Matthew S. Zawistowski

Department of Biostatistics
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Education

Postdoctoral Research Fellow — September 2011 – September 2014
The University of Michigan - Ann Arbor, MI
Advisor: Gonçalo Abecasis

Ph.D. in Biostatistics (Statistical Genetics) — Defended July 2011
The University of Michigan - Ann Arbor, MI
Advisor: Sebastian Zöllner

M.S. in Biostatistics — May 2007
The University of Michigan - Ann Arbor, MI

M.S. in Mathematics — May 2005
Lehigh University - Bethlehem, PA

B.S. in Mathematics; minor: Computer Science — May 2003
Saint Joseph's University - Philadelphia, PA

Professional Positions

- Clinical Assistant Professor — January 2019 - Present
  Department of Biostatistics
  University of Michigan, Ann Arbor, MI

- Research Area Specialist Lead — May 2016 - December 2018
  Department of Biostatistics
  University of Michigan, Ann Arbor, MI

- Biostatistician, Research Health Science Specialist — May 2014- May 2016
  Veteran's Health Affairs, VA Ann Arbor Healthcare System
  Center for Clinical Management Research, Ann Arbor, MI

Teaching Experience

- Courses taught at University of Michigan School of Public Health:
    - Biostatistics 521: Applied Biostatistics (Fall 2018, 2019)
    - Biostatistics 501-777 (online): Introduction to Biostatistics (Fall 2019)
    - Public Health 383: Data Driven Solutions in Public Health (Winter 2018, 2020)
    - Public Health 610: Introduction to Public Health (Fall 2015-17)

- Big Data Summer Institute (BDSI), Undergraduate Summer Research Program
  Department of Biostatistics, University of Michigan
  Associate Director, 2019 - current
  Research Project Group Leader, Genomics (Summer 2018, 2019), Electronic Health Records (2017)

- Teaching Assistant, 2003 - 2005
  Lehigh University, Bethlehem, PA
  Calculus I, II & III and Business Math

- Adjunct Faculty Member, Summer 2004, 2005
  Cedar Crest College, Department of Mathematics, Allentown, PA
  Primary instructor for courses in Finite Mathematics and Probability & Statistics in the Lifelong Learning Program aimed at adult students returning to complete undergraduate degrees.

- Teaching Assistant, January 2002 – May 2003
  Saint Joseph's University, Philadelphia, PA
  Business Math course and Tutor in Learning Resource Center

Service Positions

Admissions Committee for Population and Health Science online MPH/MS program, University of Michigan School of Public Health

- Chair, Fall 2020 - Present
- Committee Member, Fall 2018 - Winter 2020

Academic Honors/Affiliations

Recipient of 2019 Gilbert Whitaker Grant for the Improvement of Teaching through University of Michigan Center for Research on Learning and Teaching
NIH Cell and Molecular Dermatology Post-Doctoral Training Program (UM, 2012-2013)
2010 American Society of Human Genetics Trainee Research Semifinalist Award
NIH Biostatistics Pre-Doctoral Training Program for Research in the Biosciences (UM, 2007-08)
NIH Genome Science Pre-Doctoral Training Program (UM, 2005-07)
Teaching Assistantship (Lehigh University Mathematics Department, 2003-05)
Phi Beta Kappa, 2003
Sigma Xi, The Scientific Research Society, 2003
Pi Mu Epsilon, Mathematics Honor Society, 2002
Saint Joseph's University Honors Graduate (General & Departmental Honors)
Presidential Scholarship to Saint Joseph's University

Peer-Reviewed Publications

1. Zheng T, Ellinghaus D, Juzenas S, Cossais F, Burmeister G, Mayr G, Jørgensen IF, Teder-Laving M, Skogholt AH, Chen S, Strege PR, Ito G, Banasik K, Becker T, Bokelmann F, Brunak S, Buch S, Clausnitzer H, Datz C; DBDS Consortium, Degenhardt F, Doniec M, Erikstrup C, Esko T, Forster M, Frey N, Fritsche LG, Gabrielsen ME, Gräßle T, Gsur A, Gross J, Hampe J, Hendricks A, Hinz S, Hveem K, Jongen J, Junker R, Karlsen TH, Hemmrich-Stanisak G, Kruis W, Kupcinskas J, Laubert T, Rosenstiel PC, Röcken C, Laudes M, Leendertz FH, Lieb W, Limperger V, Margetis N, Mätz-Rensing K, Németh CG, Ness-Jensen E, Nowak-Göttl U, Pandit A, Pedersen OB, Peleikis HG, Peuker K, Rodriguez CL, Rühlemann MC, Schniewind B, Schulzky M, Skieceviciene J, Tepel J, Thomas L, Uellendahl-Werth F, Ullum H, Vogel I, Volzke H, von Fersen L, von Schönfels W, Vanderwerff B, Wilking J, Wittig M, Zeissig S, Zobel M, **Zawistowski M**, Vacic V, Sazonova O, Noblin ES; 23andMe Research Team, Farrugia G, Beyder A, Wedel T, Kahlke V, Schafmayer C, D'Amato M, Franke A. Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. *Gut*. 2021 Apr 22:gutjnl-2020-323868. doi: 10.1136/gutjnl-2020-323868. Epub ahead of print. PMID: 33888516.

2. Jia X, Goes FS, Locke AE, Palmer D, Wang W, Cohen-Woods S, Genovese G, Jackson AU, Jiang C, Kvale M, Mullins N, Nguyen H, Pirooznia M, Rivera M, Ruderfer DM, Shen L, Thai K, **Zawistowski M**, Zhuang Y, Abecasis G, Akil H, Bergen S, Burmeister M, Chapman S, DelaBastide M, Juréus A, Kang HM, Kwok PY, Li JZ, Levy SE, Monson ET, Moran J, Sobell J, Watson S, Willour V, Zöllner S, Adolfsson R, Blackwood D, Boehnke M, Breen G, Corvin A, Craddock N, DiFlorio A, Hultman CM, Landen M, Lewis C, McCarroll SA, Richard McCombie W, McGuffin P, McIntosh A, McQuillin A, Morris D, Myers RM, O'Donovan M, Ophoff R, Boks M, Kahn R, Ouwehand W, Owen M, Pato C, Pato M, Posthuma D, Potash JB, Reif A, Sklar P, Smoller J, Sullivan PF, Vincent J, Walters J, Neale B, Purcell S, Risch N, Schaefer C, Stahl EA, Zandi PP, Scott LJ. Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. *Mol Psychiatry*. 2021 Jan 22. doi: 10.1038/s41380-020-01006-9. Epub ahead of print. Erratum in: Mol Psychiatry. 2021 Mar 5;: PMID: 33483695.

3. Nielsen JB, Rom O, Surakka I, Graham SE, Zhou W, Roychowdhury T, Fritsche LG, Gagliano Taliun SA, Sidore C, Liu Y, Gabrielsen ME, Skogholt AH, Wolford B, Overton W, Zhao Y, Chen J, Zhang H, Hornsby WE, Acheampong A, Grooms A, Schaefer A, Zajac GJM, Villacorta L, Zhang J, Brumpton B, Løset M, Rai V, Lundegaard PR, Olesen MS, Taylor KD, Palmer ND, Chen YD, Choi SH, Lubitz SA, Ellinor PT, Barnes KC, Daya M, Rafaels N, Weiss ST, Lasky-Su J, Tracy RP, Vasan RS, Cupples LA, Mathias RA, Yanek LR, Becker LC, Peyser PA, Bielak LF, Smith JA, Aslibekyan S, Hidalgo BA, Arnett DK, Irvin MR, Wilson JG, Musani SK, Correa A, Rich SS, Guo X, Rotter JI, Konkle BA, Johnsen JM, Ashley-Koch AE, Telen MJ, Sheehan VA, Blangero J, Curran JE, Peralta JM, Montgomery C, Sheu WH, Chung RH, Schwander K, Nouraie SM, Gordeuk VR, Zhang Y, Kooperberg C, Reiner AP, Jackson RD, Bleecker ER, Meyers DA, Li X, Das S, Yu K, LeFaive J, Smith A, Blackwell T, Taliun D, Zollner S, Forer L, Schoenherr S, Fuchsberger C, Pandit A, **Zawistowski M**, Kheterpal S, Brummett CM, Natarajan P, Schlessinger D, Lee S, Kang HM, Cucca F, Holmen OL, Åsvold BO, Boehnke M, Kathiresan S, Abecasis GR, Chen YE, Willer CJ, Hveem K. Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nat Commun*. 2020 Dec 18;11(1):6417. doi: 10.1038/s41467-020-20086-3. PMID: 33339817; PMCID: PMC7749177.

4. Goldstein JA, Weinstock JS, Bastarache LA, Larach DB, Fritsche LG, Schmidt EM, Brummett CM, Kheterpal S, Abecasis GR, Denny JC, **Zawistowski M**. LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. *PLoS Genet.* 2020 Nov 11;16(11):e1009077. doi: 10.1371/journal.pgen.1009077. PMID: 33175840; PMCID: PMC7682892.

5. Richer J, Hill HL, Wang Y, Yang ML, Hunker KL, Lane J, Blackburn S, Coleman DM, Eliason J, Sillon G, D'Agostino MD, Jetty P, Mongeon FP, Laberge AM, Ryan SE, Fendrikova-Mahlay N, Coutinho T, Mathis MR, **Zawistowski M**, Hazen SL, Katz AE, Gornik HL, Brummett CM, Abecasis G, Bergin IL, Stanley JC, Li JZ, Ganesh SK. A Novel Recurrent COL5A1 Genetic Variant Is Associated With a Dysplasia-Associated Arterial Disease Exhibiting Dissections and Fibromuscular Dysplasia. *Arterioscler Thromb Vasc Biol.* 2020 Nov;40(11):2686-2699. doi: 10.1161/ATVBAHA.119.313885. Epub 2020 Sep 17. PMID: 32938213; PMCID: PMC7953329.

6. Saw J, Yang ML, Trinder M, Tcheandjieu C, Xu C, Starovoytov A, Birt I, Mathis MR, Hunker KL, Schmidt EM, Jackson L, Fendrikova-Mahlay N, **Zawistowski M**, Brummett CM, Zoellner S, Katz A, Coleman DM, Swan K, O'Donnell CJ; Million Veteran Program, Zhou X, Li JZ, Gornik HL, Assimes TL, Stanley JC, Brunham LR, Ganesh SK. Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. *Nat Commun*. 2020 Sep 4;11(1):4432. doi: 10.1038/s41467-020-17558-x. PMID: 32887874; PMCID: PMC7474092.

7. Zhou W, Brumpton B, Kabil O, Gudmundsson J, Thorleifsson G, Weinstock J, **Zawistowski M**, Nielsen JB, Chaker L, Medici M, Teumer A, Naitza S, Sanna S, Schultheiss UT, Cappola A, Karjalainen J, Kurki M, Oneka M, Taylor P, Fritsche LG, Graham SE, Wolford BN, Overton W, Rasheed H, Haug EB, Gabrielsen ME, Skogholt AH, Surakka I, Davey Smith G, Pandit A, Roychowdhury T, Hornsby WE, Jonasson JG, Senter L, Liyanarachchi S, Ringel MD, Xu L, Kiemeney LA, He H, Netea-Maier RT, Mayordomo JI, Plantinga TS, Hrafnkelsson J, Hjartarson H, Sturgis EM, Palotie A, Daly M, Citterio CE, Arvan P, Brummett CM, Boehnke M, de la Chapelle A, Stefansson K, Hveem K, Willer CJ, Åsvold BO. GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. *Nat Commun.* 2020 Aug 7;11(1):3981. doi: 10.1038/s41467-020-17718-z. PMID: 32769997; PMCID: PMC7414135.

8. Landi MT, Bishop DT, MacGregor S, Machiela MJ, Stratigos AJ, Ghiorzo P, Brossard M, Calista D, Choi J, Fargnoli MC, Zhang T, Rodolfo M, Trower AJ, Menin C, Martinez J, Hadjisavvas A, Song L, Stefanaki I, Scolyer R, Yang R, Goldstein AM, Potrony M, Kypreou KP, Pastorino L, Queirolo P, Pellegrini C, Cattaneo L, **Zawistowski M**, Gimenez-Xavier P, Rodriguez A, Elefanti L, Manoukian S, Rivoltini L, Smith BH, Loizidou MA, Del Regno L, Massi D, Mandala M, Khosrotehrani K, Akslen LA, Amos CI, Andresen PA, Avril MF, Azizi E, Soyer HP, Bataille V, Dalmasso B, Bowdler LM, Burdon KP, Chen WV, Codd V, Craig JE, Dębniak T, Falchi M, Fang S, Friedman E, Simi S, Galan P, Garcia-Casado Z, Gillanders EM, Gordon S, Green A, Gruis NA, Hansson J, Harland M, Harris J, Helsing P, Henders A, Hočevar M, Höiom V, Hunter D, Ingvar C, Kumar R, Lang J, Lathrop GM, Lee JE, Li X, Lubiński J, Mackie RM, Malt M, Malvehy J, McAloney K, Mohamdi H, Molven A, Moses EK, Neale RE, Novaković S, Nyholt DR, Olsson H, Orr N, Fritsche LG, Puig-Butille JA, Qureshi AA, Radford-Smith GL, Randerson-Moor J, Requena C, Rowe C, Samani NJ, Sanna M, Schadendorf D, Schulze HJ, Simms LA, Smithers M, Song F, Swerdlow AJ, van der Stoep N, Kukutsch NA, Visconti A, Wallace L, Ward SV,

Wheeler L, Sturm RA, Hutchinson A, Jones K, Malasky M, Vogt A, Zhou W, Pooley KA, Elder DE, Han J, Hicks B, Hayward NK, Kanetsky PA, Brummett C, Montgomery GW, Olsen CM, Hayward C, Dunning AM, Martin NG, Evangelou E, Mann GJ, Long G, Pharoah PDP, Easton DF, Barrett JH, Cust AE, Abecasis G, Duffy DL, Whiteman DC, Gogas H, De Nicolo A, Tucker MA, Newton-Bishop JA; GenoMEL Consortium; Q-MEGA and QTWIN Investigators; ATHENS Melanoma Study Group; 23andMe; SDH Study Group; IBD Investigators; Essen-Heidelberg Investigators; AMFS Investigators; MelaNostrum Consortium, Peris K, Chanock SJ, Demenais F, Brown KM, Puig S, Nagore E, Shi J, Iles MM, Law MH. Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. *Nat Genet*. 2020 May;52(5):494-504. doi: 10.1038/s41588-020-0611-8. Epub 2020 Apr 27. PMID: 32341527; PMCID: PMC7255059.

9. Dutta D, Gagliano Taliun SA, Weinstock JS, **Zawistowski M**, Sidore C, Fritsche LG, Cucca F, Schlessinger D, Abecasis GR, Brummett CM, Lee S. (2019) Meta-MultiSKAT: Multiple phenotype meta-analysis for region-based association test. *Genet Epidemiol. 43(7):800-814.* PMID: 31433078

10. Fritsche LG, Beesley LJ, VandeHaar P, Peng RB, Salvatore M, **Zawistowski M**, Gagliano Taliun SA, Das S, LeFaive J, Kaleba EO, Klumpner TT, Moser SE, Blanc VM, Brummett CM, Kheterpal S, Abecasis GR, Gruber SB, Mukherjee B. (2019) Exploring various polygenic risk scores for skin cancer in the phenomes of the Michigan genomics initiative and the UK Biobank with a visual catalog: PRSWeb. *PLoS Genet.* 15(6):e1008202. PMID: 31194742

11. Graham SE, Nielsen JB, **Zawistowski M**, Zhou W, Fritsche LG, Gabrielsen ME, Skogholt AH, Surakka I, Hornsby WE, Fermin D, Larach DB, Kheterpal S, Brummett CM, Lee S, Kang HM, Abecasis GR, Romundstad S, Hallan S, Sampson MG, Hveem K, Willer CJ. (2019) Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. *Nat Commun*. 10(1):1847. PMID: 31015462

12. Gasdaska A, Friend D, Chen R, Westra J, **Zawistowski M**, Lindsey W, Tintle N. (2019) Leveraging summary statistics to make inferences about complex phenotypes in large biobanks. *Pac Symp Biocomput*. 24:391-402. PMID: 30963077

13. Carlson J, Locke AE, Flickinger M, **Zawistowski M**, Levy S, Myers RM, Boehnke M, Kang HM, Scott LJ, Li JZ, Zöllner S; BRIDGES Consortium. (2018) Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. *Nat Commun*. 9(1):3753. PMID: 30218074

14. Enerbäck C, Sandin C, Lambert S, **Zawistowski M**, Stuart PE, Verma D, Tsoi LC, Nair RP, Johnston A, Elder JT. (2018) The psoriasis-protective *TYK2* I684S variant impairs IL-12 stimulated pSTAT4 response in skin-homing CD4+ and CD8+ memory T-cells. *Sci Rep.* 8(1):7043. PMID: 29728633

15. Fritsche LG, Gruber SB, Wu Z, Schmidt EM, **Zawistowski M**, Moser SE, Blanc VM, Brummett CM, Kheterpal S, Abecasis GR, Mukherjee B. (2018) Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. *Am J Hum Genet.* 102(6):1048-1061. PMID: 29779563

16. Jun G*, Manning A*, Almeida M*, **Zawistowski M***, Wood AR*, Teslovich TM*, Fuchsberger C, Feng S, Cingolani P, Gaulton KJ, Dyer T, Blackwell TW, Chen H, Chines PS, Choi S, Churchhouse C, Fontanillas P, King R, Lee S, Lincoln SE, Trubetskoy V, DePristo M, Fingerlin T, Grossman R, Grundstad J, Heath A, Kim J, Kim YJ, Laramie J, Lee J, Li H, Liu X, Livne O, Locke AE, Maller J, Mazur A, Morris AP, Pollin TI, Ragona D, Reich D, Rivas MA, Scott LJ, Sim X, Tearle RG, Teo YY, Williams AL, Zöllner S, Curran JE, Peralta J, Akolkar B, Bell GI, Burtt NP, Cox NJ, Florez JC, Hanis CL, McKeon C, Mohlke KL, Seielstad M, Wilson JG, Atzmon G, Below JE, Dupuis J, Nicolae DL, Lehman D, Park T, Won S, Sladek R, Altshuler D, McCarthy MI, Duggirala R, Boehnke M, Frayling TM, Abecasis GR, Blangero J. (2018) Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *PNAS* 115(2) 379-384. PMID: 29279374 **(* co-first authors)**

17. Dand N, Mucha S, Tsoi LC, Mahil SK, Stuart PE, Arnold A, Baurecht H, Burden AD, Callis Duffin K, Chandran V, Curtis CJ, Das S, Ellinghaus D, Ellinghaus E, Enerback C, Esko T, Gladman DD, Griffiths CEM, Gudjonsson JE, Hoffman P, Homuth G, Hüffmeier U, Krueger GG, Laudes M, Lee SH, Lieb W, Lim HW, Löhr S, Mrowietz U, Müller-Nurayid M, Nöthen M, Peters A, Rahman P, Reis A, Reynolds NJ, Rodriguez E, Schmidt CO, Spain SL, Strauch K, Tejasvi T, Voorhees JJ, Warren RB, Weichenthal M, Weidinger S, **Zawistowski M**, Nair RP, Capon F, Smith CH, Trembath RC, Abecasis GR, Elder JT, Franke A, Simpson MA, Barker JN (2017) Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signaling. *Hum Mol Genet*. 26(21):4301-4313. PMID: 28973304

18. Sussman J, Wiitala W**, Zawistowski M,** Hofer T, Bentley D, Hayward R (2017) The Veteran's Affairs cardiac risk sore: recalibrating the atherosclerotic cardiovascular disease score for applied use. *Med Care*. 55(9):864-870. PMID: 28763374

19. Tsoi LC, Stuart PE, Tian C, Gudjonsson JE, Das S, **Zawistowski M**, Ellinghaus E, Barker JN, Chandran V, Dand N, Duffin KC, Enerbäck C, Esko T, Franke A, Gladman DD, Hoffmann P, Kingo K, Kõks S, Krueger GG, Lim HW, Metspalu A, Mrowietz U, Mucha S, Rahman P, Reis A, Tejasvi T, Trembath R, Voorhees JJ, Weidinger S, Weichenthal M, Wen X, Eriksson N, Kang HM, Hinds DA, Nair RP, Abecasis GR, Elder JT (2017) Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. *Nat Commun*. 8:15382 PMID: 28537254

20. Budu-Aggrey A, Bowes J, Stuart PE, **Zawistowski M**, Tsoi LC, Nair R, Jadon DR, McHugh N, Korendowych E, Elder JT, Barton A, Raychaudhuri S (2017) A rare coding allele in IFIH1 is protective for psoriatic arthritis. *Ann Rheum Dis*. 76(7):1321-1324. PMID: 28501801

21. **Zawistowski M,** Sussman J, Hofer T, Bentley D, Hayward R, Wiitala W. (2017) Corrected ROC analysis for misclassified binary outcomes. *Statist. Med*. 36:2148–2160. PMID: 28245528

22. Hovelson DH, X Zhengyu, **Zawistowski M**, Ehm MG, Harris EC, Stocker SL, Gross AS, Jang I, Ieiri I, Lee JE, Cardon LR, Chissoe SL, Abecasis GR, Nelson MR. (2017) Characterization of ADME Gene Variation in 21 Populations Via Exome Sequencing. *Pharmacogenet Genomics* 27(3):89-100. PMID: 27984508

23. Feng S, Pistis G, Zhang H, **Zawistowski M**, Mulas A, Zoledziewska M, Holmen OL, Busonero F, Sanna S, Hveem K, Willer C, Cucca F, Liu DJ, Abecasis GR. (2015) Methods for association analysis and meta-analysis of rare variants in families. *Genet Epidemiol* 39(4):227-38. PMID: 25740221

24. **Zawistowski M***, Reppel M*, Wegmann D, St Jean PL, Ehm MG, Nelson MR, Novembre J, Zöllner S. Analysis of rare variant population structure in Europeans reveals differential stratification of gene-based tests *(2014) Eur J Hum Genet.* 22(9):1137-44. PMID: 24398795. (*** co-first authors**)

25. Liu D*, Peloso GM*, Zhan X*, Holmen O*, **Zawistowski M**, Feng S, Nikpay M, Auer PL, Goel A, Zhang H, Peters R, Farrall M, Orho-Melander M, Kooperberg C, McPherson R, Watkins H, Melander O, Willer CJ, Hveem K, Kathiresan S, Abecasis GR (2014) Meta-analysis of gene level association tests for rare variants. *Nat Genet* 46(2):200-4. PMID: 24336170.

26. Schaibley VM, **Zawistowski M**, Wegmann D, Kessner D, Ehm MG , Nelson MR , St. Jean PL , Abecasis G, Novembre J, Zoellner S, Li JZ *(*2013) The influence of genomic context on mutation patterns in the human genome inferred from rare variants. *Genome Res* 23(12):1974-84. PMID: 23990608.

27. Lui K, Fast S, **Zawistowski M***, Tintle N* *(*2013) A geometric framework for evaluating of rare variant tests of association. *Genet Epidemiol* 37(4):345-57. PMID: 23526307. (*** co-senior authors**)

28. Nelson MR, Wegmann D, Ehm MG, Kessner D, St. Jean P, Verzilli C, Shen J, Tang Z, Bacanu S, Fraser D, Warren L, Aponte J, **Zawistowski M**, Liu X, Zhang H, Zhang Y, Li J, Li Y, Li L, Woollard P, Topp S, Hall MD, Nangle K, Wang J, Abecasis G, Cardon LR, Zöllner S, Whittaker JC, Chissoe SL, Novembre J, Mooser V (2012) An abundance of rare functional variants in 202 drug target genes sequenced in 14002 people. *Science* 337(6090):100-4. PMID: 22604722.

29. Jewett E*, **Zawistowski M***, Rosenberg NA, Zöllner S (2012) A coalescent model for genotype imputation. *Genetics* 191(4):1239-55. PMID: 22595242. (*** co-first authors**)

30. **Zawistowski M**, Gopalakrishnan S, Ding J, Li Y, Grimm S, Zöllner, S (2010) Extending rare variant testing strategies: analysis of non-coding sequence and imputed genotypes. *Am J Hum Genet* 87(5):604-17. PMID: 21070896.

Consortium Publications

Majithia AR, Flannick J, Shahinian P, Guo M, Bray MA, Fontanillas P, Gabriel SB; GoT2D Consortium; NHGRI JHS/FHS Allelic Spectrum Project; SIGMA T2D Consortium; **T2D-GENES Consortium**, Rosen ED, Altshuler D. (2014) Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proc Natl Acad Sci* (36):13127-32. PMID: 25157153

Kim YJ, Lee J, Kim BJ, **T2D-GENES Consortium**, Park T. (2015) A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. *BMC Genomics* 16:1109. PMID: 26715385

Articles

Zawistowski, M. "University of Michigan's Undergraduate Big Data Summer Institute Completes Fifth Year." *AMSTAT NEWS*. 1 Dec 2019: Print. https://magazine.amstat.org/blog/2019/12/01/uofmich/

Invited Talks

"The Michigan Genomics Initiative: Managing a Dynamic University Resource." Keynote Lecture for Workshop on Rigor, Reproducibility, and Transparency, University of Michigan Department of Computational Medicine and Biology (8/25/2020)

"Teaching Biostatistics to Non-Majors." Co-organized teaching workshop with Rebecca Andridge, PhD (Ohio State University) for the University of Michigan Department of Biostatistics. We presented guidelines for good teaching practice laid out by the GAISE report and provided examples from our residential and online courses. (10/15/2019)

"The Michigan Genomics Initiative: Managing a Dynamic University Resource." Keynote Lecture for Workshop on Rigor, Reproducibility, and Transparency, University of Michigan Department of Computational Medicine and Biology (5/7/2019)

"Biobanks and Electronic Health Records in Genetics." EPID 516: Genetic Epidemiology, University of Michigan School of Public Health (3/22/2018, 4/2/2019, 3/30/2021)

"Misclassification in Electronic Health Records (and more)." BIOS 803: Cancer Seminar Series, University of Michigan School of Public Health (12/8/2017)

"Statistical analysis of next generation sequencing data." Western Michigan University, Department of Statistics, Kalamazoo, MI (11/30/12)

"Statistical analysis of next generation sequencing data." Geisinger Health System, Weis Center for Research, Danville, PA (2/1/12)

"Introduction to coalescent theory and applications." REU Seminar, Hope College, Department of Mathematics, Holland MI (6/10/11)

"Markov Chain Monte Carlo without likelihoods: correcting for the winner's curse in gene-environment association studies." Applied Bayesian Statistics Course, Department of Biostatistics, University of Michigan (4/14/11)

"Imputation accuracy for rare variants in structured populations." Platform Presentation, American Society of Human Genetics 2010 Annual Meeting, Washington D.C.

"Methods for rare variant association studies." Finland-United States Investigation of NIDDM Genetics (FUSION) Annual Meeting, Ann Arbor MI (10/2010)

"Extending rare variant testing strategies: analysis of imputed sequence data." REU Seminar, Hope College, Department of Mathematics, Holland MI (6/25/10)

Consulting Experience

Consultant and scientific advisor for the undergraduate statistical genetics research program of Dr. Nathan Tintle at Dordt College, IA (formerly Hope College, MI). Assisted in writing NIH R15 grant proposal (funded: R15HG006915), selection of student projects and feedback on progress.

Journal Peer Reviewer

Genetic Epidemiology, Bioinformatics, Human Heredity, BMC Medicine

Computer Experience: C/C++, Unix, Perl, R, Stata, SQL

Funding

1-R01-AG-067592-01 Bakulski (PI) 05/15/20-03/31/25
DNA Methylation, Genetics, and Modifiable Risk Factors of Dementia in a Nationally Representative, Multi-Ethnic Cohort This study will likely impact the field of Alzheimer's research and contribute to public health. The study will a) establish the relevance of DNA methylation on ADRD in multiple race/ethnicities; b) elucidate important biological epigenetic mechanisms; c) determine the combined and individual epigenetic-environment interplay contributions to ADRD; and d) consider the effects of sex, educational attainment, race/ethnicity, younger age groups, and urban/rural status in the same study where comparisons of relative contribution to risk can be made.
Role: co-I

Grant: (Nallamothu, Wiens) 10/1/2017-Ongoing 2.40 Cal
Name of Grant: Precision Health Data Analytics and IT
Role: Senior Personnel
Agency: University of Michigan (Internal) $2,000,000
Description:
The Precision Health Data Analytics and IT project will provide the support and infrastructure for sophisticated and timely data access and analysis to enhance precision health research and implementation. With responsibility for deploying an effective compute and storage infrastructure, as well as providing tools for data cleaning/retrieval/management, analysis/visualization, and analytics reporting, this group is tasked with creating and delivering responsive systems that will fuel precision health research.

Grant #: (Kang, Mukherjee, Zoellner) 06/01/2019-05/31/2022 0.50 Cal
Name of Grant: Transforming Analytical Learning in the Era of Big Data
Role: co-I
Agency: NIH $240,000 annual direct cost
Total Costs: Description: The program builds on the success of our existing Big Data Summer Institute (BDSI) supported by a NIH BD2K Courses and Skills grant award that is ending in 2018. We plan to expose program students to diverse techniques, skills and problems in the field of Big Data and Human Health. We enhance our ongoing summer program structure in the current proposal by involving a team of researchers working at the intersection of cardiovascular research and data science with a focus on cardiovascular precision medicine where some of the new mentored research projects will be defined. We primarily focus on three genres of health Big Data arising in Electronic Health Records/Medical Claims, Genomics and Imaging.

References

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