Ingo Ruczinski

Part I

PERSONAL DATA

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EDUCATION AND TRAINING

Degrees

- PhD, University of Washington, Seattle, WA, Statistics (2000).
- MA, University of Würzburg, Germany, Mathematics and Computer Science (1995).
- MA, State University of New York, Albany, NY, Mathematics and Statistics (1994).

Postdoctoral Training

- Public Health Sciences Division, Fred Hutchinson Cancer Research Center, Seattle, WA (2000 – 2001).
- Department of Biochemistry, University of Washington, Seattle, WA (2000 – 2001).

Visiting

- Fred Hutchinson Cancer Research Center, Seattle, WA (2011).
- Department of Statistics, University of Dortmund, Germany (2009).
- Department of Chemistry, University of California at Santa Barbara (2003 – 2008).
- Centre National de Genotypage, Paris-Evry, France (2005).

PROFESSIONAL EXPERIENCE

- Associate Chair, Department of Biostatistics, Johns Hopkins University (2018 – present).
- Professor, Department of Biostatistics, Johns Hopkins University (2014 – present).
- Preceptor, Johns Hopkins Department of Genetic Medicine (2014 – present).
- Member, Center for Computational Biology (2012 – present).
- Associate Professor, Department of Biostatistics, Johns Hopkins University (2007 – 2014).
- Member, Johns Hopkins Institute for Multiscale Modeling of Biological Interactions (2006 – 2008).
- Assistant Professor, Deptartment of Biostatistics, Johns Hopkins University (2001 – 2007).
- Postdoctoral Fellow, Department of Biochemistry, University of Washington (2000 – 2001).
- Research Associate, Public Health Sciences, Fred Hutchinson Cancer Research Center (2000 – 2001).
- Consultant, Department of Statistics, University of Washington (1998 – 1999).
- Research Assistant, Public Health Sciences, Fred Hutchinson Cancer Research Center (1998 – 2000).
- Research Assistant, Department of Biochemistry, University of Washington (1996 – 2000).
- Teaching Assistant, Department of Statistics, University of Washington (1995 – 1996).

PROFESSIONAL ACTIVITIES

Professional Memberships

- R Foundation for Statistical Computing.

Participation on Advisory Panels and Committees

- Protein Foldeomics Consortium (2004 – 2009).
- Core Faculty, Program in Predoctoral Biostatistical Training in Genetics and Genomics (2005 – 2010).
- GAIN Alternative Allele Calling working group (2008 – 2009).
- STAMPEED consortium (2008 – 2010).
- GENEVA consortium (2008 – 2012).
- NHLBI Exome Sequencing Population Genetics and Statistical Analysis working group (2010 – 2012).
- National Institute of Child Health and Human Development Expert Panel (2011).
- Appointment and Promotions Committee, Johns Hopkins Oncology Biostatistics (2013 – 2014).
- Steering Committee Member, Eye and Vision Genomics Training Program (2012 – 2018).
- Advisory Committee, Bureau / Labbe Canadian Statistical Sciences Institute Grant (2016 – 2019).
- CLUE Serology advisory committee (2005 – 2020).
- CAAPA Publications and Presentations committee (2012 – 2024).
- CAAPA Structural Variant and Population Genetics working groups (2012 – 2024).
- Core Faculty, Burroughs Wellcome Fund Training Program in Genetics and Medicine (2013 – 2020).
- Preceptor, Human Genetics Training Program, Institute of Genetic Medicine (2014 – 2023).
- Steering Committee Member, NHLBI Whole Genome Sequencing Project (2015 – 2020).
- Analysis Committee Member, NHLBI TOPMed Whole Genome Sequencing Project (2015 – 2020).
- Co-Convener, TOPMed Structural Variation working group, (2015 – present).
- Member, Johns Hopkins inHealth Individualized Health Initiative (2016 – present).
- Member, Periodontitis Characterization Clinical Study Oversight Committee, NIDCR (2022 – 2024).
- Mentor, Careers through Mentoring and Training in Omics and Data for Early Stage Investigators (2022 – 2024).
- Ad-hoc Member, Promotions Committee, Johns Hopkins Krieger School of Arts and Sciences (2024).

Program Development

- Program Chair, American Statistical Association, Section on Risk Analysis (2005 – 2006).
- Program Committee, Joint Statistical Meetings (2006).
- Program Committee, Eastern North Atlantic Region (2006, 2011).
- Program Committee, European Conference on Computational Biology (2014).
- Organizing Committee, Conference on Statistical Methods for Very Large Data Sets (2011).
- Organizing Committee, Symposium on Advances in Genomics, Epidemiology and Statistics (2014 – present).
- Co-Organizer, Symposium on Sampling in Honor of Alan Ross (2014).
- Co-Organizer, BIRS Workshop on Statistical and Computational Challenges in Genomics (2015).
- Co-Organizer, BIRS Workshop on New Statistical Methods for Family-Based Sequencing Studies (2018).
- Workshop Organizer, World Health Summit (2015).
- Organizer, TomFest - A Conference in Honor of Tom Louis (2015).
- Session Chair, Joint Statistical Meetings (2001, 2004, 2005).
- Session Chair, Eastern North Atlantic Region Meeting (2003, 2015).
- Session Chair, American Society of Human Genetics Meeting (2009, 2020).
- Session Chair, International Biometric Conference (2010).

○ Session Chair, Conference on Statistical Methods for Very Large Data Sets (2011).

○ Session Chair, Annual Conference of the International Society for Clininal Biostatistics (2013).

○ Session Chair, Symposium on Advances in Genomics, Epidemiology and Statistics (2015, 2017).

○ Session Chair, Workshop on Statistical and Computational Challenges in Genomics (2015).

○ Session Chair, Big Data - World Health Summit (2015).

○ Session Chair, BIRS Workshop on Statistical Challenges in Genomics with Application to Precision Medicine (2018).

○ Session Organizer, Joint Statistical Meetings (2002, 2005, 2006).

○ Session Organizer, Eastern North Atlantic Region Meeting (2006, 2007).

○ Session Organizer, International Biometric Conference (2010).

○ Session Organizer, Johns Hopkins Biostatistics Centennial Symposium (2017).

EDITORIAL ACTIVITIES

Editorial Board Membership

○ Associate Editor, *Biometrical Journal*, International Biometric Society / Germany (2009 – 2011).

○ Associate Editor, *Biometrics*, International Biometric Society (2008 – 2014).

○ Editorial Board, *Cancer Prevention Research*, American Association for Cancer Research (2008 – 2014).

○ Associate Editor, *BioMed Central Bioinformatics* (2011 – 2016).

Peer Review Activities

Statistical Methodology Australian and New Zealand Journal of Statistics, Biometrical Journal, Biometrics, Biostatistics, Computational Statistics and Data Analysis, International Journal of Biostatistics, Journal of the American Statistical Association, Journal of Computational and Graphical Statistics, Journal of the Royal Statistical Society (Series B), Statistics in Medicine. **Genetics, Genomics, and Proteomics** Advances in Bioinformatics, Algorithms for Molecular Biology, American Journal of Human Genetics, Annals of the American Thoracic Society, Bioinformatics, BioMed Central Bioinformatics, BioMed Central Genomics, Birth Defects Research Part A: Clinical and Molecular Teratology, Breast Cancer Research, Cancer Prevention Research, Clinical and Experimental Allergy, Expert Review of Proteomics, Genetic Epidemiology, Human Molecular Genetics, Human Mutation, Journal of Proteome Research, Mammalian Genome, Molecular and Cellular Proteomics, Nature Communications, Nature Scientific Reports, Nucleic Acids Research, Proceedings of the National Academy of Sciences, Public Library of Science (PLoS), Science, Statistical Applications in Genetics and Molecular Biology. **Biochemistry and Biophysics** Biophysical Reviews and Letters, Biotechnology Progress, Journal of Molecular Biology, Journal of Structural Biology, Protein Science, Proteins: Structure, Function and Genetics, Proteins: Structure, Function and Bioinformatics. **Other Topics and Journals** AMS-Dimacs Volume on Epidemiology and Data Mining, Faculty of 1000, Journal of Heuristics, Journal of Statistical Software, Springer Verlag New York.

Review of Proposals and Departments

○ Research and Development Program, Louisiana Board of Regents (2004).

○ National Institutes of Health, Cancer Biomarker Study Section (2006).

○ Cancer Research UK Bioinformatics Programme (2007).

○ National Science Foundation, Biological Database and Informatics Program (2007).

○ National Institutes of Health, Cancer Biomarker Study Section (2007).

○ Johns Hopkins NIEHS Center in Urban Environmental Health (2008).

○ Science Unbound Foundation (2008).

○ National Institutes of Health, Cancer Biomarker Study Section (2008).

○ National Institutes of Health, ARRA RC1 Challenge Grant Review (2009).

○ National Cancer Institute, Special Emphasis Panel, Cancer Target Discovery and Development (2011).
○ Genome Canada and the Canadian Institutes of Health Research (2012).
○ National Institute of Dental and Craniofacial Research (2013).
○ Science Unbound Foundation (2013).
○ Laboratory Reference and Research Branch, Centers for Disease Control and Prevention (2013).
○ National Cancer Institute, Special Emphasis Panel, Development of Informatics Technology (2013).
○ Yale School of Public Health Thesis Reader (2014).
○ National Institute of Child Health and Human Development, Review Panel (2014).
○ National Institute of Dental and Craniofacial Research, Review Panel (2014).
○ National Institute of Child Health and Human Development, Review Panel (2015).
○ Department of Energy Exascale Requirements Review for Biological and Environmental Research (2016).
○ Biostatistics Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute (2018).
○ National Institute of Dental and Craniofacial Research, Secondary Data Analysis Review Panel (2019).
○ National Institute of Dental and Craniofacial Research, Secondary Data Analysis Review Panel (2020).
○ National Institute of Dental and Craniofacial Research, Genomics Review Panel (2020).

Letters Supporting Appointments, Promotions, Tenure and Faculty Awards

Brigham and Women's Hospital (USA), Columbia University (USA), Fred Hutchinson Cancer Research Center (USA), George Washington University (USA), Harvard University (USA), Institut Pasteur (France), Johns Hopkins School of Public Health (USA), Johns Hopkins School of Medicine (USA), Memorial Sloan Kettering Cancer Center (USA), National Cancer Institute (USA), National Human Genome Research Institute (USA), National Institute of Allergy and Infectious Diseases (USA), National University of Singapore (Singapore), Technical University of Munich (Germany), Texas A&M University (USA), University of Alberta (Canada), University of California at Berkeley (USA), University of California at San Francisco (USA), University of Michigan (USA), University of Pennsylvania (USA), University of Regensburg (Germany), University of Virginia (USA), University of Wisconsin (USA), University of Zürich (Switzerland), Wake Forest University (USA).

HONORS AND AWARDS

○ ZW Birnbaum Award for Excellence in Teaching, University of Washington (1996).
○ Faculty Innovation Award, Johns Hopkins University (2002).
○ Maryland Cigarette Restitution Fund Grant, Johns Hopkins Medical Institutions (2002).
○ Travel Award, International Federation of Classification Societies, Cracow, Poland (2002).
○ Best Contributed Paper Award, Joint Statistical Meetings, ASA Section on Risk Analysis (2003).
○ NSF Young Researchers Travel Award, University of Florida (2003).
○ NSF Young Researchers Travel Award (University of California at Los Angeles (2004).
○ Johns Hopkins School of Public Health Faculty Research Initiative Award (2006).
○ Advising, Mentoring, and Teaching Recognition Award, Johns Hopkins University (2007).
○ Keynote Lecture, Workshop on Big Data in Medical Research, BIPS, Bremen, Germany (2010).
○ Johns Hopkins Medical Institutions Clinical and Translational Science Awards (2011).
○ Keynote Lecture, Johns Hopkins NHLBI Proteomics Technology Center Meeting (2013).
○ Elected Fellow, American Statistical Association (2016).

PUBLICATIONS *The white numbers indicate first or senior author manuscripts.*

Published Peer-Reviewed Articles

1 Li X / ⋯ 69 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl **Ruczinski I** / ⋯ 11 authors ⋯ / Lin X (2025). *A statistical framework for multi-trait rare variant analysis in large-scale whole-genome sequencing studies.* ▸ *Nature Computational Science (2): 125-143.*

2 *Mangnier L, **Ruczinski I**, Ricard J, Moreau C, Girard S, Maziade M, Bureau A (2025). RetroFun-RVS: a retrospective family-based framework for rare variant analysis incorporating functional annotations.* ▸ *Genetic Epidemiology (to appear).*

3 *Grant-McAuley W, Morgenlander WR, **Ruczinski I**, Kammers K, Laeyendecker O, Hudelson SE, Thakar M, Piwowar-Manning E, Clarke W, Breaud A, Ayles H, Bock P, Moore A, Kosloff B, Shanaube K, Meehan S, van Deventer A, Fidler S, Hayes R, Larman HB, Eshleman SH, for the HPTN 071 (PopART) Study Team (2024). Identification of antibody targets associated with lower HIV viral load and viremic control.* ▸ *PLoS One 19(9): e0305976.*

4 *Morgenlander WR, Chia WN, Parra B, Monaco DR, Ragan I, Pardo CA, Bowen R, Zhong D, Norris DE, **Ruczinski I**, Durbin A, Wang LF, Larman HB, Robinson M (2024). Precision arbovirus serology with a pan-arbovirus peptidome.* ▸ *Nature Communications 15(1): 5833.*

5 *Szczesny B, Boorgula MP, Chavan S, Campbell M, Johnson RK, Kammers K, Thompson EE, Cox MS, Shankar G, Cox C, Morin A, Lorizio W, Daya M, Kelada SN, Beaty TH, Doumatey AP, Cruz A, Watson H, Naureckas T, Giles BL, Arinola GA, Sogaolu O, Falade AG, Hansel NN, Yang I, Olopade CO, Rotimi C, Landis C, Figueiredo CA, Altman M, Kenny E, **Ruczinski I**, Liu AH, Ober C, Taub MA, Barnes KC, Mathias RA (2024). Multi-omics in nasal epithelium reveals three axes of dysregulation for asthma risk in the African Diaspora populations.* ▸ *Nature Communications 15(1): 4546.*

6 *Keener R / ⋯ 75 authors ⋯ / **Ruczinski I** / ⋯ 18 authors ⋯ / Battle A (2024). Validation of human telomere length trans-ancestry meta-analysis association signals identifies POP5 and KBTBD6 as novel human telomere length regulation genes.* ▸ *Nature Communications 15(1): 4417.*

7 *Leroux A, Crainiceanu C, Zeger S, Taub M, Ansari B, Wager TD, Bayman E, Coffey C, Langefeld C, McCarthy R, Tsodikov A, Brummet C, Clauw DJ, Edwards RR, Lindquist MA; A2CPS Consortium incl **Ruczinski I** (2024). Statistical modeling of acute and chronic pain patient-reported outcomes obtained from ecological momentary assessment.* ▸ *Pain 65(9): 1955-1965.*

8 *Liebhoff A, Venkataraman T, Morgenlander WR, Na M, Kula T, Waugh K, Morrison C, Rewers M, Longman R, Round J, Elledge S, **Ruczinski I**, Langmead B, Larman HB (2024). Efficient encoding of large antigenic spaces by epitope prioritization with Dolphyn.* ▸ *Nature Communications 15(1): 1577.*

9 *Grant-McAuley W, Morgenlander W, Hudelson S, Thakar M, Piwowar-Manning E, Clarke W, Breaud A, Blankson J, Wilson E, Ayles H, Bock P, Moore A, Kosloff B, Shanaube K, Meehan S, Van Deventer A, Fidler S, Hayes R, **Ruczinski I**, Kammers K, Laeyendecker O, Larman HB, Eshleman S (2023). Comprehensive profiling of pre-infection antibodies identifies HIV targets associated with viremic control and viral load.* ▸ *Frontiers in Immunology 14: 1178520.*

10 *Recto K, Kachroo P, Huan T, Van Den Berg D, Lee GY, Bui H, Lee DH, Gereige J, Yao C, Hwang SJ, Joehanes R, Weiss ST; NHLBI Trans-Omics in Precision Medicine (TOPMed) Consortium incl **Ruczinski I**; O'Connor GT, Levy D, DeMeo DL (2023). Epigenome-wide DNA methylation association study of circulating IgE levels identifies novel targets for asthma.* ▸ *eBioMedicine 95: 104758.*

11 *Berube S, Kobayashi T, Norris DE, **Ruczinski I**, Moss WJ, Wesolowski A, Louis TA (2023). Novel bioinformatic methods and machine learning approaches reveal candidate biomarkers of the intensity and timing of past exposure to plasmodium falciparum.* ▸ *PLoS Global Public Health 3(8): e0001840.*

12 *Wong WJ, Emdin C, Bick AG, Zekavat SM, Niroula A, Pirruccello JP, Dichtel L, Griffin G, Uddin MM, Gibson CJ, Kovalcik V, Lin AE, McConkey ME, Vromman A, Sellar RS, Kim PG, Agrawal M, Weinstock J, Long MT, Yu B, Banerjee R, Nicholls RC, Dennis A, Kelly M, Loh PR, McCarroll S, Boerwinkle E, Vasan RS, Jaiswal S, Johnson AD, Chung RT, Corey K, Levy D, Ballantyne C, NHLBI TOPMed Hematology Working Group incl **Ruczinski I**, Ebert BL, Natarajan P (2023). Clonal haematopoiesis and risk of chronic liver disease.* ▸ *Nature 616(7958): 747-754.*

13 *Weinstock JS / ⋯ 99 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I**, *Blackwell TW, Abecasis GR, Smith AV, Kang HM, Satpathy A, Natarajan P, Kitzman JO, Whitsel EA, Reiner AP, Bick AG, Jaiswal S (2023). Aberrant activation of TCL1A promotes stem cell expansion in clonal haematopoiesis. ▸ Nature 616(7958): 755-763.*

14 *Berube S, Kobayashi T, Wesolowski A, Norris DE,* **Ruczinski I**, *Moss WJ, Louis TA (2023). A Bayesian hierarchical model for signal extraction from protein microarrays. ▸ Statistics in Medicine 42(9): 1445-1460.*

15 *Li X / ⋯ 54 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I**, *TOPMed Lipids Working Group, Rotter JI, Natarajan P, Peloso GM, Li Z, Lin X (2023). Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole genome sequencing studies. ▸ Nature Genetics 55(1): 154-164.*

16 *Huffaker MF, Kanchan K, Bahnson HT,* **Ruczinski I**, *Shankar G, Leung DY, Baloh C, Du Toit G, Lack G, Nepom GT, Mathias RA (2023). FLG association with peanut allergy and eczema severity in LEAP participants. ▸ Journal of Clinical Investigation 151(4): 1137-1142.*

17 *Kanchan K, Shankar G, Huffaker MF, Bahnson HT, Chinthrajah RS, Sanda S, Ling H, Paschall JE, Manohar M, DuToit G,* **Ruczinski I**, *Togas A, Lack G, Nadeau KC, Jones SM, Nepom GT, Mathias RA (2022). HLA-associated outcomes in peanut oral immunotherapy trials identify mechanistic and clinical determinants of therapeutic success. ▸ Frontiers in Immunology 13: 941839.*

18 *Grant-McAuley W, Laeyendecker O, Monaco D, Chen A, Hudelson SE, Klock E, Brookmeyer R, Morrison D, Piwowar-Manning E, Morrison CS, Hayes R, Ayles H, Bock P, Kosloff B, Shanaube K, Mandla N, van Deventer A,* **Ruczinski I**, *Kammers K, Larman HB, Eshleman SH (2022). Evaluation of multi-assay algorithms for cross-sectional HIV incidence estimation in settings with universal antiretroviral treatment. ▸ BMC Infectious Diseases 22(1): 838.*

19 *Li Z / ⋯ 62 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I**, *TOPMed Lipids Working Group, Rotter JI, Willer CJ, Natarajan P, Peloso GM, Lin X (2022). A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. ▸ Nature Methods 9(12): 1599-1611.*

20 *Selvaraj MS / ⋯ 82 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I**, *Peloso GM, Natarajan P (2022). Whole genome sequence analysis of blood lipid levels in > 66,000 individuals. ▸ Nature Communications 13(1): 5995.*

21 *Chen A, Kammers K, Larman HB, Scharpf RB,* **Ruczinski I** *(2022). Detecting antibody reactivities in phage immuno-precipitation sequencing data. ▸ BMC Genomics 23(1): 654.*

22 *Tahir UA, Katz DH, Avila-Pachecho J, Bick AG, Pampana A, Robbins JM, Yu Z, Chen ZZ, Benson MD, Cruz DE, Ngo D, Deng S, Shi X, Zheng S, Eisman AS, Farrell L, Hall ME, Correa A, Tracy RP, Durda P, Taylor KD, Liu Y, Johnson WC, Guo X, Yao J, Chen YI, Manichaikul AW, Ruberg FL, Blaner WS, Jain D; NHLBI Trans-Omics for Precision Medicine Consortium incl* **Ruczinski I**, *Bouchard C, Sarzynski MA, Rich SS, Rotter JI, Wang TJ, Wilson JG, Clish CB, Natarajan P, Gerszten RE (2022). Whole genome association study of the plasma metabolome identifies metabolites linked to cardiometabolic disease in black individuals. ▸ Nature Communications 3(1): 4923.*

23 *Chen A, Kammers K, Larman HB, Scharpf RB,* **Ruczinski I** *(2022). Detecting and quantifying antibody reactivity in PhIP-Seq data with BEER. ▸ Bioinformatics 38(19): 4647-9.*

24 *Angkeow JW, Monaco DR, Chen A, Venkataraman T, Jayaraman S, Valencia C, Sie BM, Liechti T, Farhadi PN, Funez-dePagnier G, Sherman-Baust CA, Wong MQ,* **Ruczinski I**, *Caturegli P, Sears CL, Simner PJ, Round JL, Duggal P, Laserson U, Steiner TS, Sen R, Lloyd TE, Roederer M, Mammen AL, Longman RS, Rider LG, Larman HB (2022). Prevalence, persistence, and genetics of antibody responses to protein toxins and virulence factors. ▸ Immunity 55(6): 1051-1066.*

25 *Hu X / ⋯ 12 authors ⋯ /* **Ruczinski I** */ ⋯ 34 authors ⋯ / TOPMed Lung Working Group, Cho MH, Im HK, Manichaikul A (2022). Polygenic transcriptome risk scores improve cross-ethnic portability for COPD and lung function in the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. ▸ American Journal of Human Genetics 109(5): 857-870.*

26 *Ngwa JS, Yanek LR, Kammers K, Kanchan K, Taub MA, Scharpf RB, Faraday N, Becker LC, Mathias RA,* **Ruczinski I** *(2022). Secondary analyses for genome-wide association studies using expression quantitative trait loci. ▸ Genetic Epidemiology 46: 170-181.*

27 *Wainschtein P, Jain D, Zheng Z; TOPMed Anthropometry Working Group; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I** */ ⋯ 46 authors ⋯ / Visscher PM (2022). Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.* ► *Nature Genetics 54(3): 263-273.*

28 *Taub MA / ⋯ 114 authors ⋯ /* **Ruczinski I** */ ⋯ 10 authors ⋯ / Mathias RA on behalf of the NHLBI Trans-Omics for Precision Medicine Consortium (2022). Novel genetic determinants of telomere length from a trans-ethnic analysis of 109,122 whole genome sequences in TOPMed.* ► *Cell Genomics 2(1): 100084.*

29 *Berube S, Kobayashi T, Wesolowski A, Norris DE,* **Ruczinski I***, Moss WJ, Louis TA (2022). A pre-processing pipeline to quantify, visualize and reduce technical variation in protein microarray studies.* ► *Proteomics 22(3): e2100033.*

30 *Kanchan K, Grinek S, Bahnson TH,* **Ruczinski I***, Shankar G, Larson D, Du Toit G, Barnes KC, Sampson H, Suarez-Farinas M, Lack G, Nepom GT, Cerosaletti K, Mathias RA, Immune Tolerance Network LEAP Study Team (2022). HLA alleles and sustained peanut consumption promote IgG4 responses in subjects protected from peanut allergy.* ► *Journal of Clinical Investigation 132(1): e152070.*

31 *Mason SE, Moreta-Martinez R, Labaki WW, Strand MJ, Regan EA, Bon J, San Jose Estepar R, Casaburi R, McDonald ML, Rossiter HB, Make B, Dransfield MT, Han MK, Young K, Curtis JL, Stringer K, Kinney G, Hokanson JE, San Jose Estepar R, Washko GR; COPDGene Investigators incl* **Ruczinski I** *(2022). Longitudinal association between muscle loss and mortality in ever smokers.* ► *Chest 161(4): 960-970.*

32 *Katz DH, Tahir UA, Bick AG, Pampana A, Ngo D, Benson MD, Yu Z, Robbins JM, Chen ZZ, Cruz DE, Deng S, Farrell L, Sinha S, Schmaier AA, Shen D, Gao Y, Hall ME, Correa A, Tracy RP, Durda P, Taylor KD, Liu Y, Johnson WC, Guo X, Yao J, Ida Chen YD, Manichaikul AW, Jain D, Bouchard C, Sarzynski MA, Rich SS, Rotter JI, Wang TJ, Wilson JG, Natarajan P, Gerszten RE; National Heart, Lung, and Blood Institute TOPMed (Trans-Omics for Precision Medicine) Consortium incl* **Ruczinski I** *(2022). Whole genome sequence analysis of the plasma proteome in black adults provides novel insights into cardiovascular disease.* ► *Circulation 145(5): 357-370.*

33 *Luo Y, Kanai M, Choi W, Li X, Sakaue S, Yamamoto K, Ogawa K, Gutierrez-Arcelus M, Gregersen PK, Stuart PE, Elder JT, Forer L, Schonherr S, Fuchsberger C, Smith AV, Fellay J, Carrington M, Haas DW, Guo X, Palmer ND, Chen YI, Rotter JI, Taylor KD, Rich SS, Correa A, Wilson JG, Kathiresan S, Cho MH, Metspalu A, Esko T, Okada Y, Han B; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I***, McLaren PJ, Raychaudhuri S (2021). A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response.* ► *Nature Genetics 53(10): 1504-1516.*

34 *Daya M, Cox C, Acevedo N, Boorgula MP, Campbell M, Chavan S, Cho MH, David GL, Kachroo P, Lasky-Su J, Li X, McHugh CP, Qiao D, Rafaels N, Beck LA, Bleecker ER, Caraballo L, Cupples AL, Figueiredo CA, Gallo RL, Hanifin J, Hansel NN, Hata TR, Hersh CP, Knight-Madden J, Leung DY, Guttman-Yassky E, Meyers DA, O'Connor G, Ober C, Ong PY, Ortega VE, Paller AS, Putcha N, Reed RM, Schneider LC, Silverman EK, Slifka MK, Spergel JM, Vasan RS, Viaud-Martinez KA, Watson H, Weiss ST, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium,* **Ruczinski I***, Beaty TH, Mathias RA, Barnes KC (2021). Multi-ethnic genome-wide and HLA association study of total serum IgE.* ► *Journal of Allergy and Clinical Immunology 148(6): 1589-1595.*

35 *Kammers K, Chen A, Monaco D, Hudelson S, Greenawalt W, Moore R, Alter G, Deeks SG, Morrison CS, Eller LA, Blankson J, Laeyendecker O,* **Ruczinski I***, Eshleman SH, Larman HB (2021). Massively multiplexed antibody profiling identifies antibody targets associated with natural control of HIV infection.* ► *Frontiers Immunology 12: 740395.*

36 *Cade BE / ⋯ 23 authors ⋯ / NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl* **Ruczinski I***, Abecasis GR, Boerwinkle EA, Correa A, Cupples LA, Kaplan RC, Nickerson DA, North KE, Psaty BM, Rotter JI, Rich SS, Tracy RP, Vasan RS, Wilson JG, Zhu X, Redline S; TOPMed Sleep Working Group (2021). Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program.* ► *Genome Medicine 13(1): 136.*

37 *Yang C, Hallmark B, Chai J, O'Connor TD, Reynolds LM, Wood AC, Seeds M, Chen YI, Steffen LM, Tsai MY, Kaplan R, Qi Q, Mandarino LJ, Fretts AM, Lemaitre RN, Coletta D, Blomquist SA, Johnstone LM, Tontsch C,* **Ruczinski I***, Rich SS, Mathias RA, Chilton FH, Manichaikul A (2021). FADS genetic variation impacts cardiometabolic and inflammatory risk in Hispanics.* ► *Communication Biology 4(1): 918.*

38 *Ray D, Venkataraghavan S, Zhang W, Leslie EJ, Bidinger JA,* **Ruczinski I***, Taub MA, Marazita ML, Beaty TH (2021). Pleiotropy method identifies genetic overlap between non-syndromic orofacial clefts at multiple loci from GWAS of multi-ethnic trios.* ► *PLoS Genetics 17(7): e1009584.*

39 Keramati AR, Chen MH, Benjamin A.T. Rodriguez BA, Yanek LR, Bhan A, Gaynor BJ, Ryan K, A. Brody JA, Zhong X, Wei Q, NHLBI Trans-Omics for Precision (TOPMed) Consortium, NHLBI TOPMed Hematology and Hemostasis Working Group, Kammers K, Kanchan K, Iyer K, Kowalski MH, Pitsillides AN, Cupples LA, Li B, Schlaeger T, Shuldiner AR, O'Connell JR, **Ruczinski I,** Mitchell BD, Faraday N, Taub MA, Becker LC, Lewis JP, Mathias RA, Johnson AD (2021). Genome sequencing unveils a new regulatory landscape of platelet reactivity. ► Nature Communications 12(1): 3626.

40 Sofer T, Zheng X, Laurie CA, Gogarten SM, Brody JA, Conomos MP, Bis JC, Thornton TA, Szpiro A, O'Connell JR, Lange EM, Gao Y, Cupples LA, Psaty BM; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium incl **Ruczinski I**, Rice KM (2021). Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. ► Nature Communications 12(1): 3506.

41 Zhang W, Venkataraghavan S, Hetmanski JB, Leslie EJ, Marazita ML, Feingold E, Weinberg SM, **Ruczinski I**, Taub MA, Scott AF, Ray D, Beaty TH (2021). Detecting gene-environment interaction for maternal exposures using case-parent trios ascertained through a case with non-syndromic orofacial cleft. ► Frontiers in Cell and Developmental Biology 9: 798.

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Under Review

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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 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 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.

11 **PhIPData** ▶ The R package PhIPData, a collaboration with Athena Chen, Kai Kammers and Rob Scharpf, defines an S4 class for phage-immunoprecipitation sequencing (PhIP-seq) experiments. Buliding upon the RangedSummarizedExperiment class, PhIPData enables users to coordinate metadata with experimental data in analyses. 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.

12 **BEER** ► The R package BEER, a collaboration with Athena Chen, Kai Kammers and Rob Scharpf, implements a Bayesian model for analyzing PhIP-seq data. Given a PhIPData object, BEER returns posterior probabilities of antibody reactivity, point estimates for the relative fold-change in comparison to negative control samples, and more. 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.

TEACHING

Advisees

1 Long, Ezhou. Master of Science, Biostatistics (2004 – 2005).
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4 Chang, Howard. Doctor of Philosophy, Biostatistics (2004 – 2006).
5 Murakami, Peter. Doctor of Philosophy, Biostatistics (2006 – 2007).
6 Aripirala, Srinivas. Doctor of Philosophy, IMMBI (2007).
7 Jaffe, Andrew. Master of Science, Bioinformatics (2009 – 2010).
8 Seth, Sahil. Master of Science, Bioinformatics (2009 – 2010).
9 Wei, Yingying. Doctor of Philosophy, Biostatistics (2009 – 2010).
10 Gellar, Jonathan. Master of Science, Biostatistics (2009 – 2010).

11 Zhou, Xian Chong. Master of Science, Biostatistics (2009 – 2010).

12 Frazee, Alyssa. Doctor of Philosophy, Biostatistics (2010 – 2011).

13 Zhang, Wenze. Master of Public Health, Biostatistics (2010 – 2011).

14 Patil, Prasad. Doctor of Philosophy, Biostatistics (2011 – 2013).

15 Myint, Leslie. Doctor of Philosophy, Biostatistics (2013 – 2014).

16 Zhang, Haoyu. Doctor of Philosophy, Biostatistics (2014 – 2016).

17 Qi, Guanghao. Doctor of Philosophy, Biostatistics (2015 – 2017).

18 Zhou, Xiaobin. Master of Science, Biostatistics (2020 – 2021).

19 Lei, Jingce. Master of Science, Biostatistics (2021 – 2022).

20 Wei, Yujie. Doctor of Philosophy, Biostatistics (2021 – 2022).

21 Wagner, Elizabeth. Master of Science, Biostatistics (2022 – 2023).

22 Liu, Nora. Doctor of Philosophy, Biostatistics (2023 – 2024).

23 Hou, Christine. Master of Science, Biostatistics (2023 – 2024).

24 Zhao, Meishu. Master of Science, Biostatistics (2024 – present).

25 Ilunga, Deerspring Meucci. Doctor of Philosophy, Biostatistics (2024 – present).

Visitors

1 Pattaro, Cristian. EURAC, Bolzano, Italy (2008).

2 Bunea, Florentina. Florida State University, Tallahassee, FL (2008).

3 Schwender, Holger. University of Düsseldorf, Germany (2011, 2012, 2013, 2014, 2015).

4 Kammers, Kai. University of Dortmund, Germany (2011, 2012).

5 Bureau, Alexandre. Université Laval, Québec City, Canada (2012, 2013, 2014).

6 Dellen, Rafael. University of Düsseldorf, Germany (2013).

7 Sampson, Joshua. National Cancer Institute, Rockville, MD (2014).

8 DiRienzo, Gregory. State University of New York at Albany, Albany, NY (2018).

Faculty Mentoring Committees

1 Keet, Corinne. Johns Hopkins School of Medicine (2012 – 2015).

2 Wojciechowski, Robert. Johns Hopkins School of Public Health (2012 – 2017).

3 Corsello-Gorgun, Tiziana. University of Texas Medical Branch at Galveston (2022 – present).

4 Scharpf, Robert. Johns Hopkins School of Medicine (2010 – present).

5 Kammers, Kai. Johns Hopkins School of Medicine (2017 – present).

6 Quach, Huy. Mayo Clinic (2023 – present).

Thesis Committees / Thesis Reader

1 Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).

2 Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).

3 Sefcovic, Natasha. Doctor of Philosophy, Biology NIH/Johns Hopkins (2006).

4 Wang, Wenyi. Doctor of Philosophy, Biostatistics (2007).

5 Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).

6 Gamston, Courtney. Master of Science, Molecular Microbiology and Immunology (2007).

7 Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).

8 Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).

9 Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2008).

10 Murakami, Peter. Master of Science, Biostatistics (2008).

11 Carvalho, Benilton. Doctor of Philosophy, Biostatistics (2008).

12 Venkatesan, Meera. Doctor of Philosophy, Molecular Microbiology and Immunology (2008).

13 Chang, Yi-Ting. Master of Science, Biostatistics (2009).

14 Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2009).

15 Roberson, Eli. Doctor of Philosophy, Human Genetics, JHMI (2009).

16 Chu, Audrey. Doctor of Philosophy, Epidemiology (2010).

17 Suktitipat, Bhoom. Doctor of Philosophy, Epidemiology (2010).

18 Wu, Tao. Doctor of Philosophy, Epidemiology (2010).

19 Zhang, Tian-Xiao. Master of Science, Epidemiology (2011).

20 Toolan, Jennifer. Doctor of Philosophy, Mental Health (2011).

21 Dluzniewski, Paul. Doctor of Philosophy, Epidemiology (2011).

22 Tin, Adrienne. Doctor of Philosophy, Epidemiology (2012).

23 Provost, Katie. Doctor of Philosophy, Molecular Microbiology and Immunology (2012).

24 Shaw, Patrick. Doctor of Philosophy, Biochemistry and Molecular Biology (2012).

25 Sheppard, Brooke. Master of Science, Epidemiology (2012).

26 Behneman, Dana. Doctor of Philosophy, Epidemiology (2012).

27 Golozar, Asieh. Doctor of Philosophy, Epidemiology (2012).

28 Shirley, Matt. Doctor of Philosophy, School of Medicine (2013).

29 Halper-Stromberg, Eitan. Doctor of Philosophy, Human Genetics, JHMI (2013).

30 Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2013).

31 Higgins, Ryan. Doctor of Philosophy, School of Medicine (2013).

32 Babatz, Tim. Doctor of Philosophy, School of Medicine (2013).

33 Keet, Corinne. Doctor of Philosophy, Epidemiology (2014).

34 Ryslik, Gregory. Doctor of Philosophy, Yale School of Public Health (2014).

35 Lee, Sun Eun. Doctor of Philosophy, International Health (2015).

36 Parker, Margaret. Doctor of Philosophy, Epidemiology (2015).

37 Christ, Max. Master of Science, University of Düsseldorf (2015).

38 He, Bing. Doctor of Philosophy, Biostatistics (2017).

39 Bomotti, Samantha. Doctor of Philosophy, Epidemiology (2017).

40 Cristiano, Stephen. Doctor of Philosophy, Biostatistics (2019).

41 Longchamps, Ryan. Doctor of Philosophy, School of Medicine (2019).

42 Qi, Guanghao. Doctor of Philosophy, Biostatistics (2020).

43 Montagne, Janelle. Doctor of Philosophy, School of Medicine (2020).

44 Saha, Arkajyoti. Doctor of Philosophy, Biostatistics (2021).

45 Zhang, Jingning. Doctor of Philosophy, Biostatistics (2022).

46 Chen, Chang. Master of Science, Biostatistics (2022).

47 You, Shengjun. Master of Science, Biostatistics (2023).

48 Fu, Martina. Doctor of Philosophy, Biostatistics (2024).

49 Razi, Afrooz. Doctor of Philosophy, Human Genetics (present).

50 Lee, Elizabeth Christine. Doctor of Philosophy, Molecular Microbiology and Immunology (present).

51 Wei, Yujie. Doctor of Philosophy, Biostatistics (present).

52 Notarte, Kin Israel. Doctor of Philosophy, School of Medicine (present).

Preliminary Oral Participation * committee chair

1. Ziegler, Kathryn. Doctor of Philosophy, Biostatistics (2003).
2. Kittleson, Michelle. Doctor of Philosophy, Clinical Investigation (2004).
3. Scharpf, Robert. Doctor of Philosophy, Biostatistics (2004).
4. Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2005).
5. Naj, Adam. Doctor of Philosophy, Epidemiology (2005).
6. Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2005).
7. Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2006).
8. Li, Qing. Doctor of Philosophy, Biostatistics (2006).
9. Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2006).
10. Bowers, Katherine.* Doctor of Philosophy, Epidemiology (2007).
11. McCall, Matthew. Doctor of Philosophy, Biostatistics (2007).
12. Chu, Audrey.* Doctor of Philosophy, Epidemiology, (2008).
13. Boca, Simina. Doctor of Philosophy, Biostatistics (2008).
14. Pichard, Luis.* Doctor of Philosophy, Environmental Health Sciences (2009).
15. Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2009).
16. Wu, Tao. Doctor of Philosophy, Epidemiology (2009).
17. Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2009).
18. Garvin, Heather.* Doctor of Philosophy, School of Medicine (2009).
19. Higgins, Ryan.* Doctor of Philosophy, School of Medicine (2010).
20. Park, Yongjin. Doctor of Philosophy, Biomedical Engineering (2010).
21. Golozar, Asieh. Doctor of Philosophy, Epidemiology (2010).
22. Massie, Allan.* Doctor of Philosophy, Epidemiology (2011).
23. Jones, Katrina.* Doctor of Philosophy, School of Medicine (2011).
24. Lee, Sun Eun. Doctor of Philosophy, International Health (2012).
25. Burgess, Loring.* Doctor of Philosophy, School of Medicine (2013).
26. Squyres, Nicole.* Doctor of Philosophy, School of Medicine (2013).
27. Keet, Corinne. Doctor of Philosophy, Epidemiology (2013).
28. Hunter, David. Doctor of Philosophy, School of Medicine (2013).
29. Spampinato, Daniel. Doctor of Philosophy, School of Medicine (2013).
30. Blazeski, Adriana.* Doctor of Philosophy, School of Medicine (2014).
31. Parker, Margaret. Doctor of Philosophy, Epidemiology (2014).
32. Hatwar, Rajeev. Doctor of Philosophy, Mechanical Engineering (2014).
33. Kostecki, Geran. Doctor of Philosophy, Biomedical Engineering (2014).
34. He, Bing. Doctor of Philosophy, Biostatistics (2015).
35. Powell, Ellen. Doctor of Philosophy, Functional Anatomy and Evolution (2015).
36. Pilarowski, Genay. Doctor of Philosophy, Human Genetics (2015).
37. Fu, Jack. Doctor of Philosophy, Biostatistics (2016).
38. Prufrock, Kristen.* Doctor of Philosophy, Functional Anatomy and Evolution (2016).
39. Li, Weiyan.* Doctor of Philosophy, Epidemiology (2016).
40. Loomis, Stephanie.* Doctor of Philosophy, Epidemiology (2017).
41. Harper, Christine.* Doctor of Philosophy, Functional Anatomy and Evolution (2017).
42. Canington, Stephanie.* Doctor of Philosophy, Functional Anatomy and Evolution (2017).
43. Qi, Guanghao. Doctor of Philosophy, Biostatistics (2017).
44. Chou, Michael. Doctor of Philosophy, Epidemiology (2018).
45. Gilpatrick, Timothy.* Doctor of Philosophy, Biomedical Engineering (2018).

46 Zhang, Pengfei. Doctor of Philosophy, Biomedical Engineering (2018).

47 Orozco, Simon. Doctor of Philosophy, Biomedical Engineering (2018).

48 Goldstein, Deanna.* Doctor of Philosophy, Functional Anatomy and Evolution (2018).

49 Hogan, Aneila.* Doctor of Philosophy, Functional Anatomy and Evolution (2018).

50 Hooshangnejad, Hamed. Doctor of Philosophy, Biomedical Engineering (2018).

51 Hawthorne, Robert.* Doctor of Philosophy, Biomedical Engineering (2018).

52 Iyer, Kruthika. Doctor of Philosophy, Epidemiology (2019).

53 Berube, Sophie. Doctor of Philosophy, Biostatistics (2019).

54 Rodriguez, Marlen.* Doctor of Philosophy, Biomedical Engineering (2019).

55 Russell, Kinley.* Doctor of Philosophy, Functional Anatomy and Evolution (2019).

56 Llera, Catherine.* Doctor of Philosophy, Functional Anatomy and Evolution (2019).

57 Ayiotis, Andrianna.* Doctor of Philosophy, Biomedical Engineering (2019).

58 Fan, Hongli. Doctor of Philosophy, Biomedical Engineering (2019).

59 Hall, Franklyn. Doctor of Philosophy, Biomedical Engineering (2019).

60 Pi, Jay. Doctor of Philosophy, Biomedical Engineering (2019).

61 Chen, Athena. Doctor of Philosophy, Biostatistics (2019).

62 Omotoso, Mary.* Doctor of Philosophy, Biomedical Engineering (2020).

63 Park, Joon Soo. Doctor of Philosophy, Biomedical Engineering (2020).

64 Huang, Yi-Chieh. Doctor of Philosophy, Functional Anatomy and Evolution (2020).

65 Sims, Zana.* Doctor of Philosophy, Functional Anatomy and Evolution (2020).

66 Duchan, Dylan. Doctor of Philosophy, Epidemiology (2020).

67 Zhang, Jingning. Doctor of Philosophy, Biostatistics (2020).

68 Neshat, Sarah. Doctor of Philosophy, Biomedical Engineering (2021).

69 Luly, Kathryn.* Doctor of Philosophy, Biomedical Engineering (2021).

70 Yang, Brenda. Doctor of Philosophy, Biomedical Engineering (2021).

71 Wilson, Jacob.* Doctor of Philosophy, Functional Anatomy and Evolution (2021).

72 Fu, Martina. Doctor of Philosophy, Biostatistics (2022).

73 Cobb, Savannah.* Doctor of Philosophy, Functional Anatomy and Evolution (2022).

74 Palmer, Stephanie.* Doctor of Philosophy, Functional Anatomy and Evolution (2022).

75 Pietz, Kevin. Doctor of Philosophy, Biomedical Engineering (2023).

76 Hu, Zhen.* Doctor of Philosophy, Biomedical Engineering (2023).

77 Zhou, Julia.* Doctor of Philosophy, Biomedical Engineering (2023).

78 Torres, Fernando.* Doctor of Philosophy, Functional Anatomy and Evolution (2023).

79 Foster, Will.* Doctor of Philosophy, Functional Anatomy and Evolution (2023).

80 Batsche, Kailie.* Doctor of Philosophy, Functional Anatomy and Evolution (2023).

81 Awosika, Tolulope. Doctor of Philosophy, Biomedical Engineering (2024).

82 Daher, Jade. Doctor of Philosophy, Biomedical Engineering (2024).

83 Ornelas-Gatdula, Elysse. Doctor of Philosophy, Chemical Biology (2024).

84 Wyse-Sookoo, Kimberley.* Doctor of Philosophy, Biomedical Engineering (2024).

85 Chen, Jay. Doctor of Philosophy, Biomedical Engineering (2024).

Final Oral Participation ** committee chair*

1 Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).
2 Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).
3 Peila, Rita. Doctor of Philosophy, Epidemiology (2005).
4 Sefcovic, Natasha. Doctor of Philosophy, Biology, NIH/Johns Hopkins (2006).
5 Scharpf, Robert. Doctor of Philosophy, Biostatistics (2007).
6 Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).
7 Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).
8 Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).
9 Cheng, Yu-Ching.* Doctor of Philosophy, Epidemiology (2008).
10 Venkatesan, Meera.* Doctor of Philosophy, Molecular Microbiology and Immunology (2008).
11 Li, Qing. Doctor of Philosophy, Biostatistics (2009).
12 Chu, Audrey. Doctor of Philosophy, Epidemiology (2010).
13 Suktitipat, Bhoom. Doctor of Philosophy, Epidemiology (2010).
14 Wu, Tao.* Doctor of Philosophy, Epidemiology (2010).
15 Toolan, Jennifer.* Doctor of Philosophy, Mental Health (2011).
16 Dluzniewski, Paul. Doctor of Philosophy, Epidemiology (2011).
17 Tin, Adrienne. Doctor of Philosophy, Epidemiology (2012).
18 Provost, Katie.* Doctor of Philosophy, Molecular Microbiology and Immunology (2012).
19 Behneman, Dana.* Doctor of Philosophy, Epidemiology (2012).
20 Golozar, Asieh.* Doctor of Philosophy, Epidemiology (2012).
21 Keet, Corinne. Doctor of Philosophy, Epidemiology (2014).
22 Weitzner, Brian.* Doctor of Philosophy, Chemical and Biomolecular Engineering (2015).
23 Lee, Sun Eun. Doctor of Philosophy, International Health (2015).
24 He, Bing. Doctor of Philosophy, Biostatistics (2017).
25 Bomotti, Samantha.* Doctor of Philosophy, Epidemiology (2017).
26 Fu, Jack. Doctor of Philosophy, Biostatistics (2018).
27 Qi, Guanghao. Doctor of Philosophy, Biostatistics (2020).
28 Berube, Sophie. Doctor of Philosophy, Biostatistics (2021).
29 Chen, Athena. Doctor of Philosophy, Biostatistics (2022).

Classroom Instruction - Principal Instructor

○ 140.615 Statistics for Laboratory Scientists I (2007 – 2024).
○ 140.616 Statistics for Laboratory Scientists II (2002, 2007 – 2024).
○ 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).
○ 140.686 Advanced Methods for Statistical Genetics and Genomics (2022).
○ 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).
○ First Year Student Seminar Series, Department of Biostatistics, Johns Hopkins School of Public Health (2020 – 2021).

RESEARCH GRANT PARTICIPATION *The solid dots ● indicate grants to IR.*

Ongoing Research Support

● *Defining the Role of Viral Infections and Autoantibodies in COPD Progression (NHLBI R01).*
Dates: July 2024 - April 2028. Principal Investigators: Craig Hersh and Ingo Ruczinski.
Responsibility: Principal Investigator.

● *Differences Between the Sexes among Genetic Variants Affecting Orofacial Cleft Birth Defect Risk (NIDCR R01).*
Dates: April 2022 - March 2025. Principal Investigators: Mary Marazita and Ingo Ruczinski.
Responsibility: Principal Investigator.

○ *HIV Prevention Trials Network (NIAID UM1).*
Dates: December 2022 - November 2024. Principal Investigator: Susan Eshleman.
Responsibility: Co-Investigator.

○ *Data Center for Acute to Chronic Pain Biosignatures (NIDA U54).*
Dates: September 2019 - July 2024. Principal Investigator: Martin Lindquist.
Responsibility: Co-Investigator.

Completed

- *Design and Analysis of Displayed Peptidomes (NIGMS R01).*
  Dates: April 2020 - March 2024. **Principal Investigators:** Ben Larman and Ingo Ruczinski.
  Responsibility: Principal Investigator.

- *Genetic Epidemiology of COPD (NHLBI U01).*
  Dates: September 2017 - July 2022. **Principal Investigators:** Terri Beaty and Ingo Ruczinski.
  Responsibility: Site Principal Investigator.

- *Integrative Computational Biology Approaches to Identify Functional Determinants of Platelet Aggregation in African Americans and European Americans (NHLBI R01).*
  Dates: June 2018 - May 2021. **Principal Investigators:** Rasika Mathias and Ingo Ruczinski.
  Responsibility: 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.
  Responsibility: Principal Investigator.

- *Methods Development and Secondary Analyses for an Oral Clefts Association Study (NIDCR R03).*
  Dates: July 2011 - June 2014. **Principal Investigator:** Ingo Ruczinski.
  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.
  Responsibility: Principal Investigator.

- *Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases (NHLBI R01).*
  Dates: September 2007 - July 2011. **Principal Investigator:** Ingo Ruczinski.
  Responsibility: Principal Investigator.

- *Adaptive Function Estimation for Genomic Data (NIGMS R01).*
  Dates: September 2003 - August 2007. **Principal Investigator:** Ingo Ruczinski.
  Responsibility: Principal Investigator.

- *Analysis of SNP Data using Logic Regression (MDHMM).*
  Dates: July 2002 - June 2004. **Principal Investigator:** Ingo Ruczinski.
  Responsibility: Principal Investigator.

- *Using All-Atom Potentials to Improve Protein Structure Prediction (JHU Faculty Innovation).*
  Dates: July 2002 - June 2003. **Principal Investigator:** Ingo Ruczinski.
  Responsibility: Principal Investigator.

- *LEAP Whole Genome Sequencing Project (NIAID UM1).*
  Dates: September 2015 - January 2024. **Principal Investigator:** Rasika Mathias.
  Responsibility: Co-Investigator.

- *New Approaches for Empowering Studies of Asthma in Populations of African Descent (NHLBI R01).*
  Dates: October 2011 - November 2023. **Principal Investigator:** Kathleen Barnes.
  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 - November 2022. **Principal Investigator:** Susan Eshleman.
  Responsibility: Co-Investigator.

- *Atopic Dermatitis Research Network (NIAID U19).*
  Dates: June 2015 - March 2021. **Principal Investigator:** Rasika Mathias.
  Responsibility: Co-Investigator.

- *Integrative Analysis of Tissue Specific Transcriptomics to Identify Platelet Aggression Genes (NHLBI R21).*
  Dates: September 2017 - August 2020. **Principal Investigator:** Rasika Mathias.
  Responsibility: Co-Investigator.

- *Role of PUFA-Gene Interactions in Health Disparities (R01)*
  Dates: March 2017 - February 2019. **Principal Investigator:** Floyd Chilton.
  Responsibility: Co-Investigator.

- *Integrative Genomics in Asthmatics of African Ancestry (NHLBI R01).*
  Dates: December 2014 - November 2018. **Principal Investigator:** Kathleen Barnes.
  Responsibility: Co-Investigator.

- *A Software Framework for Exploring 1,000 Genomes of African Descent (NHLBI R01).*
  Dates: July 2015 - June 2018. **Principal Investigator:** Steven Salzberg.
  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.
  Responsibility: Co-Investigator.

- *Genetic Epidemiology of COPD (NHLBI R01).*
  Dates: August 2012 - July 2017. **Principal Investigator:** Terri Beaty.
  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.
  Responsibility: Co-Investigator.

- *Preprocessing and Analysis Tools for Contemporary Microarray Applications (NIGMS R01).*
  Dates: April 2012 - August 2016. **Principal Investigator:** Rafael Irizarry.
  Responsibility: Co-Investigator.

- *Online Mendelian Inheritance in Man: OMIM (NHGRI U41).*
  Dates: June 2015 - May 2016. **Principal Investigator:** Ada Hamosh.
  Responsibility: Co-Investigator.

- *Atopic Dermatitis Research Network Grant. (National Jewish Health subcontract)*
  Dates: July 2010 - June 2015. **Principal Investigator:** Kathleen Barnes.
  Responsibility: Co-Investigator.

- *International Genetic Epidemiology of Oral Clefts (NIDCR R01).*
  Dates: September 2009 - May 2015. **Principal Investigator:** Terri Beaty.
  Responsibility: Co-Investigator.

- *Oral Clefts: Moving from Genome Wide Studies Toward Functional Genomics (NIDCR U01).*
  Dates: May 2010 - April 2014. **Principal Investigator:** Terri Beaty.
  Responsibility: Co-Investigator.

- *Schizophrenia Heterogeneity and Toxplasma Exposure (NIMH R01).*
  Dates: December 2010 - November 2013. **Principal Investigator:** Dimitri Avramopoulos.
  Responsibility: Co-Investigator.

- *Plasma Proteomic Biomarker Indicators of Micronutrient Deficiency (Bill and Melinda Gates Foundation).*
  Dates: January 2010 - September 2012. **Principal Investigator:** Keith West.
  Responsibility: Co-Investigator.

- *Preprocessing and Analysis Tools for Contemporary Microarray Applications (NIGMS R01).*
  Dates: September 2007 - March 2012. **Principal Investigator:** Rafael Irizarry.
  Responsibility: Co-Investigator.

- *Institute for Clinical and Translational Research (NCRR UL1 Supplement).*
  Dates: September 2009 - August 2011. **Principal Investigator:** Daniel Ford.
  Responsibility: Co-Investigator.

- *Genome-Wide Associations Environmental Interactions in the Lung Health Study (NHLBI U01).*
  Dates: July 2009 - June 2011. **Principal Investigator:** Kathleen Barnes.
  Responsibility: Co-Investigator.

○ *Institute for Clinical and Translational Research (NCRR UL1).*
Dates: September 2007 - May 2011. **Principal Investigator:** Daniel Ford.
Responsibility: Co-Investigator.

○ *Hierarchical Models in Health Services Research (NIDDK R01).*
Dates: September 2007 - October 2010. **Principal Investigator:** Tom Louis.
Responsibility: Co-Investigator.

○ *DNA Repair, Skin Cancer and Overall Cancer Risk (NCI R01).*
Dates: July 2005 - March 2010. **Principal Investigator:** Anthony Alberg.
Responsibility: Co-Investigator.

○ *Genotypic Determinants of Aspirin Response in High Risk Families (NIH U01).*
Dates: January 2008 - October 2009. **Principal Investigator:** Lewis Becker.
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.
Responsibility: Co-Investigator.

○ *Protecting Childrens & Womens Health through Global Control (Bill and Melinda Gates Foundation).*
Dates: March 2009 - June 2009. **Principal Investigator:** Keith West.
Responsibility: Co-Investigator.

○ *Genetic Influences on Age-Related Decline In Strength (NIA R01).*
Dates: February 2005 - December 2007. **Principal Investigator:** Brock Beamer.
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.
Responsibility: Co-Investigator.

○ *Johns Hopkins Center in Urban Environmental Health (NIEHS P30).*
Dates: April 2003 - September 2007. **Principal Investigator:** Scott Zeger.
Responsibility: Co-Investigator.

○ *Gene-Gene Interaction Involved In Nasopharyngeal Carcinoma (NCI R01).*
Dates: September 2005 - August 2006. **Principal Investigator:** Yin Yao Shugart.
Responsibility: Co-Investigator.

○ *Gene-Environment Interactions: The Odyssey Cohort (NCI U01).*
Dates: September 1999 - June 2004. **Principal Investigator:** Kathy Helzlsouer.
Responsibility: Co-Investigator.

○ *Modeling of Mass Spectrometry MALDI Data (DARPA).*
Dates: July 2003 - December 2003. **Principal Investigator:** Fernando Pineda.
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, 2021).

- Director, Biostatistics in Cancer Epidemiology Pre-Doctoral Training Program (2010 – 2014).
- Chair, Biostatistics Events Committee (2012 – 2016).
- Chair, Faculty Recruitment Committee (2013, 2020).
- Chair, Biostatistics Retreat Planning Committee (2013).
- Biostatistics Centennial Month Coordinator (2016).
- Oncology Biostatistics Chair Recruitment Committee (2020).
- Member, Biostatistics Retreat Planning Committee (2024).
- Co-Leader, "Berlin Accord" Faculty Awards Committee (2015 – present).
- Co-Leader, Statistical Genetics Working Group (2017 – present).

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 – 2007).
- 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, 2023, 2024).

PRESENTATIONS

Scientific Meetings

1. *Detecting And Quantifying Antibody Reactivity In Phip-Seq Data.*
   Computational Biology meets Data Science, Oaxaca, Mexico (2023).

2. *Detection of Rare Disease Variants in Extended pedigrees using RVS.*
   Bioconductor Developer Meeting, New York, NY (2019).

3. *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).

4. *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).

5. *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).

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

28 *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).

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

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

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

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

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

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

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

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

37 *Assessing Variants in the Human Genome.*
Institute for Prevention Research and Medicine, Bremen, Germany (2010).

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

61 *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).

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Invited Seminars

87 *Statistical and Computational Aspects in the Analysis of Genomic Data from Family Based Designs.*
Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA (2021).

88 *Statistical and Computational Aspects in the Analysis of Genomic Data from Family Based Designs.*
Department of Biostatistics and Computational Biology, University of Rochester, NY (2019).

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

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

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

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

93 *Research Integrity: the Importance of Data Integrity (Panel Discussion).*
Deans Research Integrity Lecture Series, Johns Hopkins School of Medicine, Baltimore, MD (2013)

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

111 *On Missing Data in SNP Association Studies, and What to Do About Them.*
Department of Epidemiology, Johns Hopkins School of Public Health, Baltimore, MD (2007).

112 *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).

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

130 *Logic Regression*.
General Electric, Schenectady, NY (2002).

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

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

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

Other Meetings and Events

134 *Bayesian Genome-Wide Association Studies - A Primer*.
Johns Hopkins Statistical Genetics Group Meeting, Baltimore, MD (2019).

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

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

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

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

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

140 *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).

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

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

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

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

145 *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).

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

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

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

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

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

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

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

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

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

155 *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).

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

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

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

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

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

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

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

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

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

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