Updated August 28, 2018

CURRICULUM VITAE

MARGARET A. TAUB

PERSONAL DATA

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EDUCATION AND TRAINING

Degrees

PhD	2009	University of California, Berkeley	Statistics
BS	1999	Harvard University	Mathematics

Postdoctoral Training

Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2009-2012

Visiting

Department of Mathematical Sciences, University of Copenhagen, Denmark, 2018

PROFESSIONAL EXPERIENCE

2013-	Assistant Scientist, Public Health Studies Program Johns Hopkins Zanvyl Krieger School of Arts and Sciences
2012-	Assistant Scientist, Department of Biostatistics Johns Hopkins Bloomberg School of Public Health
2012-	Member, Center for Computational Biology Johns Hopkins University
2009-2012	Postdoctoral Fellow, Department of Biostatistics Johns Hopkins Bloomberg School of Public Health
Summer 2005	Research Assistant, Burchard Asthma Genetics Lab University of California, San Francisco

Summer 2004 Research Intern, Genomics Collaborations Group
Affymetrix Inc.

2003-2009 Graduate Student Researcher/Instructor, Department of Statistics
University of California, Berkeley

2000-2003 Associate, Applied Decision Analysis Group
Standard & Poor's

PROFESSIONAL ACTIVITIES

Society Membership & Leadership

American Society of Human Genetics
American Statistical Association
Co-organizer, R-Ladies Baltimore (2018-)

Program Development

Session Chair, American Society of Human Genetics, 2017
Abstract Reviewer, American Society of Human Genetics, 2018

EDITORIAL ACTIVITIES

Peer Review Activities

Referee for*:*
Biostatistics, BMC Bioinformatics, Statistical Applications in Genetics and Molecular Biology, Biometrics, Annals of Applied Statistics, European Journal of Human Genetics, Genome Medicine, Circulation, Bioinformatics

Ad Hoc Review of Proposals

National Institute of Dental and Craniofacial Research (2017, 2018)
MS Research Australia: Peer review of Postdoctoral Fellowship Application (2017)

HONORS AND AWARDS

2017 Johns Hopkins Center for Educational Resources Technology Fellowship
2011 Best Contribution, Statistical Challenges and Biomedical Applications of Deep Sequencing Data Workshop, Ascona, Switzerland.

2007 Outstanding Graduate Student Instructor, University of California, Berkeley.

PUBLICATIONS

Published Peer-Reviewed Articles: (* denotes equal contribution)

[1] 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. Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. *Genetic Epidemiology* (To appear)

[2] Keramati AR, Yanek LR, Iyer K, **Taub MA**, Ruczinski I, Becker DM, Becker LC, Faraday N, Mathias RA. Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. *Platelets*. 2018 Mar 19:1-7.

[3] Holzinger ER, Li Q, Parker MM, Hetmanski JB, Marazita ML, Mangold E, Ludwig KU, **Taub MA**, Begum F, Murray JC, Albacha-Hejazi H, Alqosayer K, Al-Souki G, Albasha Hejazi A, Scott AF, Beaty TH, Bailey-Wilson JE. Analysis of sequence data to identify potential risk variants for oral clefts in multiplex families. *Mol Genet Genomic Med*. 2017 Aug 9.

[4] Carlson JC, **Taub MA**, Feingold E, Beaty TH, Murray JC, Marazita ML, Leslie EJ. Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. *Birth Defects Res*. 2017 Apr 22.

[5] 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; **CAAPA Consortium**. Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome. *Sci Rep*. 2017 Apr 21

[6] Collado-Torres L, Nellore A, Kammers K, Ellis SE, **Taub MA**, Hansen KD, Jaffe AE, Langmead B, Leek JT. recount: A large-scale resource of analysis-ready RNA-seq expression data. *Nature Biotechnology*, 2017 April 11.

[7] Kammers K, **Taub MA**, Ruczinski I, Martin J, Yanek LR, Frazee A, Gao Y, Hoyle D, Faraday N, Becker DM, Cheng L, Wang ZZ, Leek JT, Becker LC, Mathias RA. Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis. *PLoS One*, 2017 Jan 20.

[8] Shringarpure SS, Mathias RA, Hernandez RD, O'Connor TD, Szpiech ZA, Torres R, De La Vega FM, Bustamante CD, Barnes KC, **Taub MA**; CAAPA consortium. Using genotype array data to compare multi- and single-sample variant calls and improve variant call sets from deep coverage whole-genome sequencing data. *Bioinformatics*. 2016 Dec 29

[9] Xiao Y, **Taub MA**, Ruczinski I, Begum F, Hetmanski JB, Schwender H, Leslie EJ, Koboldt DC, Murray JC, Marazita ML, Beaty TH. Evidence for SNP-SNP interaction identified through targeted sequencing of cleft case-parent trios. *Genet Epidemiol*. 2016 Dec 26

[10] Gomez-Cabrero D, Almgren M, Sjöholm LK, Hensvold AH, Ringh MV, Tryggvadottir R, Kere J, Scheynius A, Acevedo N, Reinius L, **Taub MA**, Montano C, Aryee MJ, Feinberg JI, Feinberg AP, Tegnér J, Klareskog L, Catrina AI, Ekström TJ. High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. *Genome Med*. 2016 Nov 22;8(1):124

[11] Mathias RA, **Taub MA**, Gignoux CR, Fu W, Musharoff S, O'Connor TD, Vergara C, Torgerson DG, Pino-Yanes M, Shringarpure SS, Huang L, Rafaels N, Boorgula MP, Johnston HR, Ortega VE, Levin AM, Song W, Torres R, Padhukasahasram B, Eng C, Mejia-Mejia DA, Ferguson T, Qin ZS, Scott AF, Yazdanbakhsh M, Wilson JG, Marrugo J, Lange LA, Kumar R, Avila PC, Williams LK, Watson H, Ware LB, Olopade C, Olopade O, Oliveira R, Ober C, Nicolae DL, Meyers D, Mayorga A, Knight-Madden J, Hartert T, Hansel NN, Foreman MG, Ford JG, Faruque MU, Dunston GM, Caraballo L, Burchard EG, Bleecker E, Araujo MI, Herrera-Paz EF, Gietzen K, Grus WE, Bamshad M, Bustamante CD, Kenny EE, Hernandez RD, Beaty TH, Ruczinski I, Akey J; CAAPA., Barnes KC. A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. *Nat Commun*. 2016 Oct 11;7:12522

[12] Kessler MD, Yerges-Armstrong L, **Taub MA**, Shetty AC, Maloney K, Jeng LJ, Ruczinski I, Levin AM, Williams LK, Beaty TH, Mathias RA, Barnes KC; Consortium on Asthma among African-ancestry Populations in the Americas (CAAPA)., O'Connor TD. Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. *Nat Commun*. 2016 Oct 11;7:12521

[13] Montano C, **Taub MA**, Jaffe A, Briem E, Feinberg JI, Trygvadottir R, Idrizi A, Runarsson A, Berndsen B, Gur RC, Moore TM, Perry RT, Fugman D, Sabunciyan S, Yolken RH, Hyde TM, Kleinman JE, Sobell JL, Pato CN, Pato MT, Go RC, Nimgaonkar V, Weinberger DR, Braff D, Gur RE, Fallin MD, Feinberg AP. Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. *JAMA Psychiatry*. 2016 May 1;73(5):506-14.

[14] Gao L, Emond MJ, Louie T, Cheadle C, Berger AE, Rafaels N, Vergara C, Kim Y, **Taub MA**, Ruczinski I, Mathai SC, Rich SS, Nickerson DA, Hummers LK, Bamshad MJ, Hassoun PM, Mathias RA; National Heart, Lung, and Blood Institute GO Exome Sequencing Project, Barnes KC. Identification of Rare Variants in ATP8B4 as a Risk Factor for Systemic Sclerosis by Whole-Exome Sequencing. *Arthritis Rheumatol*. 2016 Jan;68(1):191-200

[15] Leslie EJ*, **Taub MA***, Liu H, Steinberg KM, Koboldt DC, Zhang Q, Carlson JC, Hetmanski JB, Wang H, Larson DE, Fulton RS, Kousa YA, Fakhouri WD, Naji A, Ruczinski I, Begum F, Parker MM, Busch T, Standley J, Rigdon J, Hecht JT, Scott AF,

Wehby GL, Christensen K, Czeizel AE, Deleyiannis FW, Schutte BC, Wilson RK, Cornell RA, Lidral AC, Weinstock GM, Beaty TH, Marazita ML, Murray JC. 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. *Am J Hum Genet*. 2015 Mar 5;96(3):397-411

[16] Zeledón M, Eckart N, **Taub M**, Vernon H, Szymanski M, Wang R, Chen P-L, Nestadt G, McGrath JA, Sawa A, Pulver AE, Avramopoulos D,Valle D. Identification and Functional Studies of Regulatory Variants Responsible for the Association of NRG3 with a Delusion Phenotype in Schizophrenia. *Molecular Neuropsychiatry*, 2015;1:36-46.

[17] Neumann C, **Taub MA**, Younkin SG, Beaty TH, Ruczinski I, Schwender H. Analytic power and sample size calculation for the genotypic transmission/disequilibrium test in case-parent trio studies. *Biometrical Journal*, 2014 Nov;56(6):1076-92.

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

[19] Bureau A, Parker MM, Ruczinski I, **Taub MA**, Marazita ML, Murray JC, Mangold E, Noethen MM, Ludwig KU, Hetmanski JB, Bailey-Wilson JE, Cropp CD, Li Q, Szymczak S, Albacha-Hejazi H, Alqosayer K, Field LL, Wu-Chou YH, Doheny KF, Ling H, Scott AF, Beaty TH. Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. *Genetics*. 2014 May 2

[20] Wu T, Schwender H, Ruczinski I, Murray JC, Marazita ML, Munger RG, Hetmanski JB, Parker MM, Wang P, Murray T, **Taub M**, Li S, 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. Evidence of gene-environment interaction for two genes on chromosome 4 and environmental tobacco smoke in controlling the risk of nonsyndromic cleft palate. *PLoS One*, 2014 Feb 6;9(2)

[21] **Taub MA**, Schwender HR, Younkin SG, Louis TA, Ruczinski I. On multi-marker tests for association in case-control studies. *Front. Genet*. 2013, **4:**252

[22] Montaño CM, Irizarry RA, Kaufmann WE, Talbot K, Gur RE, Feinberg AP, **Taub MA**. Measuring cell-type specific differential methylation in human brain tissue. *Genome Biology* 2013, **14**:R94

[23] 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. Confirming genes influencing risk to cleft lip with/without cleft palate in a case-parent trio study. *Human Genetics*, 2013; AOP March 20.

[24] Liu Y, Aryee MJ, Padyukov L, Fallin MD, Hesselberg E, Runarsson A, Reinius L, Acevedo N, **Taub M**, Ronninger M, Shchetynsky K, Scheynius A, Kere J, Alfredsson L, Klareskog L, Ekström TJ, Feinberg AP. Epigenome-wide association data implicate DNA methylation as

an intermediary of genetic risk in rheumatoid arthritis. *Nature Biotechnology*, 2013; 31(2):142-7.

[25] Leek JT, **Taub MA**, Rasgon JL. A statistical approach to selecting and confirming validation targets in -omics experiments. *BMC Bioinformatics*, 2012; 13:150.

[26] Murray T*, **Taub MA***, Ruczinski I, Scott AF, Hetmanski JB, Schwender H, Patel P, Zhang TX, Munger RG, Wilcox AJ, Ye X, Wang H, Wu, T, Wu-Chou YH, Shi B, Sun HJ, Chong SS, Yeow V, Murray JC, Marazita ML, Beaty TH. Examining markers in 8q24 to explain differences in evidence for association with cleft lip with/without cleft palate between Asians and Europeans. *Genetic Epidemiology*, 2012; 36(4):392-9.

[27] **Taub MA**, Schwender H, Beaty TH, Louis TA, Ruczinski I. Incorporating genotype uncertainties into the genotypic TDT for main effects and gene-environment interactions. *Genetic Epidemiology*, 2012; 36(3):225-34.

[28] Schwender H, **Taub MA**, Beaty TH, Marazita ML, Ruczinski I. Rapid testing of SNPs and gene-environment interactions in case-parent trio data based on exact analytic parameter estimation. *Biometrics*, 2012; 68(3):766-73

[29] Leek JT, **Taub MA**, Pineda F. Cooperation between referees and authors increases review accuracy. *PLoS ONE*, 2011; 6(11):e26895

[30] Niranjan TS*, Adamczyk A*, Corrada Bravo H*, **Taub M**, Wheelan SJ, Irizarry RA, Wang T. Effective detection of rare variants in pooled DNA samples using Cross-pool tailcurve analysis. *Genome Biology*, 2011; 12:R93.

[31] **Taub MA**, Corrada Bravo H, Irizarry RA. Overcoming bias and systematic errors in next generation sequencing data. *Genome Medicine*, 2010; 2(12):87.

[32] **Taub MA**, Lipson D, Speed TP. Methods for allocating ambiguous short-reads. *Communications in Information and Systems, Special Issue in Honor of Mike Waterman*. 2010; Vol. 10, No. 2.

[33] Choudhry S*, **Taub M***, Mei R, Rodriguez-Santana J, Rogriguez-Cintron W, Shriver MD, Ziv E, Risch NJ, Burchard EG. Genome-wide screen for asthma in Puerto Ricans: evidence for association with 5q23 region. *Human Genetics*, 2008; 123(5):455-68.

[34] Zhang C, Bailey DK, Awad T, Liu G, Xing G, Cao M, Valmeekam V, Retief J, Matsuzaki H, **Taub M**, Seielstad M, Kennedy GC. A whole genome long-range haplotype (WHLRH) test for detecting imprints of positive selection in human populations. *Bioinformatics*, 2006; 22(17):2122-8.

Under Review (* denotes equal contribution)

[35] Daya M, / · · · ~50 authors · · · /, **Taub MA**, Ruczinski I, Mathias RA, and Barnes KC on behalf of the CAAPA consortium (2018). Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations.

[36] Fu J, Kammers K, Nellore A, Collado-Torres L, Leek JT, **Taub MA** (2018). RNA-seq transcript quantification from reduced-representation data in recount2.

[37] Sherman RM, / · · · ~50 authors · · · /, **Taub MA**, Beaty TH, Ruczinski I, Mathias RA, Barnes KC on behalf of CAAPA, Salzberg SL. (2018). Assembly of the pan-genome of humans of African descent reveals nearly 300 megabases of novel DNA.

[38] Boorgula MP*, **Taub MA***, Rafaels N, Daya M, Campbell MS, 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.

CURRICULUM VITAE

MARGARET A. TAUB

Part II

TEACHING

Advisees

Jing Li, ScM Biostatistics, 2018
Linda Gai, ScM Biostatistics (in progress), 2018

Academic Advisees

Lisa Rein, ScM Biostatistics, 2012-2013
Ji Soo Kim, ScM Biostatistics, 2014-2015
Wenyi Lin, ScM Biostatistics, 2015-2016
Jing Li, ScM Biostatistics, 2016-2017

Thesis Advisory Committee Participation

Julia Pringle, PhD Molecular Microbiology and Immunology (in progress), 2016-present

Preliminary Oral Participation

Margaret Parker, PhD Epidemiology, 2014 (alternate)

Final Oral Participation

Margaret Parker, PhD Epidemiology, 2015

Classroom Instruction (JHU):

Year	Course/Description	Enrollment
2012-present	Public Health Biostatistics (AS280.345) Public Health Studies Krieger School of Arts and Sciences Johns Hopkins University	165-220
2013-present	Advanced Biostatistics Lab (AS280.346) Public Health Studies Krieger School of Arts and Sciences Johns Hopkins University	11-23

2017-present Health Data Analysis Practicum (AS280.347)16-20
Public Health Studies
Krieger School of Arts and Sciences
Johns Hopkins University

Guest lecturer (JHU):

140.688 Statistics for Genomics (2010)
140.616 Statistics for Laboratory Scientists (2017)

Workshops and Short Courses:

Integrated statistical analysis of genome scale data. *Cold Spring Harbor Laboratory, NY*. June 21-22, 2010.

Statistical analysis of gene expression data with R and Bioconductor. *University of Copenhagen, Denmark*. August 17-21, 2009.

Statistics with R for Biologists. *University of California, Berkeley*. July 7-11, 2008

RESEARCH GRANT PARTICIPATION

Ongoing Research Support

Expanded analysis of whole genome sequence data in cleft case-parent trios (NIDCR R03).
Dates: Sept 2017-June 2019. Principal-investigators: Margaret A. Taub, PhD and Terri Beaty, PhD.
Objectives: Using whole genome sequencing data from case-parent trios supported by the Gabriella Miller Kids First Pediatric Research Program, to develop and implement novel statistical tools for analyzing sequence data in family-based studies of oral clefts
Responsibility: Co-Principal Investigator

Statistical Models for Biological and Technical Variation in RNA Sequencing (NIGMS R01)
Dates: Sept 2013-April 2019. Principal Investigator: Jeffrey T. Leek, PhD.
Objectives: We propose to develop statistical methods and software for analyzing RNA-seq data, accounting for biological and technological errors.
Role: Co-Investigator

HIV and Hepatitis C. Pathogenesis & the Human Genome (NIDA R01)
Dates: Sept 2014-August 2019. Principal Investigator: David Thomas, MD, MPH.
Objectives: The purpose of this research is to investigate how persons with, or at risk for, HIV recover from Hepatitis C virus (HCV) infection.
Role: Co-Investigator

Overall Atopic Dermatitis Research Network Grant (ADRN2) (NIAID U19)
Dates: April 2017-March 2020. Principal Investigator: Donald Leung, PhD, MD.
Objectives: The primary objective of the studies is to improve our understanding of mechanisms underlying cutaneous host defense, by determining the cause of different phenotypes of atopic dermatitis (AD) including Staphylococcus aureus (S. aureus) colonization, eczema herpeticum (EH) and severe AD.
Role: Co-Investigator

Integrative analysis of tissue specific transcriptomics with GTEx data to identify platelet aggregation genes (NHLBI R21)
Dates: Sept 2017-Aug 2019. Principal Investigator: Rasika A. Mathias, PhD.
Objectives: We propose the integration of genomics and transcriptomics to uncover the determinants of high residual heritability relying on cutting edge approaches of transcriptomic imputation.
Role: Co-Investigator

Multi-omic studies of asthma in an African ancestry population (NIH R01)
Dates: Feb 2018-Jan2019. Principal Investigator: Kathleen Barnes, PhD.
We will assist in the analysis of transcriptomic and microbiome data from nasal epithelial cells to characterize the human-commensal interaction associated with atopic asthma.
Role: Co-Investigator

Integrative computational biology approaches to identify functional determinants of platelet aggregation in African Americans and European Americans (NHLBI R01)
Dates: May 2018-April 2020. Principal Investigators: Rasika A. Mathias, PhD and Ingo Ruczinski, PhD.
Objectives: We propose the integration of whole genome DNA and RNA sequencing to understand the true biological mechanism of action of the previously identified genetic associations, and to uncover the determinants of high residual heritability with this multi-omics approach.
Role: Co-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.

Completed Research Support

A Family Based Exome Sequencing Approach to Identify Platelet Aggregation Genes (NHLBI R01)
Dates: Sept 2012-May 2018. Principal Investigator: Rasika A. Mathias, PhD.
Objectives: The goal of this project is to lead to a better understanding of the role of genetic variants (common and rare) in the determination of platelet aggregation native and post-ASA, including possible racial differences, and should enable genotypic tailoring of preventive therapy for CHD in high-risk individuals.
Role: Co-Investigator

Strategic Mapping of Tissue and Population Methylation for Mental Health Research (NIH U01)
Dates: April 2014-March 2018. Principal Investigator: Andrew P. Feinberg, MD, MPH.
Objectives: Our primary focus will be on discovering differentially/variably methylated regions in mental health relevant GTEx brain samples, using a large number of samples from these regions.
Role: Co-Investigator

ACADEMIC SERVICE

Johns Hopkins University:

2011, 2012	Member, organizing committee for Young Investigator Symposium on Genomics and Bioinformatics, Johns Hopkins University.
2017-present	Representative from Biostatistics to Faculty Senate

Johns Hopkins Department of Biostatistics:

2016-present	"Ombudsperson" for students
2016-present	Organizer, Biostatistics Women's Lunch series
2017	Member, departmental committee on alternative funding sources ("Los Prosperos")

PRESENTATIONS

Invited Seminars:

Telomere length estimation and analysis from WGS data. *Statistics and Probability Theory Monday Lunch Seminar*, University of Copenhagen Department of Mathematical Sciences, April 30, 2018.

Megakaryocytes derived from iPSCs show concordant eQTLs across racial groups and platelet-related signature of CD41+CD42a+ percentage. *Johns Hopkins Genomics and Bioinformatics Symposium*, October 13, 2016.

Incorporating genotype uncertainties into the genotypic transmission-disequilibrium test. *Department of Biostatistics and Epidemiology, University of Pennsylvania*. February 29, 2012.

Incorporating genotype uncertainties into the genotypic transmission-disequilibrium test. *Department of Statistics & Bioinformatics Center, University of Copenhagen, Denmark*. February 10, 2012.

Incorporating genotype uncertainties into the genotypic transmission-disequilibrium test. *Public Health Sciences Division, Fred Hutchinson Cancer Research Center*. February 1, 2012.

Incorporating genotype uncertainties into the genotypic transmission-disequilibrium test. *Department of Statistics, University of British Columbia*. January 19, 2012.

Some observations about analyzing imputed trio data with the genotypic TDT. *GENEVA Steering Committee Meeting, Washington DC*. December 12, 2011.

Understanding technical artifacts in studies to detect single nucleotide variants using Illumina high-throughput sequencing. *NIH/NCI Biostatistics Seminar*. May 4, 2011.

Incorporating genotyping uncertainties into the genotypic TDT. *Genetic Epidemiology Seminar, Johns Hopkins University*. March 28, 2011.

Detection of single-nucleotide variants with high throughput sequencing. *Young Investigator Symposium on Genomics and Bioinformatics, Johns Hopkins University*. September 23, 2010.

A method for allocating ambiguous short reads. *UC Berkeley Statistics and Genomics Seminar, Berkeley, CA*. March 5, 2009.

Population structure in genetic association studies. *Walter and Eliza Hall Institute for Medical Research Bioinformatics Seminar, Melbourne, Australia*. July 4, 2006.

Scientific Meetings (Invited):

Telomere length estimation and analysis from WGS data. *New Statistical Methods for Family-Based Sequencing Studies*, Banff International Research Station, August 9, 2018.

Computational Validation of NGS Variant Calls using Genotype Data. *INFORMS Annual Meeting, Philadelphia, PA*. November 2, 2015.

Efficient multi-marker tests for association in case-control studies. *ENAR, Washington DC*. April 2, 2012.

The effects of low-level choices on detecting genetic variants with high-throughput sequencing. *Statistical Challenges and Biomedical Applications of Deep Sequencing Data Conference, Ascona, Switzerland*. June 6, 2011. Winner: Best Contribution

Detection of single-nucleotide variants with high throughput sequencing. *Joint Statistical Meetings, Vancouver, BC*. August 2, 2010.

Detection of single-nucleotide variants with high throughput sequencing. *Workshop: Statistical Genomics in Biomedical Research, Banff International Research Station*. July 20, 2010.

Methods for allocating ambiguous short reads. *Workshop: Gene expression based on sequencing technologies. University of Copenhagen, Denmark*. August 24, 2009.

Scientific Meetings (Contributed):

Measuring cell-type specific differential methylation in human brain tissue. *WNAR, Honolulu, HI*. June 17, 2014.

Scientific Meetings (Poster Presentations):

Novel genetic loci identified for telomere length leveraging 50,000 whole genome sequences in the Trans-Omics for Precision Medicine (TOPMed) project. *American Society of Human Genetics, San Diego, CA*, Oct 18, 2018.

Telomere length estimation and analysis on large scale whole-genome sequencing data. *American Society of Human Genetics, Orlando, Florida*, Oct 18, 2017.

Gene expression analysis of megakaryocytes (MKs) derived from induced pluripotent stem cells (iPSCs) shows platelet-related signature of CD41+CD42a+ percentage. *American Society of Human Genetics, Vancouver, Canada*, Oct 20, 2016

Sequencing of *PEAR1* to identify novel genetic determinants of platelet aggregation. *American Society of Human Genetics, Baltimore, MD*. Oct 7, 2015.

Computational validation of next-generation sequencing calls using genotype array data. *American Society of Human Genetics, San Diego, CA*. Oct 21, 2014.

Whole genome sequencing in African American families to identify genetic determinants of platelet hyper-aggregation following aspirin, *American Society of Human Genetics, Boston, MA*. Oct. 24, 2013

The presence of technical artifacts in studies to detect single nucleotide variants using Illumina high-throughput sequencing. *ENAR, Miami*. March 20, 2011.