

Genevieve L. Wojcik, PhD MHS

Department of Genetics, Stanford University School of Medicine, Stanford CA, USA

E-mail: gwojcik@stanford.edu Phone: 413.530.4338 Webpage: <https://www.genevieve-wojcik.com>

CURRICULUM VITAE

I am a statistical geneticist and genetic epidemiologist whose research focuses on method development for diverse populations, as well as elucidating genetic susceptibility to infectious disease and vaccine response and host-pathogen co-evolution. My current research focuses on leveraging the complex ancestry of large-scale admixed populations, instead of overcoming it, for disease mapping. I was recently the chief analyst in a collaboration with an international team of academics and Illumina, Inc. to develop the GWAS scaffold on the Multi-Ethnic Genotyping Array (MEGA) products and the Global Screening Array (GSA). I am currently a postdoctoral fellow within the Department of Genetics at Stanford University with Dr. Carlos D. Bustamante.

Education

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

PhD, Epidemiology

December 2013

Area of Concentration: Genetic Epidemiology

MHS, Human Genetics/Genetic Epidemiology

May 2010

Certificate in Vaccine Science and Policy

Cornell University, Ithaca NY

BA, Biology

May 2008

Area of Concentration: Genetics and Development, French

Research Experience

Postdoctoral Research Scholar

2014-Present

Stanford University School of Medicine, Stanford CA

Advisor: Dr. Carlos D. Bustamante, Department of Genetics

Graduate Research Assistant

2009-2014

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

Advisor: Dr. Priya Duggal, Department of Epidemiology

Student Researcher

2007-2008

Cornell University, Ithaca NY

Advisor: Dr. Andrew Clark, Department of Molecular Biology and Genetics

Student Summer Researcher

2007

Cornell University, Ithaca NY

Advisor: Dr. Paula Cohen, Department of Biomedical Sciences, Genetics

Research Assistant

2005

Baystate Medical Center, Springfield MA

Department of Clinical Research

Summer Student Intern

2003, 2006

University of Massachusetts, Amherst MA

Advisor: Dr. Sandra Petersen, Department of Veterinary and Animal Sciences

Innovation

I was chief analyst in a large international team of academics, in collaboration with Illumina Inc., to design the GWAS scaffold for a range of Multi-Ethnic Genotyping Array (MEGA) products (MEGA, MEGA^{EX}, MEGA^{AFR/AMR}, MEGA^{EAS/EUR/SAS} and the Global Screening Array). These arrays are designed to leverage knowledge from the latest large-scale population sequencing studies and clinically relevant variants from biomedical databases, to enable low cost biobanking in very large samples sizes. As of 3rd quarter 2017 over **6M commercial units of these arrays** have been sold (see pre-print article below).

Honors and Awards

- ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist** 2016
American Society of Human Genetics, Vancouver BC
“Large-scale characterization of admixed populations and extensions of admixture mapping within the Population Architecture using Genomics and Epidemiology (PAGE)-II Study”
- ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist** 2015
American Society of Human Genetics, Baltimore MD
“Tag SNP selection for low frequency variant imputation in populations of diverse ancestry”
- The Charlotte Silverman Award Recipient** 2013
Johns Hopkins Bloomberg School of Public Health, Baltimore MD
Department of Epidemiology
- The Charlotte Ferencz Fellowship** 2012-2013
Johns Hopkins Bloomberg School of Public Health, Baltimore MD
Department of Epidemiology
- The Johns Hopkins Vaccine Initiative, Vaccine Day Poster Winner** 2012
Johns Hopkins Bloomberg School of Public Health, Baltimore MD
“Genome-wide Association Study of Response to Oral Poliovirus Vaccine in Bangladeshi Children”
- Mary Meyers Scholar, recognizing the top two doctoral students in the department** 2010-2012
Johns Hopkins Bloomberg School of Public Health, Baltimore MD
Department of Epidemiology
- Dean’s List** 2008
Cornell University, Ithaca NY

Publications

- 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; 7, 46398
- Martin AR, Gignoux CR, Walters RK, **Wojcik GL**, Neale BM, Gravel S, Daly MJ, Bustamante CD, Kenny EE. “Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations.” *Am J Hum Genet* 2017, 100(4), 635-649.

- Bien SA, **Wojcik GL**, Zubair N, Gignoux CR, Martin AR, Kocarnik JM, Martin LW, Buyske S, Haessler J, Walker RW, Cheng I, Graff M, Xia L, Franceschini N, Matise T, James R, Hindorff L, Le Marchand L, North KE, Haiman CA, Peters U, Loos RJF, Kooperberg CL, Bustamante CD, Kenny EE, Carlson CS. “Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array” *PloS one* 2016, 11(12), e0167758.
- Fan YH, Roy S, Mukhopadhyay R, Kapoor A, Duggal P, **Wojcik GL**, Pass RF, Arav-Boger R. “Role of Nucleotide Binding Oligomerization Domain 1 (NOD1) and its variants in Human Cytomegalovirus Control *in vitro* and *in vivo*” *PNAS* 2016, 113(48), E7818-E7827.
- 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, 7, 12521.
- **Wojcik GL**, Kao WH, Duggal P. “Relative performance of gene- and pathway-level methods as secondary analyses for genome-wide association studies” *BMC Genet* 2015, 16(34).
- Zignego AL, **Wojcik GL**, Cacoub P, Visentini M, Casato M, Mangia A, Latanich R, Charles E, Gragnani L, Terrier B, Piazzola V, Dustin L, Khakoo S, Busch M, Lauer G, Kim A, Alric L, Thomas D, Duggal P. Genome-wide association study of hepatitis C virus- and cryoglobulin-related vasculitis. *Genes and Immunity* 2014, 15, 500-505.
- **Wojcik GL**, Thio CL, Kao WHL, Latanich R, Goedert JJ, Mehta SH, Kirk GD, Peters MG, Cox AL, Kim AY, Chung RT, Thomas DL, Duggal P. Admixture analysis of spontaneous hepatitis C virus clearance in individuals of African descent. *Genes and Immunity* 2014, 15, 241-246.
- **Wojcik GL**, Mosbrugger T, Latanich R, Astemborski J, Kirk GL, Kim A, Seaberg EC, Busch M, Thomas DL, Duggal P, Thio CL. Variants in HAVCR1 gene region contribute to Hepatitis C persistence in African Americans. *Journal of Infectious Diseases* 2014, 209 (3): 355-359
- Duggal P, Thio C, **Wojcik GL**, Goedert JJ, Mangia A, Latanich R, Kim AY, Lauer GM, Chung RT, Peters MG, Kirk GD, Mehta SH, Cox AL, Khakoo SI, Alric L, Cramp ME, Donfield SM, Edlin BR, Tobler LH, Busch MP, Alexander G, Rosen HR, Gao X, Abdel-Hamid M, Apps R, Carrington M, Thomas DL. Genome-wide association study of spontaneous resolution of hepatitis C virus infection: data from multiple cohorts. *Annals of Internal Medicine* 2013, 158(4): 235-245.
- Arav-Boger R, **Wojcik GL**, Duggal P, Ingersoll RG, Beaty T, Pass RF, Yolken RH. Polymorphisms in Toll-like receptor genes influence antibody responses to cytomegalovirus glycoprotein B vaccine. *BMC Res Notes* 2012, 5:140.
- Jaffe A*, **Wojcik G***, Chu A, Golozar A, Maroo A, Duggal P, Klein AP. Identification of functional genetic variation in exome sequence analysis. *BMC Proc* 2011, 5(9): S13 [**shared first authorship*]

Published on Pre-Print Server

- **Wojcik GL**, Marie C, Abhyankar MM, Yoshida N, Watanabe K, Mychaleckyj J, Kirkpatrick BD, Rich SS, Concannon P, Haque R, Tsokos GC, Petri Jr. WA, Duggal P. “Genome-Wide Association Study Reveals Genetic Link Between Diarrhea-Associated *Entamoeba histolytica* Infection and Inflammatory Bowel Disease” *bioRxiv* 2017. <https://doi.org/10.1101/137448>
- Belbin GM, Odis J, Sorokin EP, Yee MC, Kohli S, Glicksberg BS, Gignoux CR, **Wojcik GL**, Van Vleck T, Jeff JM, Linderman M, Schurmann C, Ruderfer D, Cai X, Merkelson A, Justice AE, Young KL, Graff M, North KE, Peter U, James R, Hindorff L, Kornreich R, Edelmann L, Gottesman O, Stahl EEA, Cho J, Loos RJF, Bottinger EP, Nadkarni GN, Abul-Husn NS, Kenny EE. “Genetic Identification Of A Common Collagen Disease In Puerto Ricans Via Identity-By-Descent Mapping In A Health System” *bioRxiv*

2017. <https://doi.org/10.1101/141820>

- Daya M, Rafaels N, Chavan S, Johnston HR, Shetty A, Gignoux CR, Boorgula MP, Campbell M, Maul P, Maul T, Vergara C, Levin AM, **Wojcik G**, Torgerson DG, Ortega VE, Doumatey A, Araujo MI, Avila PC, Bleecker E, Bustamante C, Caraballo L, Dunston GM, Faruque MU, Ferguson T, Figueiredo C, Ford JG, Garraud PA, Hansel NN, Hernandez RD, Herrera-Paz EF, Kenny EE, Knight-Madden J, Kumar R, Lange LA, Lange EM, Lizee A, Mayorga A, Meyers D, Nicolae DL, O'Connor TD, Oliveira RR, Olopade CO, Olopade O, Qin ZS, Rotimi C, Watson H, Wilks RJ, Williams KL, Wilson JG, Ober C, Burchard EG, Beaty TH, Taub MA, Ruczinski I, Mathias RA, Barnes KC. "Genome-wide association study of asthma in individuals of African ancestry reveals novel asthma susceptibility loci" *bioRxiv* 2017. <https://doi.org/10.1101/105551>
- **Wojcik GL**, Fuchsberger C, Taliun D, Welch R, Martin AR, Shringarpure S, Carlson CS, Abecasis G, Kang HM, Boehnke M, Bustamante CD, Gignoux CR, and Kenny EE. "Imputation aware tag SNP selection to improve power for large, multi-ethnic association studies" *bioRxiv* 2017. <https://doi.org/10.1101/112953>

Platform and Invited Talks

- **Wojcik GL** (invited session) "Improved strategies to leverage complex genetic architecture for trait mapping in diverse admixed populations" **American Society of Human Genetics (ASHG)**, Orlando FL, *October 2017
- **Wojcik GL**, Graff M, Haessler J, Belbin GM, Sorokin EP, Bustamante CD, Gignoux CR, Kenny EE, PAGE-II Study. "Testing the generalizability of current GWAS findings within the multi-ethnic PAGE-II Study" **Society of Molecular Biology and Evolution**, Austin TX, 2017
- **Wojcik GL** (invited panelist) "The Meaning of Race: Examining the Role of Race and Ethnicity in Genomic Research and Medicine" **ELSI Congress**, Farmington CT, 2017
- **Wojcik GL**. "Genetic characterization of admixed populations within the Population Architecture using Genomics and Epidemiology (PAGE)-II Study demonstrates wide spectrum of diversity" **Stanford Center for Computational, Evolutionary, and Human Genomics (CEHG)**, Stanford CA, 2017
- **Wojcik GL**, Marie C, Mychaleckyj J, Rich SS, Concannon P, Haque R, Kirkpatrick BD, Petri Jr. WA, Duggal P. "Genetic links between symptomatic *Entamoeba histolytica* infection and inflammatory bowel disease" **American Society of Tropical Medicine and Hygiene (ASTMH)**, Atlanta GA, 2016
- **Wojcik GL**, Nishimura K, Reiner A, Hodonsky C, Shringarpure S, Belbin G, Conomos MP, Haessler J, Thornton TA, Laurie C, Hindorff L, James R, Haiman C, LeMarchand L, Matisse T, Buyske S, Thyagarajan B, Carlson C, Loos R, North KE, Avery C, Kooperberg C, Bustamante CD, Gignoux CR, Kenny EE, on behalf of the PAGE Study. "Large-scale characterization of admixed populations and extensions of admixture mapping within the Population Architecture using Genomics and Epidemiology (PAGE)-II Study" **American Society of Human Genetics (ASHG)**, Vancouver BC, 2016
- **Wojcik GL**. "Leveraging large-scale diverse multi-ethnic data to improve precision medicine for all" **Illumina Array Seminar: San Francisco**, San Francisco CA, 2016
- **Wojcik GL**. "Participant privacy in a large multi-ethnic consortium: exercises and thoughts in the PAGE-II Consortium" **NIH/NHGRI Aggregate Genomics Workshop**, Rockville MD, 2016
- **Wojcik GL**, Mondal D, Alam M, Mychaleckyj J, Rich S, Concannon P, Haque R, Petri WA, Duggal P. "Age-dependent genetic associations with *Cryptosporidium* infection in Bangladeshi children" **American Society of Tropical Medicine and Hygiene (ASTMH)**, Atlanta GA, 2012

Teaching Experience

Assistant, Stanford Data Carpentry Workshop, Stanford CA

Data Carpentry Genomics Workshop 2017

Instructor, Stanford University School of Medicine, Stanford CA

Configuration of the US Healthcare System and the Application of Big Data/Analytics 2016

Demo Facilitator, Stanford University School of Medicine, Stanford CA

AVID CEHG Outreach 2016

Teaching Assistant, Johns Hopkins Bloomberg School of Public Health, Baltimore MD

Infectious Disease Dynamics, 4th Term 2013

Principles of Genetic Epidemiology, 1st Term 2012

Summer Institute Population Genetics 2011, 2012

Methods for Linkage Analysis in Genetic Epidemiology, 4th Term 2010, 2011, 2012

Epidemiological Methods III, 3rd Term (Lead TA) 2012

Epidemiological Methods III, 3rd Term 2010, 2011

Principles of Epidemiology, Summer Term 2009

Introduction to Population Genetics, 2nd Term 2009

Introduction to Genetic Epidemiology, 1st Term 2009

Volunteer Instructor, Community Educational Outreach, Baltimore, MD

STARS (Students Teaching and Reaching Students) Instructor 2008-2013

Teaching Assistant, Cornell University, Ithaca NY

BioG112: Current Topics in Biology and Society 2008

BioGD281: Genetics 2007, 2008

Biology and Genetics Tutor 2007, 2008

BioBM330: Biochemistry 2006

Service

Peer Reviewer

Genes & Immunity, International Society for Computational Biology, Virology, Science Translational Medicine

2015-present

President, Epidemiology Student Organization

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

2011-2012

Chair, STARS (Students Teaching and Reaching Students)

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

2009-2010

Student Mentor

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

2009-2013

Volunteer, STARS (Students Teaching and Reaching Students)

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

2008-2013

Volunteer EMT-Basic

Dryden Ambulance, Dryden NY

2007-2008

Scientific Consortia

- Participating analyst, NHGRI, The Genome Sequencing Program, Center for Common Disease Genomics, 2016-present
- Participating analyst, Sanger/Stanford Big Data Initiative, The Oceanic Genome Variation Project Consortium (Design and Analysis group), 2014-present
- Participating analyst, NHGRI, The Population Architecture using Genomics and Epidemiology Study (Analysis Committee, Chip Design Working Group, Clinically Relevant Variant Working Group, Inflammatory Trait Group), 2013-present

Professional Membership

- American Society of Tropical Medicine and Hygiene (2012-Present)
- American Society of Human Genetics (2010-Present)
- International Genetic Epidemiology Society (2010-Present)