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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

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
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

American Society of Human Genetics
American Statistical Association

EDITORIAL ACTIVITIES

Served as *referee* for*:*

Biostatistics, BMC Bioinformatics, Statistical Applications in Genetics and Molecular Biology, Biometrics

HONORS AND AWARDS

2011 Best Contribution, Statistical Challenges and Biomedical Applications of Deep Sequencing Data, Ascona, Switzerland.

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

PUBLICATIONS

Journal Articles: (* denotes equal contribution)

[1] 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

[2] 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

[3] Zeledón M., Eckart N., **Taub M**., Vernon H., Szymanski M., Wang R., Chen P.-L., Nestadt G., McGrath J.A., Sawa A, Pulver A.E., 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.

[4] 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.

[5] 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.

[6] 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

[7] 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)

[8] **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

[9] 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

[10] 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.

[11] 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.

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

[13] 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.

[14] **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.

[15] 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

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

[17] 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.

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

[19] **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.

[20] 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.

[21] 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.

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Part II

TEACHING

Master's Advisees

Lisa Rein, ScM Biostatistics, 2012
Ji Soo Kim, ScM Biostatistics, 2014
Wenyi Lin, ScM Biostatistics, 2015

Preliminary Oral Participation

Margaret Parker, PhD Epidemiology, 2014 (alternate)

Final Oral Participation

Margaret Parker, PhD Epidemiology, 2015

Classroom Instruction (JHU):

AS280.345 Public Health Biostatistics (2012, 2013, 2014, 2015)
AS280.346 Advanced Biostatistics Lab (2012, 2013, 2014, 2015)

Guest lecturer (JHU):

140.688.01 Statistics for Genomics (2010)

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

ACADEMIC SERVICES

Johns Hopkins University:

2011, 2012 Member, organizing committee for Young Investigator Symposium on Genomics and Bioinformatics, Johns Hopkins University.

PRESENTATIONS

Invited Seminars:

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):

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.

Poster Presentations:

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.