnia N, Rotter JI, Psaty BM, Jackson RD, Herrington DM, O'Donnell CJ, Reiner AP, Rich SS, Rieder MJ, Bamshad MJ, Nickerson DA; NHLBI GO Exome Sequencing Project incl. Ruczinski I (2014). Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. ► Human Molecular Genetics 23(8): 1957-63.

55 Taub MA, Schwender HR, Younkin SG, Louis TA, Ruczinski I (2013). On multi-marker tests for association in case-control studies. ► Frontiers in Statistical Genetics and Methodology 4-252: 1-12.

56 Rosenthal EA, Ranchalis J, Crosslin DR, Burt A, Brunzell JD, Motulsky AG, Nickerson DA, NHLBI GO Exome Sequencing Project (incl. Ruczinski I), Wijsman EM, Jarvik GP (2013). Joint linkage and association analysis with exome sequence data implicates SLC25A40 in hypertriglyceridemia. ► American Journal of Human Genetics 93(6): 1035-45.

57 Stephens SH / ⋯ 82 authors ⋯ / Ruczinski I / ⋯ 51 authors ⋯ / Ehringer ME (2013). Distinct loci in the CHRNA5 / CHRNA3 / CHRNB4 gene cluster are associated with onset of regular smoking. ► Genetic Epidemiology 37(8): 846-59.

58 Beaty TH, Taub MA, Scott AF, Murray JC, Marazita ML, Schwender H, Parker MM, Hetmanski JB, Balakrishnan P, Mansilla MA, Mangold E, Ludwig KU, Noethen MM, Rubini M, Elcioglu N, Ruczinski I (2013). Confirming genes influencing risk to cleft lip with/without cleft palate in a case-parent trio study. ► Human Genetics 132(7): 771-81.

59 Cole RN / Ruczinski I / Schulze K, Christian P, Herbrich SM, Wu L, DeVine LR, O'Meally RN, Shrestha S, Boronina TN, Yager JD, Groopman JD, West Jr KP (2013). The plasma proteome identifies expected and novel proteins correlated with micronutrient status in undernourished Nepalese children. ► The Journal of Nutrition 143(10): 1540-8.

60 Guo DC, Regalado E, Casteel DE, Santos-Cortez RL, Gong L, Kim JJ, Dyack S, Horne SG, Chang G, Jondeau G, Boileau C, Coselli JS, Li Z, Leal SM, Shendure J, Rieder MJ, Bamshad MJ, Nickerson DA; GenTAC Registry Consortium; National Heart, Lung, and Blood Institute Grand Opportunity Exome Sequencing Project (incl. Ruczinski I), Kim C, Milewicz DM (2013). Recurrent gain-of-function mutation in PRKG1 causes thoracic aortic aneurysms and acute aortic dissections. ► American Journal of Human Genetics 93(2): 398-404.

61 O'Connor TD, Kiezun A, Bamshad M, Rich SS, Smith JD, Turner E; NHLBI GO Exome Sequencing Project; ESP Population Genetics, Statistical Analysis Working Group (incl. Ruczinski I), Leal SM, Akey JM (2013). Fine-scale patterns of population stratification confound rare variant association tests. ► PLoS One 8(7): e65834.

62 Johnsen JM, Auer PL, Morrison AC, Jiao S, Wei P, Haessler J, Fox K, McGee SR, Smith JD, Carlson CS, Smith N, Boerwinkle E, Kooperberg C, Nickerson DA, Rich SS, Green D, Peters U, Cushman M, Reiner AP; NHLBI Exome Sequencing Project incl. Ruczinski I (2013). Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. ► Blood 122(4): 590-7.

63 Li Q, Schwender H, Louis TA, Fallin MD, Ruczinski I (2013). Efficient simulation of epistatic interactions in case-parent trios. ► Human Heredity 75(1): 12-22.

64 May DH, Navarro SL, Ruczinski I, Hogan J, Ogata Y, Schwarz Y, Levy L, Holzman T, McIntosh MW, Lampe JW (2013). Metabolomic profiling of urine: response to a randomized, controlled feeding study of select fruits and vegetables, and application to an observational study. ► British Journal of Nutrition 9: 1-11.

65 Vergara C, Murray T, Rafaels N, Lewis R, Campbell M, Foster C, Gao L, Faruque M, Oliveira RR, Carvalho E, Araujo MI, Cruz A, Watson H, Caraballo L, Mercado D, Knight-Madden J, Ruczinski I, Dunston G, Beaty TH, Mathias RA, Barnes KC (2013). African ancestry is a risk factor for asthma and high total IgE levels in African admixed populations. ► Genetic Epidemiology 37(4): 393-401.

66 Omoumi A, Wang Z, Yeow V, Cheng J, Wu-Chou YH, Chen PK, Cheah FS, Ruczinski I, Lee CG, Beaty TH, Chong SS (2013). Fetal polymorphisms at the ABCB1-transporter gene locus are associated with susceptibility to non-syndromic oral cleft malformations. ► European Journal of Human Genetics 12: 1436-41.

67 Norton N, Li D, Rampersaud E, Morales A, Martin ER, Zuchner S, Guo S, Gonzalez M, Hedges DJ, Robertson PD, Krumm N, Nickerson DA, Hershberger RE; National Heart, Lung, and Blood Institute GO Exome Sequencing Project (incl. Ruczinski I) and the Exome Sequencing Project Family Studies Project Team (2013). Exome sequencing and genome-wide linkage analysis in 17 families illustrate the complex contribution of TTN truncating variants to dilated cardiomyopathy. ► Circulation: Cardiovascular Genetics 6(2): 144-53.

68 Herbrich SM, Cole RN, West Jr KP, Schulze K, Yager JD, Groopman JD, Christian P, Wu L, O'Meally RN, May DH, McIntosh MW, Ruczinski I (2013). Statistical inference from multiple iTRAQ experiments without using common reference standards. ► Journal of Proteome Research 12(2): 594-604.

69 Fu W, O'Connor TD, Jun G, Kang HM, Abecasis G, Leal SM, Gabriel S, Altshuler D, Shendure J, Nickerson DA, Bamshad MJ; NHLBI Exome Sequencing Project (incl. Ruczinski I), Akey JM (2013). Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. ► Nature 493(7431): 216-20.

70 Patel PJ, Beaty TH, Ruczinski I, Murray JC, Marazita ML, Munger RG, Hetmanski JB, Wu T, Murray T, Rose M, Redett RJ, Jin SJ, Lie RT, Wu-Chou YH, Wang H, Ye X, Yeow V, Chong SS, Jee SH, Shi B, Scott AF (2013). X-linked genetic variants in DMD associated with oral clefts. ► European Journal of Oral Science 121(2): 63-8.

71 Hansel NN, Ruczinski I, Mathias RA, Neptune ER, Sin D, Rafaels N, Malinina A, Daley D, Murray T, Vergara C, Huang L, Sandford A, Heckbert SR, Psaty B, Li G, Berger A, Cheadle C, Dupuis J, O'Connor G, Crystal R, Toshiko T, Ferruci L, Boezen M, Postma DS, Smolonska J, Silverman E, Wan E, Vestbo J, Lomas D, Wise RA, Connett J, Neptune ER, Pare P, Beaty TH, Barnes KC (2013). Genome-wide study identifies two loci associated with lung function decline in mild to moderate COPD. ► Human Genetics 132(1): 79-90.

72 Alberg AJ, Jorgensen TJ, Ruczinski I, Wheless L, Shugart YY, Berthier-Schaud Y, Kessing B, Hoffman-Bolton J, Helzlsouer KJ, Linda Kao WH, Francis L, Alani R, Smith MW, Strickland PT (2013). DNA repair gene variants in relation to overall cancer risk: a population-based study. ► Carcinogenesis 34(1): 86-92.

73 Wang H, Zhang T, Wu T, Hetmanski JB, Ruczinski I, Schwender H, Murray T, Fallin MD, Redett RJ, Raymond GV, Jin SC, Wu-Chou YH, Chen PK, Yeow V, Chong SS, Cheah FS, Jee SH, Jabs EW, Liang KY, Scott A, Beaty TH (2013). The FGF & FGFR gene family and risk of cleft lip with/without cleft palate. ► The Cleft Palate-Craniofacial Journal 50(1): 96-103.

74 Scharpf RB, Beaty TH, Schwender H, Younkin S, Scott AF, Ruczinski I (2012). Fast detection of de novo copy number variants from SNP arrays of case-parent trios. ► BMC Bioinformatics 13(1): 330.

75 Mathias RA, Fu W, Akey JM, Ainsworth H, Torgerson DG, Hugenschmidt CE, Ruczinski I, Sergeant S, Barnes KC, Chilton FH (2012). Adaptive evolution of the FADS gene cluster in Africa. ► PLoS One 7(9): e44926.

76 Ruczinski I, Jorgensen TJ, Shugart YY, Berthier-Schaud Y, Kessing B, Hoffman-Bolton J, Helzlsouer KJ, Linda Kao WH, Wheless L, Francis L, Alani R, Strickland PT, Smith MW, Alberg AJ (2012). A population-based study of DNA repair gene variants in relation to nonmelanoma skin cancer as a marker of a cancer-prone phenotype. ► Carcinogenesis 33(9): 1692-8.

77 Ludwig KU, Mangold E, Herms S, Nowak S, Reutter H, Paul A, Becker J, Herberz R, AlChawa T, Nasser E, Boehmer A, Mattheisen M, Alblas MA, Barth S, Kluck N, Lauster C, Braumann B, Reich RH, Hemprich A, Poetzsch S, Blaumeiser B, Daratsianos N, Kreusch T, Murray JC, Marazita ML, Scott AF, Beaty TH, Ruczinski I, Kramer FJ, Wienker TF, Steegers-Theunissen RP, Rubini M, Mossey PA, Hoffmann P, Lange C, Cichon S, Propping P, Knapp M, Noethen MM (2012). First genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci including one subtype-specific locus. ► Nature Genetics 44(9): 968-71.

78 Boileau C, Guo DC, Hanna N, Regalado ES, Detaint D, Gong L, Varret M, Prakash SK, Li AH, d'Indy H, Braverman AC, Grandchamp B, Kwartler CS, Gouya L, Santos-Cortez RL, Abifadel M, Leal SM, Muti C, Shendure J, Gross MS, Rieder MJ, Vahanian A, Nickerson DA, Michel JB; National Heart, Lung, and Blood Institute (NHLBI) Go Exome Sequencing Project (incl. Ruczinski I), Jondeau G, Milewicz DM (2012). TGFB2 mutations cause familial thoracic aortic aneurysms and dissections associated with mild systemic features of Marfan syndrome. ► Nature Genetics 44(8): 916-21.

79 Emond MJ, Louie T, Emerson J, Zhao W, Mathias RA, Knowles MR, Wright FA, Rieder MJ, Tabor HK, Nickerson DA, Barnes KC; National Heart, Lung, and Blood Institute (NHLBI) GO Exome Sequencing Project (incl. Ruczinski I); Lung GO, Gibson RL, Bamshad MJ (2012). Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic Pseudomonas aeruginosa infection in cystic fibrosis. ► Nature Genetics 44(8): 886-9.

80 Schwender H, Taub M, Beaty TH, Marazita ML, Ruczinski I (2012). Testing SNPs in case-parent trio data based on exact analytic parameter estimations. ► Biometrics 68(3): 766-73.

81 Jorgensen TJ, Ruczinski I, Shugart YY, Wheless L, Berthier-Schaud Y, Kessing B, Hoffman-Bolton J, Helzlsouer KJ, Linda Kao WH, Francis L, Alani R, Strickland PT, Smith MW, Alberg AJ (2012). A population-based study of hedgehog pathway gene variants in relation to the dual risk of contracting both basal cell carcinoma and another cancer. ► Cancer Epidemiology 36(5): e288-93.

82 Laurie CC / ··· 18 authors ··· / Ruczinski I / ··· 52 authors ··· / Weir BS (2012). Somatic mosaicism for large chromosomal anomalies from birth to old age and its relationship to cancer. ► Nature Genetics 44(6): 642-50.

83 Hartz SM / ··· 86 authors ··· / Ruczinski I / ··· 64 authors ··· / Bierut LJ (2012). Increased genetic vulnerability to smoking at CHRNA5 in early-onset smokers. ► Archives of General Psychiatry 69(8): 854-60.

84 Chen Q, Wang H, Hetmanski JB, Zhang T, Ruczinski I, Schwender H, Liang KY, Fallin MD, Redett RJ, Raymond GV, Wu-Chou YH, Chen PK, Yeow V, Chong SS, Cheah FS, Jabs EW, Scott A, Beaty TH (2012). BMP4 is associated with NSCL/P in an Asian population. ► PLoS One 7(4): e35347.

85 Murray T, Taub M, Ruczinski I, Scott AF, Hetmanski JB, Schwender H, Patel P, Zhang TX, Munger RG, Wilcox AJ, Ye X, Wang H, Wu-Chou YH, Shi B, Chong SS, Yeow V, Lie RT, Murray JC, Marazita ML, Beaty TH (2012). The impact of genetic distance and SNP selection bias on the strength of cleft lip/palate signal in chromosome 8q24 between Asians and Europeans. ► Genetic Epidemiology 36(4): 392-9.

86 Shi M, Murray JC, Marazita ML, Munger RG, Ruczinski I, Hetmanski J, Wu T, Murray T, Redett RA, Wilcox AJ, Lie RT, Wu-Chou YH, Chen PK, Wang H, Ye X, Yeow V, Chong S, Shi B, Christensen K, Scott AF, Patel P, Cheah F, Beaty TH (2012). Genome wide study of maternal and parent-of-origin effects on the etiology of orofacial clefts. ► American Journal of Medical Genetics 8A(4): 784-94.

87 Taub M, Schwender H, Beaty TH, Louis TA, Ruczinski I (2012). Incorporating genotype uncertainties into the genotypic TDT for main effects and gene-environment interactions. ► Genetic Epidemiology 36(3): 244-52.

88 Scholl PF, Cole RN, Ruczinski I, Gucek M, Diez R, Rennie A, Nathasingh C, Schulze K, Christian P, Yager J, Groopman JD, West KP (2012). Serum proteome changes between the first and third trimester in undernourished Nepalese women during uncomplicated pregnancy. ► Placenta 33(5): 424-32.

89 Saxena R / ··· 72 authors ··· / Ruczinski I / ··· 78 authors ··· / Keating BJ (2012). Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. ► American Journal of Human Genetics 90(3): 410-25.

90 Wheless L, Kistner-Griffin E, Jorgensen TJ, Ruczinski I, Berthier-Schaad Y, Kessing B, Hoffman-Bolton J, Woodward L, Yao Y, Strickland PT, Alani RM, Smith MW, Alberg AJ (2012). A community-based study of nucleotide excision repair polymorphisms in relation to risk of non-melanoma skin cancer. ► Journal of Investigative Dermatology 132(5): 1354-62.

91 Zhang TX, Beaty TH, Ruczinski I (2012). Candidate pathway based analysis for cleft lip with or without cleft palate. ► Statistical Applications in Genetics and Molecular Biology 11(2): Article 10.

92 Wu T, Fallin MD, Shi M, Ruczinski I, Liang KY, Hetmanski JB, Wang H, Ingersoll RG, Huang S, Ye X, Wu−Chou YH, Chen PK, Jabs EW, Shi B, Redett R, Scott AF, Beaty TH (2012). Evidence of gene-environment interaction for the RUNX2 gene and environmental tobacco smoke in controlling the risk of cleft lip with/without cleft palate. ► Birth Defects Research 94(2): 76-83.

93 Wang H, Hetmanski JB, Ruczinski I, Liang KY, Murray T, Fallin MD, Redett RA, Raymond G, Wu-Chou YH, Chen PK, Yeow V, Park BY, Chong SS, Cheah F, Jee SH, Ingersoll RG, Jabs EW, Scott AF, Beaty TH (2012). ROR2 gene is associated with risk of non-syndromic cleft palate in an Asian population. ► Chinese Medical Journal 125(3): 476-480.

94 Bhatia G / ··· 23 authors ··· / Ruczinski I / ··· 13 authors ··· / Price AL (2011). Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection. ► American Journal of Human Genetics 89(3): 368-81.

95 Torgerson DG / ⋯ 45 authors ⋯ / Ruczinski I / ⋯ 25 authors ⋯ / Nicolae DL (2011). Meta-analysis of genome-wide association studies of asthma in ethnically diverse North American populations. ► Nature Genetics 43(9): 887-92.

96 Faraday N, Yanek L, Yang XP, Mathias R, Herrera-Galeano E, Suktitipat B, Qayyum R, Johnson AD, Chen MH, Tofler GH, Ruczinski I, Friedman AD, Gylfason A, Thorsteinsdottir U, Bray PF, O'Donnell CJ, Becker DM, Becker LC (2011). Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. ► Blood 118(12): 3367-75.

97 Wegmann D, Kessner D, Veeramah K, Mathias RA, Nicolae DL, Yanek LR, Sun YV, Torgerson DG, Rafaels N, Becker LC, Ruczinski I, Beaty TH, Kardia SL, Meyers D, Barnes KC, Becker DM, Freimer N, Novembre J (2011). Recombination rates in admixed individuals revealed by ancestry-based inference. ► Nature Genetics 43(9): 847-53.

98 Beaty TH, Ruczinski I, Murray JC, Marazita ML, Munger RG, Hetmanski JB, Murray T, Redett RJ, Fallin MD, Liang KY, Wu T, Patel PJ, Jin SC, Zhang TX, Schwender H, Wu-Chou YH, Chen PK, Chong SS, Cheah F, Yeow V, Ye X, Wang H, Huang S, Jabs EW, Shi B, Wilcox AJ, Lie RT, Jee SH, Christensen K, Doheny K, Pugh EW, Ling H, Scott AF (2011). Evidence for gene-environment interaction in a genome wide study of isolated, non-syndromic cleft palate. ► Genetic Epidemiology 35(6): 469-78.

99 Mathias RA, Sergeant S, Ruczinski I, Torgerson DG, Hugenschmidt C, Kubala M, Vaidya D, Suktitipat B, Ziegler JT, Ivester P, Case D, Yanek L, Freedman B, Rudock ME, Barnes KC, Langefeld C, Becker LC, Bowden DW, Becker DM, Chilton FH (2011). The impact of FADS genetic variants on omega-6 polyunsaturated fatty acid metabolism in African Americans. ► BMC Genetics 12(1): 50.

100 Pasaniuc B, Zaitlen N, Lettre G, Chen G, Tandon A, Kao WH, Ruczinski I / ⋯ 37 authors ⋯ / Price AL (2011). Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a breast cancer consortium. ► PLoS Genetics 7(4):e1001371.

101 Scharpf RB, Irizarry RA, Ritchie M, Carvalho B, Ruczinski I (2011). Using the R package crlmm for genotyping and copy number estimation. ► Journal of Statistical Software 40(12): 1-32.

102 Halper-Stromberg E, Frelin L, Ruczinski I, Scharpf R, Jie C, Carvalho B, Hao H, Hetrick K, Jedlicka A, Dziedzic A, Doheny K, Scott AF, Baylin S, Pevsner J, Spencer F, Irizarry RA (2011). Performance assessment of copy number microarray platforms using a spike-in experiment. ► Bioinformatics 27(8): 1052-1060.

103 Kral BG, Mathias RA, Suktitipat B, Ruczinski I, Vaidya D, Yanek LR, Quyyumi AA, Patel RS, Zafari AM, Vaccarino V, Shah SH, Granger CB, Hauser ER, Kraus WE, Becker LC, Becker DM (2011). A common variant in the CDNK2B gene on chromosome 9p21 protects against coronary artery disease in Americans of African ancestry. ► Journal of Human Genetics 56(3): 224-9.

104 Schwender H, Bowers K, Fallin MD, Ruczinski I (2011). Importance measures for epistatic interactions in case-parent trios. ► Annals of Human Genetics 75(1): 122-32.

105 Scharpf RB, Ruczinski I, Carvalho B, Doan B, Chakravarti A, Irizarry RA (2011). A multilevel model to address batch effects in copy number estimation using SNP arrays. ► Biostatistics 12(1): 33-50.

106 Schwender H, Ruczinski I, Ickstadt K (2011). Testing SNPs and sets of SNPs for importance in association studies. ► Biostatistics 12(1): 18-32.

107 Scharpf RB, Iacobuzio-Donahue CA, Cope L, Ruczinski I, Lakkar S, Garrett-Mayer E, Parmigiani G (2010). Cross-platform comparison of two pancreatic cancer phenotypes. ► Cancer Informatics 9: 257-64.

108 Assimes TL / ⋯ 35 authors ⋯ / Ruczinski I / ⋯ 94 authors ⋯ / Quertermous T (2010). Lack of association between the Trp719Arg polymorphism in kinesin-like protein 6 and coronary artery disease in 19 case-control studies. ► Journal of the American College of Cardiology 56(19): 1552-63.

109 Lam TK, Ruczinski I, Helzlsouer K, Shugart YY, Li KE, Caulfield LE, Alberg AJ (2010). Cruciferous vegetable intake and lung cancer risk: a nested case-control study matched on cigarette smoking. ► Cancer Epidemiology Biomarkers and Prevention 19(10): 2534-40.

110 Wu T, Liang KY, Hetmanski JB, Ruczinski I, Fallin MD, Ingersoll RG, Wang H, Huang S, Ye X, Wu-Chou Y, Chen PK, Jabs EW, Shi B, Redett R, Scott AF, Beaty TH (2010). Evidence of gene-environment interaction for the IRF6 gene and maternal multivitamin supplementation in controlling the risk of cleft lip with/without cleft palate. ► Human Genetics 28(4): 401-10.

111 Murray T, Beaty T, Mathias R, Rafaels N, Faraque M, Watson H, Ruczinski I, Dunston G, Barnes KC (2010). African and non-African admixture components in African Americans and an African Caribbean population. ► Genetic Epidemiology 34(6): 561-8.

112 Li Q, Fallin MD, Louis TA, Lasseter VK, McGrath JA, Avramopoulos D, Wolyniec PS, Valle D, Liang KY, Pulver AE, Ruczinski I (2010). Detection of SNP-SNP interactions in trios of parents with schizophrenic children. ► Genetic Epidemiology 34(5): 396-406.

113 Hunninghake GM, Soto-Quiros ME, Avila L, Kim HP, Lasky-Su J, Rafaels N, Ruczinski I, Beaty TH, Mathias RA, Barnes KC, Wilk JB, O'Connor GT, Gauderman WJ, Baurley JW, Gilliland F, Liang C, Sylvia JS, Klanderman BJ, Sharma SS, Himes BE, Bossley C, Israel E, Raby BA, Bush A, Choi AM, Weiss ST, Celedon JC (2010). TSLP polymorphisms are associated with asthma in a sex-specific fashion. ► Allergy 65(12): 1566-75.

114 Mathias RA, Kim Y, Sung H, Yanek LR, Hererra-Galeano JE, Ruczinski I, Wilson AF, Faraday N, Becker LC, Becker DM, Mantese VJ (2010). A combined genome-wide linkage and association approach to find susceptibility loci for platelet function phenotypes in Caucasian and African American families with coronary artery disease. ► BMC Medical Genomics 3(1): 22.

115 Beaty TH, Hetmanski JB, Murray JC, Marazita ML, Munger RG, Ruczinski I, Liang KY, Wu T, Murray T, Fallin MD, Redett RA, Raymond G, Schwender H, Jin SJ, Rose M, Cooper ME, Dunnwald M, Mansilla MA, Leslie E, Bullard S, Lidral A, Moreno LM, Menezes R, Vieira AR, Petrin A, Wilcox A, Lie RT, Jabs EW, Wu-Chou YH, Wang H, Ye X, , Huang S, Yeow V, Chong SS, Jee SH, Shi B, Christensen K, Doheny K, Pugh EW, Ling H, Castilla EE, Czeizel AE, Ma L, Field LL, Brody L, Pangilinan F, Mills JL, Molloy AM, Kirke PN, Scott JM, Arcos-Burgos M, Scott AF (2010). A genome-wide association study of cleft lip with and without cleft palate identifies risk variants near MAFB and ABCA4. ► Nature Genetics 42(6): 525-9.

116 Louis TA, Ruczinski I (2010). Efficient evaluation of ranking procedures when the number of units is large, with application to SNP identification. ► Biometrical Journal 52(1): 34-49.

117 Mathias RA, Grant AV, Rafaels R, Hand T, Gao L, Vergara C, Tsai YJ, Yang M, Campbell M, Foster C, Gao P, Togias A, Hansel N, Diette G, Adkinson NF, Liu M, Faruque M, Dunston GM, Watson H, Bracken MB, Hoh J, Maul P, Maul T, Murray T, Hetmanski JB, Ashworth R, Ongaco C, Hendricks K, Doheney K, Pugh E, Scott AF, Kabesch M, Liang L, Abecasis G, Moffatt MF, Cookson WO, Ruczinski I, Beaty TH, Barnes KC (2010). A genome-wide association study on african-ancestry populations identifies novel asthma genes. ► Journal of Allergy and Clinical Immunology 125(2): 336-46.

118 Sleiman PM, Flory J, Imielinski M, Bradfield JP, Annaiah K, Willis-Owen SA, Wang K, Rafaels NM, Michel S, Bonnelykke K, Zhang H, Kim CE, Frackelton EC, Glessner JT, Hou C, Otieno FG, Santa E, Thomas K, Smith RM, Glaberson WR, Garris M, Chiavacci RM, Beaty TH, Ruczinski I, Orange J, Allen J, Spergel JM, Grundmeier R, Mathias RA, Christie JD, von Mutius E, Cookson WO, Kabesch M, Moffatt MF, Grunstein MM, Barnes KC, Devoto M, Magnusson M, Li H, Struan FA, Grant SF, Bisgaard H, Hakonarson H (2010). Common variants in DENND1B associate with pediatric asthma. ► New England Journal of Medicine 362(1): 36-44.

119 Scharpf RB, Ruczinski I (2010). R classes and methods for SNP array data. ► Methods in Molecular Biology 593: 67-79.

120 Gallicchio L, Chang H, Christo DK, Thuita L, Huang HY, Strickland P, Ruczinski I, Hoffman SC, Helzlsouer KJ (2009). Single nucleotide polymorphisms in obesity-related genes and all-cause and cause-specific mortality: a prospective cohort study. ► BMC Medical Genetics 10: 103.

121 Jorgensen TJ, Ruczinski I, Kessing B, Smith MW, Shugart YY, Alberg AJ (2009). Hypothesis-driven candidate gene association studies: practical design and analytical considerations. ► American Journal of Epidemiology 170(8): 986-93.

122 Wheless L, Ruczinski I, Alani R, Clipp S, Hoffman-Bolton J, Jorgensen TJ, Liégeois NJ, Strickland PT, Alberg AJ (2009). The association between skin characteristics and skin cancer prevention behaviors. ► Cancer Epidemiology, Biomarkers, and Prevention 18(10): 2613-9.

123 Price AL, Tandon A, Patterson N, Barnes KC, Rafaels N, Ruczinski I, Beaty TH, Mathias R, Reich D, Myers S (2009). Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. ► PLoS Genetics 5(6): e1000519.

124 Miller CL, Murakami P, Ruczinski I, Ross RG, Sinkus M, Sullivan B, Leonard S (2009). The risk for schizophrenia and bipolar disorder conveyed by two complex genotypes incorporating loci relevant to the kynurenine pathway and melanotropin function. ► Schizophrenia Research 113(2-3): 259-67.

125 Lam TK, Ruczinski I, Helzlsouer K, Shugart YY, Li KE, Clipp S, Alberg AJ (2009). Copy number variants of GSTM1 and GSTT1 in relation to lung cancer risk in a prospective cohort study. ► Annals of Epidemiology 19(8): 546-52.

126 Köttgen A, Glazer NL, Dehghan A, Hwang SJ, Katz R, Li M, Yang Q, Gudnason V, Launer LJ, Harris TB, Smith AV, Arking DE, Astor BC, Boerwinkle E, Ehret GB, Ruczinski I, Scharpf RB, Chen YI, de Boer IH, Haritunians T, Lumley T, Sarnak M, Siscovick D, Benjamin EJ, Levy D, Upadhyay A, Aulchenko YS, Hofman A, Rivadeneira F, Uitterlinden AG, van Duijn CM, Chasman DI, Paré P, Ridker PM, Kao WH, Witteman JC, Coresh J, Shlipak MG, Fox CS (2009). Multiple loci associated with indices of renal function and chronic kidney disease. ► Nature Genetics 41(6): 712-717.

127 Himes BE, Hunninghake GM, Baurley JW, Rafaels NM, Sleiman P, Strachan DP, Wilk JB, Willis-Owen SA, Klanderman B, Lasky-Su J, Lazarus R, Murphy AJ, Soto-Quiros ME, Avila L, Beaty T, Mathias RA, Ruczinski I, Barnes KC, Celedón JC, Cookson WO, Gauderman WJ, Gilliland FD, Hakonarson H, Lange C, Moffatt MF, O'Connor GT, Raby BA, Silverman EK, Weiss ST (2009). Genome-wide association analysis identifies PDE4D as an asthma-susceptibility gene. ► American Journal of Human Genetics 84: 581-93.

128 Ruczinski I, Plaxco KW (2009). Some recommendations for the practitioner to improve the precision of experimentally determined protein folding rates and Φ values. ► Proteins: Structure, Function and Bioinformatics 74(2): 461-74.

129 Schulze KJ, Christian P, Ruczinski I, Ray AL, Nath A, Wu LS, Semba RD (2008). Hepcidin and iron status among pregnant women in Bangladesh. ► Asia Pacific Journal of Clinical Nutrition 17(3): 451-6.

130 Pattaro C, Ruczinski I, Fallin DM, Parmigiani G (2008). Haplotype block partitioning as a tool for dimensionality reduction in SNP association studies. ► BMC Genomics 9(1): 405.

131 Chen J, Ruczinski I, Jorgensen TJ, Yenokyan G, Yao Y, Alani R, Liegeois NJ, Hoffman SC, Hoffman-Bolton J, Strickland PT, Helzlsouer KJ, Alberg AJ (2008). Nonmelanoma skin cancer as a marker of risk for subsequent malignancy: a community-based prospective cohort study. ► Journal of the National Cancer Institute 100(17): 1215-22.

132 Sull JW, Liang KY, Hetmanski JB, Fallin MD, Ingersoll RG, Park J, Wu-Chou YH, Chen PK, Chong SS, Cheah F, Yeow V, Park BY, Jee SH, Jabs EW, Redett R, Jung E, Ruczinski I, Scott AF, Beaty TH (2008). Differential parental transmission of markers in RUNX2 among cleft case-parent trios from four populations. ► Genetic Epidemiology 32(6): 505-12.

133 Scharpf R, Parmigiani G, Pevsner J, Ruczinski I (2008). Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays. ► Annals of Applied Statistics 2(2): 687-713.

134 Gallicchio L, Chang H, Christo DK, Thuita L, Huang HY, Strickland P, Ruczinski I, Hoffman SC, Helzlsouer KJ (2008). Single nucleotide polymorphisms in imflammation-related genes and mortality in a community-based cohort in Washington county, Maryland. ► American Journal of Epidemiology 167(7): 807-13.

135 Ting JC, Roberson ED, Miller N, Lysholm-Bernacchi A, Stephan DA, Capone GT, Ruczinski I, Thomas GH, Pevsner J (2007). Visualization of uniparental inheritance, Mendelian inconsistencies, deletions and parent of origin effects in single nucleotide polymorphism trio data with SNPtrio. ► Human Mutation 28(12): 1225-35.

136 Scharpf RB, Ting JC, Pevsner J, Ruczinski I (2007). SNPchip: R classes and methods for SNP array data. ► Bioinformatics 23(5): 627-8.

137 Visvanathan K, Crum RM, Strickland PT, You X, Ruczinski I, Berndt S, Alberg AJ, Hoffman SC, Comstock GW, Bell DA, Helzlsouer KJ (2007). Alcohol dehydrogenase genetic polymorphisms, low-to-moderate alcohol consumption and risk of breast cancer. ► Alcoholism: Clinical and Experimental Research 31(3): 467-76.

138 Jorgensen J, Visvanathan K, Ruczinski I, Thuita L, Helzlsouer KJ (2007). Breast cancer risk is not associated with polymorphic forms of Xeroderma Pigmentosum genes in a cohort of women from Washington County, Maryland. ► Breast Cancer Research and Treatment 101(1): 65-71.

139 Dai J / Ruczinski I, LeBlanc M, Kooperberg C (2006). Imputation methods to improve inference in SNP association studies. ► Genetic Epidemiology 30(8): 690-702.

140 Ruczinski I, Sosnick TR, Plaxco KW (2006). Methods for the accurate estimation of confidence intervals on protein folding Φ-values. ► Protein Science 15(10): 2257-64.

141 Brown EE, Fallin D, Ruczinski I, Hutchinson A, Staats B, Vitale F, Lauria C, Serraino D, Rezza G, Mbisa G, Whitby D, Messina A, Goedert JJ, Chanock SJ, and the Kaposi Sarcoma Working Group (2006). Associations of classic kaposi sarcoma with common variants in genes that modulate host immunity. ► Cancer Epidemiology, Biomarkers and Prevention 15(5): 926-34.

142 De Los Rios MA, Muralidhara BK, Wildes D, Sosnick TR, Marqusee S, Wittung-Stafshede P, Plaxco KW, Ruczinski I (2006). On the precision of experimentally determined protein folding rates and Φ-values. ► Protein Science 15(3): 553-63.

143 Brewster AM, Jorgensen TJ, Ruczinski I, Huang HY, Hoffman S, Thuita L, Newschaffer C, Lunn RM, Bell D, Helzlsouer KJ (2006). Polymorphisms of the DNA repair genes XPD (Lys751Gln) and XRCC1 (Arg399Gln and Arg194Trp): relationship to breast cancer risk and familial predisposition to breast cancer. ► Breast Cancer Research and Treatment 95(1): 73-80.

144 Ting JC, Ye Y, Thomas GH, Ruczinski I, Pevsner J (2006). Analysis and visualization of chromosomal abnormalities in SNP data with SNPscan. ► BMC Bioinformatics, 18:7(1): 25.

145 Mao R, Wang X, Spitznagel Jr EL, Frelin LP, Ting JC, Ding H, Kim J, Ruczinski I, Downey TJ, Pevsner J (2005). Primary and secondary transcriptional effects in the developing human Down syndrome brain and heart. ► Genome Biology, 6(13): R107.

146 McCarney ER, Werner JH, Bernstein SL, Ruczinski I, Makarov DE, Goodwin PM, Plaxco KW (2005). Site-specific dimensions across a highly denatured protein: a single molecule study. ► Journal of Molecular Biology, 352(3): 672-82.

147 Kooperberg C, Ruczinski I (2005). Identifying interacting SNPs using monte carlo logic regression. ► Genetic Epidemiology 28(2): 157-70.

148 Maxwell KL, Wildes D, Zarrine-Afsar A, De Los Rios MA, Brown AG, Friel CT, Hedberg L, Horng JC, Bona D, Miller EJ, Vallee-Belisle A, Main ER, Bemporad F, Qiu L, Teilum K, Vu ND, Edwards AM, Ruczinski I, Poulsen FM, Kragelund BB, Michnick SW, Chiti F, Bai Y, Hagen SJ, Serrano L, Oliveberg M, Raleigh DP, Wittung-Stafshede P, Radford SE, Jackson SE, Sosnick TR, Marqusee S, Davidson AR, Plaxco KW (2005). Protein folding: defining a standard set of experimental conditions and a preliminary kinetic data set of two-state proteins. ► Protein Science 14(3): 602-16.

149 Ruczinski I, Kooperberg C, LeBlanc M (2004). Exploring interactions in high dimensional genomic data: an overview of logic regression, with applications. ► Journal of Multivariate Analysis 90: 178-95.

150 Kohn JE, Millett IS, Jacob J, Zagrovic B, Dillon TM, Cingel N, Dothager RS, Seifert S, Thiyagarajan P, Sosnick TR, Hasan MZ, Pande VS, Ruczinski I, Doniach S, Plaxco KW (2004). Random-coil behavior and the dimensions of chemically unfolded proteins. ► Proceedings of the National Academy of Sciences 101(34): 12491-6.

151 Ruczinski I, Kooperberg C, LeBlanc M (2003). Logic regression. ► Journal of Computational and Graphical Statistics 12(3): 475-511.

152 Bonneau R, Tsai J, Ruczinski I, Baker D (2002). Contact order and ab initio protein structure prediction. ► Protein Science 11(8): 1937-44.

153 Ruczinski I, Kooperberg C, Bonneau R, Baker D (2002). Distributions of β sheets in proteins with application to structure prediction. ► Proteins: Structure, Function and Genetics 48: 85-97.

154 Larson S, Ruczinski I, Davidson AR, Baker D, Plaxco KW (2002). Residues participating in the folding nucleus do not exhibit preferential evolutionary conservation. ► Journal of Molecular Biology 316: 225-33.

155 Kooperberg C, Ruczinski I, LeBlanc M, Hsu L (2001). Sequence analysis using logic regression. ► Genetic Epidemiology 21(S1): 626-31.

156 Bonneau R, Tsai J, Ruczinski I, Chivian D, Rohl C, Strauss C, Baker D (2001). Rosetta in CASP4: progress in ab initio protein structure prediction. ► Proteins: Structure, Function and Genetics 45(S5): 119-26.

157 Bonneau R, Tsai J, Ruczinski I, Baker D (2001). Functional inferences from blind ab initio protein structure predictions. ► Journal of Structural Biology 134(2-3): 186-90.

158 Plaxco KW, Simons KT, Ruczinski I, Baker D (2000). Topology, stability, sequence, and length: defining the determinants of two-state protein folding kinetics. ► Biochemistry 39(37): 11177-83.

159 Plaxco KW, Larson S, Ruczinski I, Riddle DS, Thayer EC, Buchwitz B, Davidson AR, Baker D (2000). Evolutionary conservation in protein folding kinetics. ► Journal of Molecular Biology 298: 303-12.

160 Simons KT, Bonneau R, Ruczinski I, Baker D (1999). Ab initio protein structure prediction of CASP3 targets using ROSETTA. ► Proteins 37(S3): 171-6.

161 Riddle DS, Grantcharova VP, Santiago J, Alm E, Ruczinski I, Baker D (1999). Experiment and theory highlight role of native state topology in SH3 folding. ► Nature Structural Biology 6: 1016-24.

162 Simons KT, Ruczinski I, Kooperberg C, Fox B, Bystroff C, Baker D (1999). Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. ► Proteins 34(1): 82-95.

Refereed Letters, Communications, Book Chapters, Proceedings, Technical Reports, Other

163 Kammers K, Foster DB, Ruczinski I (2016). Chapter 12: Analysis of proteomic data. ► Manual of Cardiovascular Proteomic - A Primer for Clinicians, Scientists and Students 275-292. Springer Verlag, London UK.

164 Ruczinski I, Mathias RA (2012). Consideration of family history in the design of case control studies of rare variants for complex diseases. ► Johns Hopkins University, Department of Biostatistics Working Papers.

165 Louis TA, Carvalho BS, Fallin MD, Irizarry RA, Li Q, Ruczinski I (2010). Association tests that accommodate genotyping errors: Response to Rice and Dukić. ► Bayesian Statistics 9: 417-20.

166 Louis TA, Carvalho BS, Fallin MD, Irizarry RA, Li Q, Ruczinski I (2010). Association tests that accommodate genotyping errors. ► Bayesian Statistics 9: 393-413 (Bernardo JM, Bayarri MJ, Berger JO, Dawid AP, Heckerman D, Smith AF, West M, Eds), Oxford University Press, Oxford UK.

167 Schwender H, Ruczinski I (2010). Logic regression and extensions. ► Advances in Genetics 72: 25-45.

168 Scientists for Reproducible Research (2010). Disclose all data in publications. ► Nature 467: 401.

169 Li Q, Louis TA, Fallin MD, Ruczinski I (2009). Trio logic regression - detection of SNP-SNP interactions in case-parent trios. ► Johns Hopkins University, Department of Biostatistics Working Papers # 194.

170 Ruczinski I, Kooperberg C (2009). Logic regression. ► Encyclopedia of Medical Decision Making, Kattan MW (Editor), Thousand Oaks, CA: Sage Publications, 678-81.

171 Alberg AJ, Chen J, Ruczinski I, Jorgensen TJ, Alani R, Liegeois NJ (2009). Response: Re: Nonmelanoma skin cancer and risk for subsequent malignancy. ► Journal of the National Cancer Institute 101(3): 210-1.

172 Ruczinski I (2007). Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays. ► Proceedings of the INSERM Workshop #179, 11-5.

173 Ruczinski I, Kooperberg C, LeBlanc M (2003). Logic regression - methods and software. ► Nonlinear Estimation and Classification - Lecture Notes in Statistics 171: 333-44.

Under Review

174 Laurie CC / ··· 73 authors ··· / Ruczinski I / ··· 23 authors ··· / Jaquish C, and the NHLBI Trans-Omics for Precision Medicine Consortium (2018). The NHLBI trans-omics for precision medicine (TOPMed) program.

175 Vince N, Limou S, Daya M, Morii W, Rafaels N, Geffard E, Douillard V, Walencik A, Boorgula MP, Chavan S, Vergara C, Ortega VE, Levin AM, Eng C, Wilson JG, Lange LA, Williams K, Watson H, Ober C, Nicolae DL, Meyers DA, Hansel NN, Ford JG, Faruque MU, Burchard EG, Bleecker ER, Campbell M, Taub MA, Beaty TH, Ruczinski I, Mathias RA, Noguchi E, Barnes KC, Torgerson D, Gourraud PA (2018). Association of HLA-DRB1*09:01 with IgE levels among asthmatics from the African ancestry CAAPA consortium.

176 Winters A, Bahnson TH, Ruczinski I, Boorgula M, Malley C, Keramati A, Chavaan S, Cerosaletti K, Sayre PH, Plaut M, DuToit G, Lack G, Barnes KC, Nepom J, Mathias RA, for the Immune Tolerance Network LEAP Study Team (2018). Interaction between the MALT1 locus and peanut exposure in the risk for peanut allergy in the LEAP study.

177 Obeidat M, Faiz A, Li X, van den Berge M, Hansel NN, Joubert P, Brandsma C, Rafaels N, Mathias RA, Ruczinski I, Beaty TH, Barnes KC, Man SF, Pare PD, Sin DD (2018). The pharmacogenomics of inhaled corticosteroids and lung function decline in COPD.

178 Wang A, Avramopoulos D, Lori A, Mulle J, Conneely K, Powers A, Duncan E, Almi L, Massa N, McGrath J, Schwartz A, Goes FS, Weng L, Nestadt G, Wang R, Yolken R, Ruczinski I, Gillespie CR, Jovanovic T, Ressler K, Pulver AE, Pearce BD (2018). Genome-wide association study in two populations to determine genetic variants associated with Toxoplasma gondii infection and relationship to schizophrenia risk.

179 Eshleman SH, Laeyendecker O, Kammers K, Chen A, Sivay MV, Kottapalli S, Sie BM, Yuan T, Mohan D, Wansley D, Kula T, Morrison C, Stephen J. Elledge SJ, Brookmeyer R, Ruczinski I, Larman HB (2018). Comprehensive profiling of HIV antibody evolution.

180 Yuan T, Mohan D, Laserson U, Ruczinski I, Baer AN, Larman HB (2018). Improved analysis of phage immunoprecipitation sequencing (PhIP-Seq) data using a z-score algorithm.

181 Boorgula MP, Taub MA, Rafaels N, Daya M, Chavan S, Shetty A, Cheadle C, Barkataki S, Fan J, David G, Beaty TH, Ruczinski I, Hanifin J, Schneider LC, Gallo R, Paller AS, Beck LA, Leung DY, Mathias RA, KC Barnes (2018). Replicated methylation changes associated with Eczema Herpeticum and allergic response.

182 Hecker J, Coull B, Ruczinski I, Lange C (2018). On the feasibility of permutation testing for single locus analysis in whole genome-sequencing studies: an optimal sequential strategy and its application to a whole-genome sequencing study for a quantitative trait.

183 Harris DN, Ruczinski I, Yanek LR, Becker L, Becker D, Guio H, Chilton FH, Mathias RA, O'Connor TD (2018). Evolution of hominin polyunsaturated fatty acid metabolism: from Africa to the New World.

184 Boorgula MP, Taub MA, Rafaels N, Daya M, Chavan S, Shetty A, Cheadle C, Barkataki S, Fan J, David G, Beaty TH, Ruczinski I, Hanifin J, Schneider LC, Gallo R, Paller AS, Beck LA, Leung DY, Mathias RA, Barnes KC (2018). Methylation patterns in whole blood from patients with atopic dermatitis with eczema herpeticum.

185 Tietz T, Selinski S, Golka K, Hengstler J, Gripp S, Ickstadt K, Ruczinski I, Schwender H (2018). Identification of interactions of binary variables associated with survival time using survivalFS.

186 Parker MM, Hobbs BD, Ruczinski I, Mathias RA, Lutz SM, Hokanson JE, Begum F, Castaldi PJ, Crapo J, Silverman EK, Cho MH, Beaty TH and the COPDGene Investigators (2018). Exome array analysis of quantitative lung function measurements in the COPDGene study.

Software

1 Logic regression ► Logic regression is a regression methodology primarily developed for the detection of gene-gene and gene-environment interactions in SNP association studies. The Logic Regression methodology and software was developed in collaboration with Charles Kooperberg and Michael LeBlanc at the Fred Hutchinson Cancer Research Center. Logic Regression is available as Free Software under the terms of the Free Software Foundation's GNU General Public License in source code form.

2 Φ estimation ► Methods and software for the analysis of kinetic data derived from denaturing experiments were developed in collaboration with Kevin Plaxco at the University of California Santa Barbara, and Tobin Sosnick at the University of Chicago. The software was implemented as a web tool, using Perl, HTML, and the statistical software environment R.

3 Rosetta ab initio ► Rosetta is a software suite relevant for the prediction and design of protein structures, protein folding mechanisms, and protein-protein interactions. Rosetta ab initio is a tool for de novo prediction of protein structures, and was developed in collaboration with members in the laboratory of David Baker at the University of Washington. The license for the Rosetta code is available through the Baker laboratory.

4 SNPchip ► The R package SNPchip contains S4 classes and methods useful for storing, visualizing, and analyzing high density SNP data. SNPchip was developed in collaboration with Robert Scharpf at the Johns Hopkins Bloomberg

School of Public Health, and Jonathan Pevsner and Jason Ting in the Kennedy Krieger Institute. The R package SNPchip is freely available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

5 VanillaICE ► The R package ICE contains the software for fitting hidden Markov models on genomic array data to infer chromosomal alterations, including deletions, amplifications, and regions with loss of heterozygosity, using measures of uncertainty for the genotype and copy number estimates. VanillaICE was developed in collaboration with Robert Scharpf and Giovanni Parmigiani at the Johns Hopkins Bloomberg School of Public Health. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

6 Trio ► The R package trio was developed in collaboration with Qing Li and Holger Schwender, and provides functionality relevant for the analysis of case-parent trio data, in particular to test for SNP main effects and GxE interactions with the genotypic TDT, and epistatic interactions with trio logic regression. Implemented are functions that aid in the transformation of the trio data from standard linkage files into objects suitable as input for trio logic regression, and a framework that allows for the simulation of case-parent data where the risk of disease is specified by higher order SNP interactions. The R package is available as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

7 CRLMM Copy Number ► The CRLMM software, originally implemented as a method for SNP array genotype calling, was extended to a copy number analysis tool for Affymetrix and Illumina SNP arrays in collaboration with Rob Scharpf, Rafael Irizarry, Matthew Ritchie, and Benilton Carvalho. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

8 MinimumDistance ► The R package MinimumDistance, a collaboration with Rob Scharpf, Sam Younkin, and Moiz Bootwalla, was specifically developed for fast detection of de-novo copy number changes in case-parent trios from SNP array data. MinimumDistance is an effective approach for reducing technical and experimental sources of noise which can generate false positives in experimental datasets. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

9 RVS ► The R package RVS, a collaboration with Tom Sherman and Alexandre Bureau, implements a suite of tools to assess association and linkage between rare genetic variants and a dichotomous disease indicator in family pedigrees. Calculating sharing probabilities of rare genomic variants among multiple affected members of an extended pedigree, RVS can be used to detect highly penetrant causal variants segregating in families. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

10 MDTS ► The R package MDTS, a collaboration with Jack Fu and Rob Scharpf, was developed to infer de novo copy number deletions simultaneously across multiple trios from targeted sequencing data. MDTS has sensitivity competitive with existing methods, but much better specificity, rarely generating any false positives. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

CURRICULUM VITAE
Ingo Ruczinski

Part II

TEACHING

Advisees

Long, Ezhou. Master of Science, Biostatistics (2004 – 2005).
Scharpf, Robert. Doctor of Philosophy, Biostatistics (2004 – 2007).
Paithankar, Sameer. Master of Science, Bioinformatics (2007 – 2008).
Li, Qing. Doctor of Philosophy, Biostatistics (2004 – 2009).
Liu, Yun. Master of Health Sciences, Biostatistics (2008 – 2009).
Scharpf, Robert. Post-Doctoral Fellow, Biostatistics (2007 – 2010).
Schwender, Holger. Post-Doctoral Fellow, Biostatistics (2009 – 2010).
Oikawa, Robert. Master of Public Health, Biostatistics (2010 – 2011).
Herbrich, Shelley. Master of Science, Biostatistics (2010 – 2012).
Taub, Margaret. Post-Doctoral Fellow, Biostatistics (2009 – 2012).
Golozar, Asieh. Master of Health Sciences, Biostatistics (2012 – 2013).
Li, Shengchao. Research Scientist, Biostatistics (2010 – 2013).
Younkin, Samuel. Post-Doctoral Fellow, Biostatistics (2011 – 2013).
Wang, Hang. Master of Health Sciences, Biostatistics (2012 – 2014).
Begum, Ferdouse. Post-Doctoral Fellow, Epidemiology (2013 – 2015).
Fuller, John. Post-Doctoral Fellow, Medicine (2014 – 2015).
Kammers, Kai. Post-Doctoral Fellow, Biostatistics (2013 – 2016).
Fu, Jack. Doctor of Philosophy, Biostatistics (2013 – 2018).
Sherman, Thomas. Research Scientist, Biostatistics (2017 – 2018).
Ngwa, Julius. Post-Doctoral Fellow, Biostatistics (2015 – present).
Keramati, Ali. Cardiovascular Medicine Fellow (2016 – present).
Chen, Athena. Doctor of Philosophy, Biostatistics (2017 – present).

Academic Advisees

Wang, Jian. Master of Science, Biostatistics (2001 – 2002).
Shum, Kenny. Doctor of Philosophy, Biostatistics (2002 – 2004).
Ho, Yen-Yi. Doctor of Philosophy, Biostatistics (2003 – 2005).
Chang, Howard. Doctor of Philosophy, Biostatistics (2004 – 2006).
Murakami, Peter. Doctor of Philosophy, Biostatistics (2006 – 2007).
Aripirala, Srinivas. Doctor of Philosophy, IMMBI (2007).
Jaffe, Andrew. Master of Science, Bioinformatics (2009 – 2010).
Seth, Sahil. Master of Science, Bioinformatics (2009 – 2010).
Wei, Yingying. Doctor of Philosophy, Biostatistics (2009 – 2010).
Gellar, Jonathan. Master of Science, Biostatistics (2009 – 2010).
Zhou, Xian Chong. Master of Science, Biostatistics (2009 – 2010).
Frazee, Alyssa. Doctor of Philosophy, Biostatistics (2010 – 2011).
Zhang, Wenze. Master of Public Health, Biostatistics (2010 – 2011).
Patil, Prasad. Doctor of Philosophy, Biostatistics (2011 – 2013).
Myint, Leslie. Doctor of Philosophy, Biostatistics (2013 – 2014).
Zhang, Haoyu. Doctor of Philosophy, Biostatistics (2014 – 2016).
Qi, Guanghao. Doctor of Philosophy, Biostatistics (2015 – 2017).

Visitors

Pattaro, Cristian. EURAC, Bolzano, Italy (2008).
Bunea, Florentina. Florida State University, Tallahassee, FL (2008).
Schwender, Holger. University of Düsseldorf, Germany (2011, 2012, 2013, 2014, 2015).
Kammers, Kai. University of Dortmund, Germany (2011, 2012).
Bureau, Alexandre. Université Laval, Québec City, Canada (2012, 2013, 2014).
Dellen, Rafael. University of Düsseldorf, Germany (2013).
Sampson, Joshua. National Cancer Institute, Rockville, MD (2014).
DiRienzo, Gregory. State University of New York at Albany, Albany, NY (2018).

Faculty Mentoring Committees

Keet, Corinne. Johns Hopkins School of Medicine (2012 – 2015).
Wojciechowski, Robert. Johns Hopkins School of Public Health (2012 – 2017).
Scharpf, Robert. Johns Hopkins School of Medicine (2010 – present).
Kammers, Kai. Johns Hopkins School of Medicine (2017 – present).

Thesis Committees / Thesis Reader

Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).
Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).
Sefcovic, Natasha. Doctor of Philosophy, Biology NIH/Johns Hopkins (2006).
Wang, Wenyi. Doctor of Philosophy, Biostatistics (2007).
Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).
Gamston, Courtney. Master of Science, Molecular Microbiology and Immunology (2007).
Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).
Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).
Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2008).
Murakami, Peter. Master of Science, Biostatistics (2008).
Carvalho, Benilton. Doctor of Philosophy, Biostatistics (2008).
Venkatesan, Meera. Doctor of Philosophy, Molecular Microbiology and Immunology (2008).
Chang, Yi-Ting. Master of Science, Biostatistics (2009).
Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2009).
Roberson, Eli. Doctor of Philosophy, Human Genetics, JHMI (2009).
Chu, Audrey. Doctor of Philosophy, Epidemiology (2010).
Suktitipat, Bhoom. Doctor of Philosophy, Epidemiology (2010).
Wu, Tao. Doctor of Philosophy, Epidemiology (2010).
Zhang, Tian-Xiao. Master of Science, Epidemiology (2011).
Toolan, Jennifer. Doctor of Philosophy, Mental Health (2011).
Dluzniewski, Paul. Doctor of Philosophy, Epidemiology (2011).
Tin, Adrienne. Doctor of Philosophy, Epidemiology (2012).
Provost, Katie. Doctor of Philosophy, Molecular Microbiology and Immunology (2012).
Shaw, Patrick. Doctor of Philosophy, Biochemistry and Molecular Biology (2012).
Sheppard, Brooke. Master of Science, Epidemiology (2012).
Behneman, Dana. Doctor of Philosophy, Epidemiology (2012).
Golozar, Asieh. Doctor of Philosophy, Epidemiology (2012).
Shirley, Matt. Doctor of Philosophy, School of Medicine (2013).
Halper-Stromberg, Eitan. Doctor of Philosophy, Human Genetics, JHMI (2013).

Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2013).
Higgins, Ryan. Doctor of Philosophy, School of Medicine (2013).
Babatz, Tim. Doctor of Philosophy, School of Medicine (2013).
Keet, Corinne. Doctor of Philosophy, Epidemiology (2014).
Ryslik, Gregory. Doctor of Philosophy, Yale School of Public Health (2014).
Lee, Sun Eun. Doctor of Philosophy, International Health (2015).
Parker, Margaret. Doctor of Philosophy, Epidemiology (2015).
Christ, Max. Master of Science, University of Düsseldorf (2015).
He, Bing. Doctor of Philosophy, Biostatistics (2017).
Bomotti, Samantha. Doctor of Philosophy, Epidemiology (2017).
Cristiano, Stephen. Doctor of Philosophy, Biostatistics (2018, expected).
Longchamps, Ryan. Doctor of Philosophy, School of Medicine (2018, expected).
Montagne, Janelle. Doctor of Philosophy, School of Medicine (2019, expected).
Qi, Guanghao. Doctor of Philosophy, Biostatistics (2020, expected).

Preliminary Oral Participation * committee chair

Ziegler, Kathryn. Doctor of Philosophy, Biostatistics (2003).
Kittleson, Michelle. Doctor of Philosophy, Clinical Investigation (2004).
Scharpf, Robert. Doctor of Philosophy, Biostatistics (2004).
Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2005).
Naj, Adam. Doctor of Philosophy, Epidemiology (2005).
Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2005).
Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2006).
Li, Qing. Doctor of Philosophy, Biostatistics (2006).
Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2006).
Bowers, Katherine*. Doctor of Philosophy, Epidemiology (2007).
McCall, Matthew. Doctor of Philosophy, Biostatistics (2007).
Chu, Audrey*. Doctor of Philosophy, Epidemiology, (2008).
Boca, Simina. Doctor of Philosophy, Biostatistics (2008).
Pichard, Luis*. Doctor of Philosophy, Environmental Health Sciences (2009).
Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2009).
Wu, Tao. Doctor of Philosophy, Epidemiology (2009).
Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2009).
Garvin, Heather*. Doctor of Philosophy, School of Medicine (2009).
Higgins, Ryan*. Doctor of Philosophy, School of Medicine (2010).
Park, Yongjin. Doctor of Philosophy, Biomedical Engineering (2010).
Golozar, Asieh. Doctor of Philosophy, Epidemiology (2010).
Massie, Allan*. Doctor of Philosophy, Epidemiology (2011).
Jones, Katrina*. Doctor of Philosophy, School of Medicine (2011).
Lee, Sun Eun. Doctor of Philosophy, International Health (2012).
Burgess, Loring*. Doctor of Philosophy, School of Medicine (2013).
Squyres, Nicole*. Doctor of Philosophy, School of Medicine (2013).
Keet, Corinne. Doctor of Philosophy, Epidemiology (2013).
Hunter, David. Doctor of Philosophy, School of Medicine (2013).
Spampinato, Daniel. Doctor of Philosophy, School of Medicine (2013).
Blazeski, Adriana*. Doctor of Philosophy, School of Medicine (2014).
Parker, Margaret. Doctor of Philosophy, Epidemiology (2014).

Hatwar, Rajeev. Doctor of Philosophy, Mechanical Engineering (2014).
Kostecki, Geran. Doctor of Philosophy, Biomedical Engineering (2014).
He, Bing. Doctor of Philosophy, Biostatistics (2015).
Powell, Ellen. Doctor of Philosophy, Functional Anatomy and Evolution (2015).
Pilarowski, Genay. Doctor of Philosophy, Human Genetics (2015).
Fu, Jack. Doctor of Philosophy, Biostatistics (2016).
Prufrock, Kristen*. Doctor of Philosophy, Functional Anatomy and Evolution (2016).
Li, Weiyan*. Doctor of Philosophy, Epidemiology (2016).
Loomis, Stephanie*. Doctor of Philosophy, Epidemiology (2017).
Harper, Christine*. Doctor of Philosophy, Functional Anatomy and Evolution (2017).
Canington, Stephanie*. Doctor of Philosophy, Functional Anatomy and Evolution (2017).
Qi, Guanghao. Doctor of Philosophy, Biostatistics (2017).
Chou, Michael. Doctor of Philosophy, Epidemiology (2018).
Gilpatrick, Timothy*. Doctor of Philosophy, Biomedical Engineering (2018).
Zhang, Pengfei. Doctor of Philosophy, Biomedical Engineering (2018).
Orozco, Simon. Doctor of Philosophy, Biomedical Engineering (2018).
Goldstein, Deanna*. Doctor of Philosophy, Functional Anatomy and Evolution (2018).
Hogan, Aneila*. Doctor of Philosophy, Functional Anatomy and Evolution (2018).
Hooshangnejad, Hamed. Doctor of Philosophy, Biomedical Engineering (2018).
Hawthorne, Robert*. Doctor of Philosophy, Biomedical Engineering (2018).

Final Oral Participation * committee chair

Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).
Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).
Peila, Rita. Doctor of Philosophy, Epidemiology (2005).
Sefcovic, Natasha. Doctor of Philosophy, Biology, NIH/Johns Hopkins (2006).
Scharpf, Robert. Doctor of Philosophy, Biostatistics (2007).
Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).
Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).
Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).
Cheng, Yu-Ching*. Doctor of Philosophy, Epidemiology (2008).
Venkatesan, Meera*. Doctor of Philosophy, Molecular Microbiology and Immunology (2008).
Li, Qing. Doctor of Philosophy, Biostatistics (2009).
Chu, Audrey. Doctor of Philosophy, Epidemiology (2010).
Suktitipat, Bhoom. Doctor of Philosophy, Epidemiology (2010).
Wu, Tao*. Doctor of Philosophy, Epidemiology (2010).
Toolan, Jennifer*. Doctor of Philosophy, Mental Health (2011).
Dluzniewski, Paul. Doctor of Philosophy, Epidemiology (2011).
Tin, Adrienne. Doctor of Philosophy, Epidemiology (2012).
Provost, Katie*. Doctor of Philosophy, Molecular Microbiology and Immunology (2012).
Behneman, Dana*. Doctor of Philosophy, Epidemiology (2012).
Golozar, Asieh*. Doctor of Philosophy, Epidemiology (2012).
Keet, Corinne. Doctor of Philosophy, Epidemiology (2014).
Weitzner, Brian*. Doctor of Philosophy, Chemical and Biomolecular Engineering (2015).
Lee, Sun Eun. Doctor of Philosophy, International Health (2015).
He, Bing. Doctor of Philosophy, Biostatistics (2017).
Bomotti, Samantha*. Doctor of Philosophy, Epidemiology (2017).
Fu, Jack. Doctor of Philosophy, Biostatistics (2018).

Classroom Instruction - Principal Instructor

- 140.615 Statistics for Laboratory Scientists I (2007 – 2018).
- 140.616 Statistics for Laboratory Scientists II (2002, 2007 – 2018).
- 140.652 Methods in Biostatistics II (2015).
- 140.751 Advanced Methods in Biostatistics I (2002 – 2005).
- 140.752 Advanced Methods in Biostatistics II (2002 – 2005).
- 390.672 Quantitative Analysis of Clinical Data (2010).

Classroom Instruction - Co-Instructor

- 140.668 Statistical Topics in Genetics and Genomics (2004).
- 140.776 Statistical Computing (2003, 2004).
- 260.655 Protein Bioinformatics (2004 – 2006, 2008, 2010).

Classroom Instruction - Invited Guest Lecturer (JHSPH)

- 100.804 Topics in Macromolecular Structure and Function (2010).
- 140.636 Perl for Bioinformatics (2003, 2004).
- 140.638 Analysis of Biological Sequences (2005 – 2008).
- 140.649 Statistical Learning: Algorithmic and Nonparametric Approaches (2007).
- 140.668 Statistical Topics in Genetics and Genomics (2008, 2014).
- 140.753 Advanced Methods in Biostatistics III (2010).
- 140.754 Advanced Methods in Biostatistics IV (2002, 2004 – 2007).
- 140.756 Advanced Methods in Biostatistics VI (2008, 2010).
- 140.776 Statistical Computing (2009).
- 140.778 Advanced Statistical Computing (2002).
- 260.602 Introduction to Bioinformatics (2006, 2007).
- 260.655 Protein Bioinformatics (2007).
- 340.611 Methodologic Issues in Cancer Epidemiology (2005).
- 340.631 Methods for Association Analysis in Genetic Epidemiology (2007 – 2012).
- 340.725 Methods for Clinical and Translational Research (2013).
- 340.734 Principles of Genetic Epidemiology (2014).
- 340.860 Current Topics in Epidemiological Research (2014).
- 550.865 Public Health Perspectives on Research (2005).

Classroom Instruction - Invited Lecturer (Other)

- EnviroHealth Connections Summer Institute, Johns Hopkins School of Medicine (2007).
- Course in Epidemiology, Technische Universität Dortmund, Dortmund, Germany (2009).
- Bioinformatics, BCMB Core Course, Johns Hopkins School of Medicine (2009).
- Research in Cellular and Molecular Medicine, Johns Hopkins School of Medicine (2012 – 2015).
- Introduction to Biomedical Research, Johns Hopkins Department of Biophysics (2013).
- Short Course, Asian Institute in Statistical Genetics and Genomics, Seoul, South Korea (2014 – 2017).
- Effective Science Communication, Johns Hopkins School of Medicine (Spring 2015, Fall 2015).
- Method, Logic, and Experimental Design in Biology, BCMB Program, Johns Hopkins Medicine (2016).

RESEARCH GRANT PARTICIPATION The solid dots • indicate grants to IR.

Ongoing Research Support

- Integrative Computational Biology Approaches to Identify Functional Determinants of Platelet Aggregation in African Americans and European Americans (NHLBI R01).
  Dates: June 2018 - May 2020. Principal Investigators: Rasika Mathias, PhD and Ingo Ruczinski, PhD.
  Responsibility: Co-Principal Investigator.
- Methods, Software, and Analyses of Genomic Data in Multiplex Oral Cleft Families (NIDCR R03).
  Dates: September 2015 - August 2019. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.
- ◦ New Approaches for Empowering Studies of Asthma in Populations of African Descent (NHLBI R01).
  Dates: October 2011 - November 2022. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.
- ◦ Genetic Epidemiology of COPD (NHLBI R01).
  Dates: December 2017 - November 2022. Principal Investigator: Terri Beaty, PhD.
  Responsibility: Co-Investigator.
- ◦ HIV incidence testing in an evolving epidemic: identification of accurate multi-assay algorithms that include serosignatures from a novel antibody profiling system. (NIAID R01).
  Dates: November 2016 - October 2021. Principal Investigator: Susan Eshleman, MD.
  Responsibility: Co-Investigator.
- ◦ Atopic Dermatitis Research Network (NIAID U19).
  Dates: June 2015 - March 2020. Principal Investigator: Rasika Mathias, PhD.
  Responsibility: Co-Investigator.
- ◦ Integrative Analysis of Tissue Specific Transcriptomics to Identify Platelet Aggression Genes (NHLBI R21).
  Dates: September 2017 - August 2019. Principal Investigator: Rasika Mathias, PhD.
  Responsibility: Co-Investigator.
- ◦ Role of PUFA-Gene Interactions in Health Disparities (R01)
  Dates: March 2017 - February 2019. Principal Investigator: Floyd Chilton, PhD.
  Responsibility: Co-Investigator.
- ◦ LEAP Whole Genome Sequencing Project (NIAID UM1).
  Dates: September 2015 - January 2019. Principal Investigator: Rasika Mathias, PhD.
  Responsibility: Co-Investigator.
- ◦ Integrative Genomics in Asthmatics of African Ancestry (NHLBI R01).
  Dates: December 2014 - November 2018. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.

Completed

- Methods Development and Secondary Analyses for an Oral Clefts Association Study (NIDCR R03).
  Dates: July 2011 - June 2014. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.
- Grant from the Johns Hopkins Institute for Clinical and Translational Research (NCRR Subcontract).
  Dates: June 2011 - June 2012. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.
- Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases (NHLBI R01).
  Dates: September 2007 - July 2011. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.
- Adaptive Function Estimation for Genomic Data (NIGMS R01).
  Dates: September 2003 - August 2007. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.

- Analysis of SNP Data using Logic Regression (MDHMM).
  Dates: July 2002 - June 2004. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.
- Using All-Atom Potentials to Improve Protein Structure Prediction (JHU Faculty Innovation).
  Dates: July 2002 - June 2003. Principal Investigator: Ingo Ruczinski, PhD.
  Responsibility: Principal Investigator.

- A Software Framework for Exploring 1,000 Genomes of African Descent (NHLBI R01).
  Dates: July 2015 - June 2018. Principal Investigator: Steven Salzberg, PhD.
  Responsibility: Co-Investigator.
- Functional Impact of IL33 Polymorphisms on Asthma & other Th2-mediated Diseases (NHLBI R01).
  Dates: March 2012 - September 2017. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.
- Genetic Epidemiology of COPD (NHLBI R01).
  Dates: August 2012 - July 2017. Principal Investigator: Terri Beaty, PhD.
  Responsibility: Co-Investigator.
- A Family-based Exome Sequencing Approach to Identify Platelet Aggregation Genes (NHLBI R01).
  Dates: July 2012 - May 2017. Principal Investigator: Rasika Mathias, PhD.
  Responsibility: Co-Investigator.
- Preprocessing and Analysis Tools for Contemporary Microarray Applications (NIGMS R01).
  Dates: April 2012 - August 2016. Principal Investigator: Rafael Irizarry, PhD.
  Responsibility: Co-Investigator.
- Online Mendelian Inheritance in Man: OMIM (NHGRI U41).
  Dates: June 2015 - May 2016. Principal Investigator: Ada Hamosh, MD.
  Responsibility: Co-Investigator.
- Atopic Dermatitis Research Network Grant. (National Jewish Health subcontract)
  Dates: July 2010 - June 2015. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.
- International Genetic Epidemiology of Oral Clefts (NIDCR R01).
  Dates: September 2009 - May 2015. Principal Investigator: Terri Beaty, PhD.
  Responsibility: Co-Investigator.
- Oral Clefts: Moving from Genome Wide Studies Toward Functional Genomics (NIDCR U01).
  Dates: May 2010 - April 2014. Principal Investigator: Terri Beaty, PhD.
  Responsibility: Co-Investigator.
- Schizophrenia Heterogeneity and Toxplasma Exposure (NIMH R01).
  Dates: December 2010 - November 2013. Principal Investigator: Dimitri Avramopoulos, PhD.
  Responsibility: Co-Investigator.
- Plasma Proteomic Biomarker Indicators of Micronutrient Deficiency (Bill and Melinda Gates Foundation).
  Dates: January 2010 - September 2012. Principal Investigator: Keith West, PhD.
  Responsibility: Co-Investigator.
- Preprocessing and Analysis Tools for Contemporary Microarray Applications (NIGMS R01).
  Dates: September 2007 - March 2012. Principal Investigator: Rafael Irizarry, PhD.
  Responsibility: Co-Investigator.
- Institute for Clinical and Translational Research (NCRR UL1 Supplement).
  Dates: September 2009 - August 2011. Principal Investigator: Daniel Ford, MD.
  Responsibility: Co-Investigator.
- Genome-Wide Associations Environmental Interactions in the Lung Health Study (NHLBI U01).
  Dates: July 2009 - June 2011. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.

- Institute for Clinical and Translational Research (NCRR UL1).
  Dates: September 2007 - May 2011. Principal Investigator: Daniel Ford, MD.
  Responsibility: Co-Investigator.
- Hierarchical Models in Health Services Research (NIDDK R01).
  Dates: September 2007 - October 2010. Principal Investigator: Tom Louis, PhD.
  Responsibility: Co-Investigator.
- DNA Repair, Skin Cancer and Overall Cancer Risk (NCI R01).
  Dates: July 2005 - March 2010. Principal Investigator: Anthony Alberg, PhD.
  Responsibility: Co-Investigator.
- Genotypic Determinants of Aspirin Response in High Risk Families (NIH U01).
  Dates: January 2008 - October 2009. Principal Investigator: Lewis Becker, MD.
  Responsibility: Co-Investigator.
- Genome-Wide Association Studies of Asthma In Populations Of African Descent (NHLBI R01).
  Dates: October 2006 - September 2009. Principal Investigator: Kathleen Barnes, PhD.
  Responsibility: Co-Investigator.
- Protecting Childrens & Womens Health through Global Control (Bill and Melinda Gates Foundation).
  Dates: March 2009 - June 2009. Principal Investigator: Keith West, PhD.
  Responsibility: Co-Investigator.
- Genetic Influences on Age-Related Decline In Strength (NIA R01).
  Dates: February 2005 - December 2007. Principal Investigator: Brock Beamer, MD.
  Responsibility: Co-Investigator.
- Novel Approaches to Studying the In Situ Bioremediation Potential of Complex Mixtures (NIEHS R01).
  Dates: September 2006 - December 2007. Principal Investigator: Rolf Halden, PhD.
  Responsibility: Co-Investigator.
- Johns Hopkins Center in Urban Environmental Health (NIEHS P30).
  Dates: April 2003 - September 2007. Principal Investigator: Scott Zeger, PhD.
  Responsibility: Co-Investigator.
- Gene-Gene Interaction Involved In Nasopharyngeal Carcinoma (NCI R01).
  Dates: September 2005 - August 2006. Principal Investigator: Yin Yao Shugart, PhD.
  Responsibility: Co-Investigator.
- Gene-Environment Interactions: The Odyssey Cohort (NCI U01).
  Dates: September 1999 - June 2004. Principal Investigator: Kathy Helzlsouer, MD.
  Responsibility: Co-Investigator.
- Modeling of Mass Spectrometry MALDI Data (DARPA).
  Dates: July 2003 - December 2003. Principal Investigator: Fernando Pineda, PhD.
  Responsibility: Co-Investigator.

ACADEMIC SERVICE

Department of Biostatistics

- Member, Committee for Biostatistics Information Technology (2001 – present).
- Member, Second Year Oral Examination Committee (2003 – 2005).
- Chair, Honors and Awards Committee (2003 – 2012).
- Seminar Coordinator (2004 – 2005).
- Faculty Senate Representative (2004 – 2006).
- Member, Intellectual Environment Committee (2005 – 2010).
- Member, Faculty Recruitment Committee (2009 – 2011, 2018).
- Director, Biostatistics in Cancer Epidemiology Pre-Doctoral Training Program (2010 – 2014).

- Chair, Biostatistics Events Committee (2012 – 2016).
- Chair, Faculty Recruitment Committee (2013).
- Chair, Biostatistics Retreat Planning Committee (2013).
- Biostatistics Centennial Month Coordinator (2016).
- Co-Leader, "Berlin Accord" Faculty Awards Committee (2015 – present).
- Co-Leader, Statistical Genetics Working Group (2017 – present).

Bloomberg School of Public Health

- Member, Steering Committee, Malaria Research Institute (2002 – 2009).
- Member, Curriculum Committee MHS in Bioinformatics (2003 – 2011).
- Member, Bioinformatics and Biostatistics Core, Urban Environmental Health Center (2003 – present).
- Affiliate, Cancer Epidemiology Prevention & Control Training Fellowship Program (2005 – present).
- Co-Director, MHS in Bioinformatics Program (2007 – 2011).
- Committee on Information Technology (2007 – 2010).
- Co-Chair, CTSA Innovative Working Group on Genome-wide Association Studies (2008 – 2012).
- Member, Joint High Performance Computing Exchange Oversight Committee (2012 – present).
- Member, Genetic Epidemiology Faculty Recruitment Committee (2013).
- Co-Chair, Bloomberg Distinguished Professor Recruitment Committee (2013).
- Participant, Council on Education for Public Health Accreditation Site Visit (2015).
- Ad-hoc Member, Appointments and Promotions Committee (2016).

PRESENTATIONS

Scientific Meetings

1 Detection of De Novo Copy Number Deletions from Targeted Sequencing of Trios.
Statistical Challenges in High-Throughput Genomics with Application to Precision Medicine, Oaxaca, Mexico (2018).

2 Sharing of Rare Nucleotide and Copy Number Variants in Extended Multiplex Families.
Statistical Challenges in High-Throughput Genomics with Application to Precision Medicine, Oaxaca, Mexico (2018).

3 Sharing of Rare Nucleotide and Copy Number Variants in Extended Multiplex Families.
BIRS Workshop on New Statistical Methods for Family-Based Sequencing Studies, Banff, Canada (2018).

4 A New Method to Detect de novo Copy Number Deletions from Targeted Sequencing Data.
European Society of Human Genetics Meeting, Copenhagen, Denmark (2017).

5 From Sequence to Function.
DoE Exascale Requirements for Biological and Environmental Research, Rockville, MD (2016).

6 Statistical and Computational Aspects in the Analysis of Genomic Data from Family Based Designs.
International Biometric Society ENAR Spring Meeting, Austin, TX (2016).

7 Big Data in Health and Biomedicine.
World Health Summit, Berlin, Germany (2015).

8 A Brief Note about Genetic Variation.
BIRS Workshop on Functional Genomics, Epigenomics and Disease Genetics, Banff, Canada (2015).

9 New Methods for Family Based Studies Identify Genetic Regions Underlying Oral Cleft Risk.
European Society of Human Genetics Meeting, Glasgow, Scotland (2015).

10 Proteomic Data Analyses pour les Nuls.
Annual Retreat, Johns Hopkins NHLBI Innovative Proteomics Center, Baltimore, MD (2015).

11 DNA Copy Number Analyses for Family Based Designs.
International Biometric Society ENAR Spring Meeting, Miami, FL (2015).

12 Detecting Differentially Expressed Proteins.
10th Siena Meeting, From Genome to Proteome, Siena, Italy (2014).

13 Statistical Genomics - Methods and Analysis for Multi-Omics Data.
9th Asian Institute in Statistical Genetics and Genomics, Seoul, South Korea (2014).

14 Inferring Rare Disease Risk Variants Based on Exact Probabilities of Sharing by Multiple Affected Relatives.
European Society of Human Genetics Meeting, Milan, Italy (2014).

15 Inferring Rare Disease Risk Variants Based on Exact Probabilities of Sharing by Multiple Affected Relatives.
American Society of Human Genetics Meeting, Boston, MA (2013).

16 Finding Proteomic Biomarker Signatures to Assess the Nutritional Status in Populations.
Annual Conference of the International Society for Clininal Biostatistics, Munich, Germany (2013).

17 Sequencing Family Members to Detect Disease Risk Variants.
BIRS Workshop on Data Integration Challenges in Computational Biology, Banff, Canada (2013).

18 Your Friend, the Biostatistician.
Keynote Lecture, Johns Hopkins NHLBI Proteomics Technology Center, Baltimore, MD (2013).

19 Fast Detection of De Novo Copy Number Variants from Case-Parent Trio SNP Arrays.
European Society of Human Genetics Meeting, Paris, France (2013).

20 Methods for Genetic Studies with Case-Parent Trios.
Mid-Atlantic Genetic Epidemiology and Statistics Conference, Philadelphia, PA (2013).

21 On Study Designs and Statistical Analyses in Sequencing Studies.
Howard Hughes Medical Institute, Janelia Farm Research Campus, Ashburn, VA (2013).

22 Statistical Inference from Multiple iTRAQ Experiments without Using Common Reference Standards.
Proteomic Forum, Berlin, Germany (2013).

23 Fast Detection of De-Novo Copy Number Variants from Case-Parent SNP Arrays.
American Society of Human Genetics Meeting, San Francisco, CA (2012).

24 Estimation of Relative Protein Abundance and Analysis of Proteomic Data from Multiple iTRAQ Experiments.
9th Siena Meeting, From Genome to Proteome, Siena, Italy (2012).

25 Estimation of Relative Protein Abundance and Analysis of Proteomic Data from Multiple iTRAQ Experiments.
19th International Mass Spectrometry Conference, Kyoto, Japan (2012).

26 Estimation of Relative Protein Abundance and Analysis of Proteomic Data from Multiple iTRAQ Experiments.
ASMS Conference on Mass Spectrometry and Allied Topics, Vancouver, BC, Canada (2012).

27 Estimation of Relative Protein Abundances in Multiple iTRAQ Experiments.
Bioconductor Developer Meeting, Manchester, United Kingdom (2011).

28 On High-Throughput Tandem Mass Spectrometry Data.
Conference on Statistical Methods for Very Large Data Sets, Baltimore, MD (2011).

29 Some Study Designs to Improve Statistical Power in Association Tests for Rare Variants.
Statistical Challenges and Biomedical Applications of Sequencing Data, Ascona, Switzerland (2011).

30 Micronutrient Deficiencies and the Human Plasma Nutriproteome.
Second Conference of the Central European Network, Zürich, Switzerland (2011).

31 Micronutrient Deficiencies and the Human Plasma Nutriproteome.
Human Proteome World Congress, Geneva, Switzerland (2011).

32 Assessing Variants in the Human Genome.
Workshop on Statistical Methods for Genomics and Systems Biology, Montreal, Canada (2011).

33 SNP Associations with Lung Function Decline.
GENEVA Steering Committee Meeting, Washington, DC (2011).

34 Assessing Multiple Micronutrient Deficiencies in Populations through the Plasma Nutriproteome.
International Biometric Conference, Florianopolis, Brazil (2010).

35 Genotype and DNA Copy Number Estimation.
Bioconductor Developer Meeting, Heidelberg, Germany (2010).

36 Assessing Multiple Micronutrient Deficiencies in Populations through the Plasma Nutriproteome.
Human Proteome World Congress, Sydney, Australia (2010).

37 Detection of Epistatic Interactions in Schizophrenic Children.
Annual Conference of the International Society for Clininal Biostatistics, Montpellier, France (2010).

38 Assessing DNA Copy Numbers in Large Scale Studies using Genomic Arrays.
19th International Conference on Computational Statistics, Paris, France (2010).

39 SNP Association Studies with Case-Parent Trios.
BIRS Workshop on Statistical Genomics in Biomedical Research, Banff, Canada (2010).

40 New Statistical Methods to Assess Interactions in Genomic Studies.
GEI Methods of Analysis Investigators Meeting, Bethesda, MD (2010).

41 Detection of SNP-SNP Interactions in Case-Parent Trios.
59th Annual ASHG Meeting, Honolulu, HI (2009).

42 Detection of SNP-SNP Interactions in Case-Parent Trios.
18th Annual IGES Meeting, Kahuku, HI (2009).

43 Inference for SNPchip Data in the Presence of Genotype and Copy Number Uncertainty.
BioC2009 Conference, Seattle, WA (2009).

44 Some New Methods to Detect Signal in Association Studies.
NHLBI PROGENI Analysis Workshop, Baltimore, MD (2009).

45 On Protein Folding Kinetics and Structure Prediction.
International Biometric Society WNAR Meeting, Portland, OR (2009).

46 On Genotype Uncertainty in Association Studies.
SFB 475, Reduction of Complexity in Multivariate Data Structures, Dortmund, Germany (2009).

47 New Statistical Methods to Assess Interactions in Complex Disease.
The Genes, Environment, and Health Initiative Investigators Meeting, Bethesda, MD (2009).

48 On Missing Data and Genotyping Errors in Association Studies.
GEI Analyze This! Workshop, National Institutes of Health, Bethesda, MD (2008).

49 On Missing Data and Genotyping Errors in Association Studies.
Emerging Challenges in Genome and Translational Research, Banff, Canada (2008).

50 Some Basic Considerations with Regards to Chevron Curves and Φ-Value Estimation.
Gordon Research Conference on Protein Folding Dynamics, Ventura, CA (2008).

51 Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases.
GEI Investigators Meeting, National Institutes of Health, Bethesda, MD (2008).

52 On Genotyping Errors and Missing Data in Genome-Wide Association Studies.
GENEVA Investigator Meeting, National Institues of Health, Bethesda, MD (2008).

53 Assessment of Chromosomal Alterations using Copy Number and Genotype Estimates.
INSERM Workshop, LaLonde les Maures, France (2007).

54 An Integrated Approach for the Assessment of Chromosomal Abnormalities.
BIRS Workshop Statistical Methods for High-Throughput Genetic Data, Banff, Canada (2007).

55 An Integrated Approach for the Assessment of Chromosomal Abnormalities.
Statistics for Biomolecular Data Integration and Modeling, Ascona, Switzerland (2007).

56 Detecting Genetic Interactions in Disease.
Dementia Consortium Retreat, JHM Alzheimer's Disease Research Center, Baltimore, MD (2007).

57 An Integrated Approach for the Assessment of Chromosomal Abnormalities.
Chapter Meeting, International Society of Genetic Epidemiology, Boston, MA (2007).

58 Inference in Gene Association Studies of Cancer Risks with Partially Missing Family History Data.
Annual Meeting of the American Association for Cancer Research, Washington, DC (2006).

59 On the Precision of Experimentally Determined Protein Folding Rates and Φ Values.
Structural Bioinformatics and Computational Biophysics Meeting, Fortaleza, Brazil (2006).

60 Computational and Statistical Tools Relevant for the Exploration of the Protein Folding Process.
BIRS Workshop on Computational and Statistical Genomics, Banff, Canada (2006).

61 Visualizing and Analyzing High Density SNP Data with SNPscan.
International Biometric Society Spring Meeting, Tampa, FL (2006).

62 On Missing Data and Interactions in SNP Association Studies.
Statistical Methods in Molecular Epidemiology, Ruhr University, Bochum, Germany (2005).

63 Logic Regression and its Applications in SNP Association Studies.
Annual Conference of the International Society for Clininal Biostatistics, Szeged, Hungary (2005).

64 Uncertainty about Φ Values.
The 8th Johns Hopkins Folding Meeting, St. Michaels, MD (2005).

65 Logic Regression in SNP Association Studies.
BIRS Workshop on Statistical Science for Genome Biology, Banff, Canada (2004).

66 Protein Folding and Structure Prediction.
North American New Researchers Conference, York University, Toronto, Canada (2004).

67 Improvements for Logic Regression.
Meeting of the International Federation of Classification Societies IFCS, Chicago, IL (2004).

68 Statistical and Computational Issues in Protein Folding and Structure Prediction.
Interface 2004: Computational Biology and Bioinformatics, Baltimore, MD (2004).

69 Protein Structure Prediction using Rosetta.
IPAM Workshop on Structural Proteomics at UCLA, Los Angeles, CA (2004).

70 Finding Interactions and Assessing Variable Importance in SNP Association Studies.
DIMACS Workshop, Data Mining and Epidemiology, Rutgers University, New Brunswick, NJ (2004).

71 Statistical Issues in Protein Folding.
Johns Hopkins Biostatistics Retreat, St. Michaels, MD (2004).

72 Interactions and Variable Importance in Genomic Data.
Data Mining, Statistical Learning, & Bioinformatics Workshop, U Florida, Gainesville, FL (2004).

73 Finding Simple Classification Rules in Risk Analysis.
Joint Statistical Meetings, San Francisco, CA (2003).

74 Distributions of β Sheets in Proteins with Application to Structure Prediction.
Johns Hopkins Biostatistics Retreat, St.Michaels, MD (2003).

75 Exploring Interactions in Genomic Data using Logic Regression.
International Conference on Research in Computational Molecular Biology, Berlin, Germany (2003).

76 Exploring Interactions in Genomic Data.
International Biometric Society Meeting, Tampa, FL (2003).

77 Statistical and Computational Issues in Ab Initio Protein Structure Prediction.
Joint Statistical Meetings, New York, NY (2002).

78 Classification using Boolean Functions.
Conference of the International Federation of Classification Societies, Cracow, Poland (2002).

79 Logic Regression.
Annual Meeting, Classification Society of North America, Madison, WI (2002).

80 Computational and Statistical Issues in Ab Initio Protein Structure Prediction.
American Statistical Association Chapter Meeting, Albany, NY (2002).

81 Logic Regression.
International Biometric Society ENAR Spring Meeting, Arlington, VA (2002).

82 A New Regression Methodology using Boolean Logic.
Joint Statistical Meetings, Atlanta, GA (2001).

83 Logic Regression.
MSRI Workshop on Nonlinear Estimation and Classification, Berkeley, CA (2001).

Invited Seminars

84 Inferring Rare Disease Risk Variants Based on Exact Probabilities of Sharing among Multiple Affected Relatives.
Centre de Recherches Mathématiques, Montreal, Canada (2016).

85 Statistical and Computational Aspects in the Analysis of Genomic Data from Family Based Designs.
Department of Biostatistics, Columbia University, New York, NY (2015).

86 Summarizing and Presenting Data.
Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2014).

87 Some New Statistical Methods for Family-Based Association Studies.
National Cancer Institute Biostatistics Branch, Rockville, MD (2013).

88 Research Integrity: the Importance of Data Integrity (Panel Discussion).
Dean's Research Integrity Lecture Series, Johns Hopkins School of Medicine, Baltimore, MD (2013)

89 Estimation of Relative Protein Abundance and Analysis of Proteomic Data from Multiple iTRAQ Experiments.
National Institute of Allergy and Infectious Diseases, Bethesda, MD (2012).

90 Power in Association Tests for Rare Variants.
Bioinformatics & Computational Biology Group, Genentech Inc, San Francisco, CA (2011).

91 Power in Association Tests for Rare Variants.
Department of Epidemiology and Biostatistics, University of California, San Francisco, CA (2011).

92 Some New Methods for Family-Based Association Studies.
Department of Biostatistics and Medical Informatics, University of Wisconsin, Madison, WI (2011).

93 Logic Regression.
Department of Applied Mathematics and Statistics, Johns Hopkins University, Baltimore, MD (2010).

94 SNP Association Studies with Case-Parent Trios.
Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA (2010).

95 SNP Association Studies with Case-Parent Trios.
Department of Statistical Science, Duke University, Durham, NC (2010).

96 Variation in the Human Genome, and Disease.
Department of Biophysics & Biophysical Chemistry, Johns Hopkins University, Baltimore, MD (2010).

97 Assessing Genomic Variability using High-Throughput SNP Arrays.
Clinical Research Grand Rounds, Welch Center, Baltimore, MD (2010).

98 SNP Association Studies with Case-Parent Trios.
Statistics and Genomics Seminar, University of California, Berkeley, CA (2009).

99 Detection of SNP-SNP Interactions in Case-Parent Trios.
Fakultät Statistik, Technische Universität Dortmund, Germany (2009).

100 On Missing Data and Genotyping Errors in Association Studies.
Seminar für Statistik, Eidgenössische Technische Hochschule Zürich, Switzerland (2008).

101 Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.
Department of Bioinformatics and Comp. Biology, George Mason University, Manassas, VA (2008).

102 Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.
Department of Biostatistics, University of Alabama, Birmingham AL (2008).

103 Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.
Statistics and Genomics Seminar, University of California, Berkeley CA (2007).

104 On Missing Data and Interactions in SNP Association Studies.
Institute of Genetic Medicine, EURAC, Bolzano, Italy (2007).

105 An Integrated Approach for the Assessment of Chromosomal Abnormalities.
Institut für Statistik, Ludwig-Maximilians Universität München, Munich, Germany (2007).

106 On Missing Data in SNP Association Studies, and What to Do About Them.
Department of Epidemiology, JH Bloomberg School of Public Health, Baltimore, MD (2007).

107 Logic Regression as a Statistical Tool to Assess Interactions in SNP Association Studies.
Center for Prevention and Clinical Research, Johns Hopkins University, Baltimore, MD (2007).

108 Statistics Schmatistics: On the Folded, the Unfolded, and the Transition State.
Johns Hopkins Institute for Multiscale Modeling of Biological Interactions, Baltimore, MD (2006).

109 On Missing Data and Interactions in SNP Association Studies.
Department of Statistics, University of British Columbia, Canada (2006).

110 On Missing Data and Interactions in SNP Association Studies.
Department of Biostatistics and Biomathematics, Georgetown University, Washington, DC (2006).

111 Logic Regression.
Department of Statistics, Florida State University, Tallahassee, FL (2006).

112 Logic Regression.
Department of Statistics and Applied Probability, University of California, Santa Barbara, CA (2006).

113 Uncertainty about Φ Values.
Department of Biophysics, Johns Hopkins University, Baltimore, MD (2005).

114 Assessing Interactions in High-Dimensional Genomic Data.
Department of Epidemiology and Public Health, Yale School of Medicine, New Haven, CT (2005).

115 Missing Data and Gene Interactions in SNP Association Studies.
Centre National de Genotypage, Paris-Evry, France (2005).

116 Protein Folding and Structure Prediction - A Statistician's View.
Seminar für Statistik, Eidgenössische Technische Hochschule Zürich, Switzerland (2005).

117 A Statistician's View on Protein Folding.
Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA (2005).

118 Protein Folding and Structure Prediction - A Statistician's View.
Department of Statistics, Rutgers University, Piscataway, NJ (2005).

119 Protein Folding and Structure Prediction - A Statistician's View.
Department of Mathematics and Statistics, McGill University, Montreal, Canada (2005).

120 Functional Inferences from Blind Ab Initio Protein Structure Predictions.
Institut für Statistik, Ludwig-Maximilians Universität München, Munich, Germany (2004).

121 Logic Regression.
US Census Bureau, Suitland, MD (2004).

122 Logic Regression and Interactions in High Dimensional Genomic Data.
Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD (2003).

123 Logic Regression and Interactions in High Dimensional Genomic Data.
Memorial Sloan-Kettering Cancer Center, New York, NY (2003).

124 Logic Regression and its Applications to SNP Association Studies.
NCI National Cancer Institute, Rockville, MD (2002).

125 Logic Regression.
General Electric, Schenectady, NY (2002).

126 Logic Regression with Application to SNP Data Analysis.
Wadsworth Center for Labs and Research, Albany, NY (2002).

127 A New Regression Methodology using Boolean Logic.
Department of Biostatistics, Johns Hopkins University, Baltimore, MD. (2001).

128 A New Regression Methodology using Boolean Logic.
Department of Statistics, Columbia University, New York, NY (2001).

Other Meetings and Events

129 Overview of Statistical Methods for Case-Parent Trio Data.
Johns Hopkins Statistical Genetics Group Meeting, Baltimore, MD (2017).

130 A Public Health Researcher's Commentary on Wagner's Ring.
JHSPH Dean's Lecture Series, Baltimore, MD (2016).

131 Variant Sharing in Multiplex Families.
TOPMed Whole Genome Sequencing Project Analysis Committee (2015).

132 Das Leben ist Grausam (Life is Cruel).
Johns Hopkins Center for Computational Biology Group Meeting, Baltimore, MD (2015).

133 On Family-Based Genetic Association Studies.
Johns Hopkins Center for Computational Biology Group Meeting, Baltimore, MD (2014).

134 Estimation of Relative Protein Abundance and Analysis of Proteomic Data from Multiple iTRAQ Experiments.
The Bill and Melinda Gates Foundation, Johns Hopkins Site Visit, Baltimore, MD (2012).

135 Biomarker Informatics and Future Clusters of Vitamin A Biomarkers.
Biomarkers of Nutrition for Human Development Expert Panel, Bethesda MD (2011).

136 Some Experimental Design and Estimation Considerations in Proteomic and Genomic Studies.
Computational Biology Working Group, Fred Hutchinson Cancer Research Center, Seattle, WA (2011).

137 Assessing Multiple Micronutrient Deficiencies in Populations through the Plasma Nutriproteome.
The Bill and Melinda Gates Foundation, Seattle, WA (2011).

138 Update for the Lung Health Study on Lung Function Decline.
GENEVA Steering Committee Meeting, Rockville, MD (2011).

139 Study Designs to Improve Statistical Power in Association Tests for Rare Variants.
Biostatistics Pre-Happy Hour Talk, Johns Hopkins School of Public Health, Baltimore, MD (2011).

140 Basic Statistical and Experimental Design Considerations in some OMICs Examples.
Johns Hopkins Environmental Health Sciences Research Retreat, Baltimore, MD (2011).

141 Good Practices for Running Simulations.
Biostatistics Student Computing Club, Johns Hopkins School of Public Health, Baltimore, MD (2010).

142 Genomewide Association Studies - A Time for Multidisciplinary Research.
Johns Hopkins School of Medicine, Baltimore, MD (2010).

143 On Missing Data and Genotyping Errors in Association Studies.
Welch Center, Johns Hopkins University, Baltimore, MD (2008).

144 Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases.
National Institutes of Health, Bethesda MD (2008).

145 Bioinformatics - Some Selected Examples and a Bit of an Overview.
EnviroHealth Connections Summer Institute, Baltimore MD (2007).

146 Statistical Approaches to assess Gene Copy Number and Loss of Heterozygosity.
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2007).

147 On Missing Genotype Data.
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2006).

148 Visualizing and Analyzing High Density SNP Data with SNPscan.
Deptartment of Biostatistics Retreat, Johns Hopkins University, Baltimore, MD (2006).

149 A Web Based Tool and R Package to Visualize and Analyze Affymetrix SNP Chip Data.
SNP Working Group, School of Public Health, Johns Hopkins University, Baltimore, MD (2005).

150 Are You Gellin'?
Bayview NHLBI Proteomics Center, Johns Hopkins University, Baltimore, MD (2005).

151 MCMC Methods to Detect Gene-Gene Interactions.
SNP Working Group, School of Public Health, Johns Hopkins University, Baltimore, MD (2005).

152 Are You Gellin'?
Genome Cafe Opening, Bloomberg School of Public Health, Baltimore, MD (2005).

153 An Add-On R Package for Rosetta.
Rosetta Developers Meeting, Leavenworth, WA (2005).

154 The Standard Error of the Lab Scientist.
Wall of Wonder, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2005).

155 Some SNP Related Stuff I am Working On.
Pulver Lab, Department of Psychiatry, Johns Hopkins School of Medicine, Baltimore, MD (2005).

156 How Do Proteins Fold?
Department of Biostatistics Faculty Meeting, Johns Hopkins University, Baltimore, MD (2004).

157 Protein Structure and Folding.
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2004).

158 On β Sheets in Proteins with Application to Structure Prediction.
Rosetta Developers Meeting, Leavenworth, WA (2003).

159 A Journey from Gene Expression to Protein Structure.
American Statistical Association Chapter Meeting, Albany, NY (2002).