

Genevieve L. Wojcik, PhD MHS

Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore MD, USA

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CURRICULUM VITAE

I am an Assistant Professor of Epidemiology at the Johns Hopkins Bloomberg School of Public Health in Baltimore, Maryland. As a statistical geneticist and genetic epidemiologist, my research focuses on method development for diverse populations, as well as elucidating genetic susceptibility to infectious disease and vaccine response. As infectious disease burden falls mostly on populations of non-European descent, I have developed and applied tools for complex trait mapping in diverse populations. For the past several years, I have been a lead analyst for two major multi-ethnic NHGRI consortia: the Population Architecture using Genomics and Epidemiology (PAGE) Study and the Genome Sequencing Program (GSP). These projects have utilized my training in expertise in multiple complementary fields, including statistical genetics, traditional epidemiology, and population genetics. I am also currently the co-chair of the Complex Disease Working Group of NHGRI's Clinical Genome Resource (ClinGen), which has developed an updated framework for polygenic risk score reporting and is developing disease-specific best practices with an eye towards downstream clinical utility.

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

Professional Experience

Assistant Professor

2019-present

Johns Hopkins Bloomberg School of Public Health, Baltimore MD

Department of Epidemiology

Postdoctoral Research Scholar

2014-2019

Stanford University School of Medicine, Stanford CA

Advisor: Dr. Carlos D. Bustamante, Departments of Genetics, Biomedical Data Science

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

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.

Honors and Awards

ASHG Reviewer's Choice Abstract Award American Society of Human Genetics, Vancouver BC <i>"The influence of population structure on complex trait architecture: Insights from the PAGE study"</i>	2018
ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist American Society of Human Genetics, Vancouver BC <i>"Large-scale characterization of admixed populations and extensions of admixture mapping within the Population Architecture using Genomics and Epidemiology (PAGE)-II Study"</i>	2016
ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist American Society of Human Genetics, Baltimore MD <i>"Tag SNP selection for low frequency variant imputation in populations of diverse ancestry"</i>	2015
The Charlotte Silverman Award Recipient Johns Hopkins Bloomberg School of Public Health, Baltimore MD Department of Epidemiology	2013
The Charlotte Ferencz Fellowship Johns Hopkins Bloomberg School of Public Health, Baltimore MD Department of Epidemiology	2012-2013
The Johns Hopkins Vaccine Initiative, Vaccine Day Poster Winner Johns Hopkins Bloomberg School of Public Health, Baltimore MD <i>"Genome-wide Association Study of Response to Oral Poliovirus Vaccine in Bangladeshi Children"</i>	2012
Mary Meyers Scholar, recognizing the top two doctoral students in the department Johns Hopkins Bloomberg School of Public Health, Baltimore MD Department of Epidemiology	2010-2012
Dean's List Cornell University, Ithaca NY	2008

Publications

1. Wand H, Lambert SA, Tamburro C, Iacocca MA, O'Sullivan JW, Sillari C, Kullo IJ, Rowley R, Dron JS, Brockman D, Venner E, McCarthy MI, Antoniou AC, Easton DF, Hegele RA, Khera AV, Chatterjee N, Kooperberg C, Edwards K, Vlessis K, Kinnear K, Danesh JN, Parkinson H, Ramos EM, Roberts MC, Ormond KE, Khoury MJ, Janssens ACJW, Goddard KAB, Kraft P, MacArthur JAL, Inouye M, **Wojcik GL**. [Improving reporting standards for polygenic scores in risk prediction studies](#). *Nature*, in press.
2. Lopez Pineda A, Pourshafeie A, Ioannidis A, Leibold CM, Chan AL, Bustamante CD, Frankovich J, **Wojcik GL**. [Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients](#). *J Biomed Inform*. 2020 Dec 28;113:103664. doi: 10.1016/j.jbi.2020.103664. Epub ahead of print. PMID: 33359113.
3. Vergara C, Duggal P, Thio CL, Valencia A, O'Brien TR, Latanich R, Timp W, Johnson EO, Kral AH, Mangia A, Goedert JJ, Piazzola V, Mehta SH, Kirk GD, Peters MG, Donfield SM, Edlin BR, Busch MP, Alexander G, Murphy EL, Kim AY, Lauer GM, Chung RT, Cramp ME, Cox AL, Khakoo SI, Rosen HR, Alric L, Wheelan SJ, **Wojcik GL**, Thomas DL, Taub MA. [Multi-ancestry fine mapping of interferon lambda and the outcome of acute hepatitis C virus infection](#). *Genes Immun*. 2020 Nov;21(5):348-359. doi: 10.1038/s41435-020-00115-3. Epub 2020 Oct 28. PubMed PMID: 33116245; PubMed Central PMCID: PMC7657970.
4. Baldassari AR, Sitlani CM, Highland HM, Arking DE, Buyske S, Darbar D, Gondalia R, Graff M, Guo X, Heckbert SR, Hindorff LA, Hodonsky CJ, Ida Chen YD, Kaplan RC, Peters U, Post W, Reiner AP, Rotter JI, Shohet RV, Seyerle AA, Sotoodehnia N, Tao R, Taylor KD, **Wojcik GL**, Yao J, Kenny EE, Lin HJ, Soliman EZ, Whitsel EA, North KE, Kooperberg C, Avery CL. [Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex](#)

- [Traits](#). *Circ Genom Precis Med*. 2020 Aug;13(4):e002680. doi: 10.1161/CIRCGEN.119.002680. Epub 2020 Jun 30. PubMed PMID: 32602732; PubMed Central PMCID: PMC7520945.
5. Ioannidis AG, Blanco-Portillo J, Sandoval K, Hagelberg E, Miquel-Poblete JF, Moreno-Mayar JV, Rodríguez-Rodríguez JE, Quinto-Cortés CD, Auckland K, Parks T, Robson K, Hill AVS, Avila-Arcos MC, Sockell A, Homburger JR, **Wojcik GL**, Barnes KC, Herrera L, Berríos S, Acuña M, Llop E, Eng C, Huntsman S, Burchard EG, Gignoux CR, Cifuentes L, Verdugo RA, Moraga M, Mentzer AJ, Bustamante CD, Moreno-Estrada A. [Native American gene flow into Polynesia predating Easter Island settlement](#). *Nature*. 2020 Jul;583(7817):572-577. doi: 10.1038/s41586-020-2487-2. Epub 2020 Jul 8. PubMed PMID: 32641827.
 6. Fernández-Rhodes L, Young KL, Lilly AG, Raffield LM, Highland HM, **Wojcik GL**, Agler C, Love SM, Okello S, Petty LE, Graff M, Below JE, Divaris K, North KE. [Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations](#). *Circ Res*. 2020 Jun 5;126(12):1816-1840. doi: 10.1161/CIRCRESAHA.120.315893. Epub 2020 Jun 4. PubMed PMID: 32496918; PubMed Central PMCID: PMC7285892.
 7. Walker RW, Belbin GM, Sorokin EP, Van Vleck T, **Wojcik GL**, Moscati A, Gignoux CR, Cho J, Abul-Husn NS, Nadkarni G, Kenny EE, Loos RJJ. [A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank](#). *J Hepatol*. 2020 Jun;72(6):1070-1081. doi: 10.1016/j.jhep.2020.01.029. Epub 2020 Mar 5. PubMed PMID: 32145261.
 8. Hodonsky CJ, Baldassari AR, Bien SA, Raffield LM, Highland HM, Sittani CM, **Wojcik GL**, Tao R, Graff M, Tang W, Thyagarajan B, Buyske S, Fornage M, Hindorff LA, Li Y, Lin D, Reiner AP, North KE, Loos RJJ, Kooperberg C, Avery CL. [Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics](#). *BMC Genomics*. 2020 Mar 14;21(1):228. doi: 10.1186/s12864-020-6626-9. PubMed PMID: 32171239; PubMed Central PMCID: PMC7071748.
 9. **Wojcik GL**, Korpe P, Marie C, Mentzer AJ, Carstensen T, Mychaleckyj J, Kirkpatrick BD, Rich SS, Concannon P, Faruque ASG, Haque R, Petri WA Jr, Duggal P. [Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates PRKCA](#). *mBio*. 2020 Feb 4;11(1). doi: 10.1128/mBio.03343-19. PubMed PMID: 32019797; PubMed Central PMCID: PMC7002356.
 10. Bien SA, **Wojcik GL**, Hodonsky CJ, Gignoux CR, Cheng I, Matise TC, Peters U, Kenny EE, North KE. [The Future of Genomic Studies Must Be Globally Representative: Perspectives from PAGE](#). *Annu Rev Genomics Hum Genet*. 2019 Aug 31;20:181-200. doi: 10.1146/annurev-genom-091416-035517. Epub 2019 Apr 12. PubMed PMID: 30978304.
 11. Vishnu A, Belbin GM, Wojcik GL, Bottinger EP, Gignoux CR, Kenny EE, Loos RJJ. [The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans](#). *Am J Clin Nutr*. 2019 Jul 1;110(1):16-23. doi: 10.1093/ajcn/nqz098. PubMed PMID: 31161206; PubMed Central PMCID: PMC6599741.
 12. **Wojcik GL**, Graff M, Nishimura KK, Tao R, Haessler J, Gignoux CR, Highland HM, Patel YM, Sorokin EP, Avery CL, Belbin GM, Bien SA, Cheng I, Cullina S, Hodonsky CJ, Hu Y, Huckins LM, Jeff J, Justice AE, Kocarnik JM, Lim U, Lin BM, Lu Y, Nelson SC, Park SL, Poisner H, Preuss MH, Richard MA, Schurmann C, Setiawan VW, Sockell A, Vahi K, Verbanck M, Vishnu A, Walker RW, Young KL, Zubair N, Acuña-Alonso V, Ambite JL, Barnes KC, Boerwinkle E, Bottinger EP, Bustamante CD, Caberto C, Canizales-Quinteros S, Conomos MP, Deelman E, Do R, Doheny K, Fernández-Rhodes L, Fornage M, Hailu B, Heiss G, Henn BM, Hindorff LA, Jackson RD, Laurie CA, Laurie CC, Li Y, Lin DY, Moreno-Estrada A, Nadkarni G, Norman PJ, Pooler LC, Reiner AP, Romm J, Sabatti C, Sandoval K, Sheng X, Stahl EA, Stram DO, Thornton TA, Wassel CL, Wilkens LR, Winkler CA, Yoneyama S, Buyske S, Haiman CA, Kooperberg C, Le Marchand L, Loos RJJ, Matise TC, North KE, Peters U, Kenny EE, Carlson CS. [Genetic analyses of diverse populations improves discovery for complex traits](#). *Nature*. 2019 Jun;570(7762):514-518. doi: 10.1038/s41586-019-1310-4. Epub 2019 Jun 19. PubMed PMID: 31217584; PubMed Central PMCID: PMC6785182.
 13. Huddart R, Fohner AE, Whirl-Carrillo M, **Wojcik GL**, Gignoux CR, Popejoy AB, Bustamante CD, Altman RB, Klein TE. [Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research](#). *Clin Pharmacol Ther*. 2019 May;105(5):1256-1262. doi: 10.1002/cpt.1322. Epub 2019 Jan 21. PubMed PMID: 30506572; PubMed Central PMCID: PMC6465129.
 14. Vergara C, Thio CL, Johnson E, Kral AH, O'Brien TR, Goedert JJ, Mangia A, Piazzolla V, Mehta SH, Kirk GD, Kim AY, Lauer GM, Chung RT, Cox AL, Peters MG, Khakoo SI, Alric L, Cramp ME, Donfield SM, Edlin BR, Busch MP, Alexander G, Rosen HR, Murphy EL, Latanich R, **Wojcik GL**, Taub MA, Valencia A, Thomas DL, Duggal P. [Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C](#)

- [Virus](#). Gastroenterology. 2019 Apr;156(5):1496-1507.e7. doi: 10.1053/j.gastro.2018.12.014. Epub 2018 Dec 26. PubMed PMID: 30593799; PubMed Central PMCID: PMC6788806.
15. Daya M, Rafaels N, Brunetti TM, Chavan S, Levin AM, Shetty A, Gignoux CR, Boorgula MP, **Wojcik G**, Campbell M, Vergara C, Torgerson DG, Ortega VE, Doumatey A, Johnston HR, Acevedo N, Araujo MI, Avila PC, Belbin G, Bleecker E, Bustamante C, Caraballo L, Cruz A, Dunston GM, Eng C, Faruque MU, Ferguson TS, Figueiredo C, Ford JG, Gan W, Gourraud PA, Hansel NN, Hernandez RD, Herrera-Paz EF, Jiménez S, Kenny EE, Knight-Madden J, Kumar R, Lange LA, Lange EM, Lizee A, Maul P, Maul T, Mayorga A, Meyers D, Nicolae DL, O'Connor TD, Oliveira RR, Olopade CO, Olopade O, Qin ZS, Rotimi C, Vince N, Watson H, Wilks RJ, Wilson JG, Salzberg S, Ober C, Burchard EG, Williams LK, Beaty TH, Taub MA, Ruczinski I, Mathias RA, Barnes KC. [Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations](#). Nat Commun. 2019 Feb 20;10(1):880. doi: 10.1038/s41467-019-08469-7. PubMed PMID: 30787307; PubMed Central PMCID: PMC6382865.
 16. Schurz H, Kinnear CJ, Gignoux C, **Wojcik G**, van Helden PD, Tromp G, Henn B, Hoal EG, Möller M. [A Sex-Stratified Genome-Wide Association Study of Tuberculosis Using a Multi-Ethnic Genotyping Array](#). Front Genet. 2018;9:678. doi: 10.3389/fgene.2018.00678. eCollection 2018. PubMed PMID: 30713548; PubMed Central PMCID: PMC6346682.
 17. **Wojcik GL**, Fuchsberger C, Taliun D, Welch R, Martin AR, Shringarpure S, Carlson CS, Abecasis G, Kang HM, Boehnke M, Bustamante CD, Gignoux CR, Kenny EE. [Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies](#). G3 (Bethesda). 2018 Oct 3;8(10):3255-3267. doi: 10.1534/g3.118.200502. PubMed PMID: 30131328; PubMed Central PMCID: PMC6169386.
 18. **Wojcik GL**, Marie C, Abhyankar MM, Yoshida N, Watanabe K, Mentzer AJ, Carstensen T, Mychaleckyj J, Kirkpatrick BD, Rich SS, Concannon P, Haque R, Tsokos GC, Petri WA Jr, Duggal P. [Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated Entamoeba histolytica Infection and Inflammatory Bowel Disease](#). MBio. 2018 Sep 18;9(5). doi: 10.1128/mBio.01668-18. PubMed PMID: 30228239; PubMed Central PMCID: PMC6143743.
 19. Fregel R, Méndez FL, Bokbot Y, Martín-Socas D, Camalich-Massieu MD, Santana J, Morales J, Ávila-Arcos MC, Underhill PA, Shapiro B, **Wojcik G**, Rasmussen M, Soares AER, Kapp J, Sockell A, Rodríguez-Santos FJ, Mikdad A, Trujillo-Mederos A, Bustamante CD. [Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe](#). Proc Natl Acad Sci U S A. 2018 Jun 26;115(26):6774-6779. doi: 10.1073/pnas.1800851115. Epub 2018 Jun 12. PubMed PMID: 29895688; PubMed Central PMCID: PMC6042094.
 20. Belbin GM, Odgis 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, Peters U, James R, Hindorff L, Kornreich R, Edelmann L, Gottesman O, Stahl EE, Cho JH, Loos RJ, 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](#). Elife. 2017 Sep 12;6. doi: 10.7554/eLife.25060. PubMed PMID: 28895531; PubMed Central PMCID: PMC5595434.
 21. 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. [Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome](#). Sci Rep. 2017 Apr 21;7:46398. doi: 10.1038/srep46398. PubMed PMID: 28429804; PubMed Central PMCID: PMC5399604.
 22. 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 Apr 6;100(4):635-649. doi: 10.1016/j.ajhg.2017.03.004. Epub 2017 Mar 30. PubMed PMID: 28366442; PubMed Central PMCID: PMC5384097.
 23. 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 RJ, 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. doi: 10.1371/journal.pone.0167758. eCollection 2016. PubMed PMID: 27973554; PubMed Central PMCID: PMC5156387.

24. 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](#). Proc Natl Acad Sci U S A. 2016 Nov 29;113(48):E7818-E7827. doi: 10.1073/pnas.1611711113. Epub 2016 Nov 16. PubMed PMID: 27856764; PubMed Central PMCID: PMC5137695.
25. Kessler MD, Yerges-Armstrong L, Taub MA, Shetty AC, Maloney K, Jeng LJB, 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. doi: 10.1038/ncomms12521. PubMed PMID: 27725664; PubMed Central PMCID: PMC5062569.
26. **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 Apr 8;16:34. doi: 10.1186/s12863-015-0191-2. PubMed PMID: 25887572; PubMed Central PMCID: PMC4391470.
27. Zignego AL, **Wojcik GL**, Cacoub P, Visentini M, Casato M, Mangia A, Latanich R, Charles ED, Gragnani L, Terrier B, Piazzola V, Dustin LB, Khakoo SI, Busch MP, Lauer GM, Kim AY, Alric L, Thomas DL, Duggal P. [Genome-wide association study of hepatitis C virus- and cryoglobulin-related vasculitis](#). Genes Immun. 2014 Oct;15(7):500-5. doi: 10.1038/gene.2014.41. Epub 2014 Jul 17. PubMed PMID: 25030430; PubMed Central PMCID: PMC4208981.
28. **Wojcik GL**, Thio CL, Kao WH, 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 Immun. 2014 Apr;15(4):241-6. doi: 10.1038/gene.2014.11. Epub 2014 Mar 13. PubMed PMID: 24622687; PubMed Central PMCID: PMC4308959.
29. **Wojcik G**, Latanich R, Mosbrugger T, Astemborski J, Kirk GD, Mehta SH, Goedert JJ, Kim AY, Seaberg EC, Busch M, Thomas DL, Duggal P, Thio CL. [Variants in HAVCR1 gene region contribute to hepatitis C persistence in African Americans](#). J Infect Dis. 2014 Feb 1;209(3):355-9. doi: 10.1093/infdis/jit444. Epub 2013 Aug 20. PubMed PMID: 23964107; PubMed Central PMCID: PMC3883167.
30. Duggal P, Thio CL, **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](#). Ann Intern Med. 2013 Feb 19;158(4):235-45. doi: 10.7326/0003-4819-158-4-201302190-00003. PubMed PMID: 23420232; PubMed Central PMCID: PMC3638215.
31. 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 Mar 13;5:140. doi: 10.1186/1756-0500-5-140. PubMed PMID: 22414065; PubMed Central PMCID: PMC3317442.
32. 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 Nov 29;5 Suppl 9:S13. doi: 10.1186/1753-6561-5-S9-S13. PubMed PMID: 22373437; PubMed Central PMCID: PMC3287847. *shared first authorship

Pre-print Articles

1. Belbin GM, Wenric S, Cullina S, Blichsberg BS, Moscati A, **Wojcik GL**, Shemirani R, Beckmann ND, Cohain A, Sorokin EP, Park DS, Ambite JL, Ellis S, Auton A, CBIPM Genomics Team, Regeneron Genetics Center, Bottinger EP, Cho JH, Loos RJF, Abul-husn NS, Zaitlen NA, Gignoux CR, Kenny EE. "Towards a fine-scale population health monitoring system" *bioRxiv* (2019) 780668; doi: <https://doi.org/10.1101/780668>
2. Severson AL, Shortt JA, Mendex FL, Wojcik GL, Bustamante CD, Gignoux CR. "SNAPPY: Single Nucleotide Assignment of Phylogenetic Parameters on the Y chromosome" *bioRxiv* (2018) 454736; doi: <https://doi.org/10.1101/454736>

Platform and Invited Talks

- **2020:** Society for Epidemiological Research, Boston MA; University of California Berkeley, Berkeley CA; Eastern Virginia Medical School, Norfolk VA; Johns Hopkins Bloomberg School of Public Health, Baltimore MD; National Genetic Counselor Society Polygenic Risk Score Education Module (virtual).
- **2019:** American Society of Human Genetics, Houston TX; Genomic Medicine XII: Genomics and Risk Prediction, Silver Spring MD.
- **2018:** Chan Zuckerberg Initiative, San Francisco CA; Department of Human Genetics Pymatuning Retreat, University of Pittsburgh, Pittsburgh, PA; Genetics across Diverse Populations: Integration into Everyday Life, Stanford University, Stanford CA.
- **2017:** American Society of Human Genetics (ASHG), Orlando FL; Society of Molecular Biology and Evolution, Austin TX; Ethical, Legal, and Social Implications (ELSI) Congress, Farmington CT; Stanford Center for Computational, Evolutionary, and Human Genomics (CEHG), Stanford CA.
- **2016 and earlier:** American Society of Tropical Medicine and Hygiene (ASTMH), Atlanta GA; American Society of Human Genetics (ASHG), Vancouver BC, 2016; Illumina Array Seminar: San Francisco, San Francisco CA; NIH/NHGRI Aggregate Genomics Workshop, Rockville MD, 2016; American Society of Tropical Medicine and Hygiene (ASTMH), Atlanta GA, 2012.

Teaching Experience

Instructor, Johns Hopkins Bloomberg School of Public Health, Baltimore MD

Principles of Genetic Epidemiology 2 (340.732.01), Department of Epidemiology 2020-present

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