September 15, 2023

1. Biographical Information

- Matthew P. Conomos
- University of Washington
  Department of Biostatistics Genetic Analysis Center
  UW Tower Box 359461
  4333 Brooklyn Ave NE, Seattle, WA 98195-9461
- Office Phone: (206) 543-3463
- Cell Phone: (585) 957-2101
- Email: mconomos@uw.edu

2. Education

- University of Rochester, Rochester, NY. B.S. Applied Mathematics and B.A. Statistics, conferred Magna Cum Laude and with Highest Distinction, 2008
- University of Washington, Seattle, WA. Ph.D. Biostatistics, Statistical Genetics Pathway, 2014

3. Licensure

- Not applicable

4. Professional Positions

- Research Scientist, University of Washington, Department of Biostatistics, Genetic Analysis Center, January 2015 - March 2016
- Statistical Geneticist, Arivale Inc., May 2016 - August 2017
- Senior Research Scientist: Statistical Genetics, Arivale Inc., August 2017 - July 2018
- Senior Research Scientist, University of Washington, Department of Biostatistics, Genetic Analysis Center, August 2018 - Present

5. Honors, Awards, Scholarships

- Rush Rhees Scholarship for academic excellence, University of Rochester, 2004
- Phi Beta Kappa Honor Society, University of Rochester, 2008
- Trainee, National Institutes of Health (NIH) Statistical Genetics Training Grant, University of Washington 2009-2011
- First Place Student Paper Competition, The Western North American Region of The International Biometric Society (WNAR) Meeting, June 2014
- Robert C. Elston Best Paper Award in Genetic Epidemiology in 2015

6. Professional Activities (outside of UW)

- Reviewer: Bioinformatics, Genealogy, Genetic Epidemiology, Genetics, PLoS Genetics, PLoS ONE, Statistical Applications in Genetics and Molecular Biology (SAGMB), Statistics in Medicine
- Professional Societies: American Society of Human Genetics, The Western North American Region of The International Biometric Society

7. Bibliography

a) Refereed research articles

1. Recto, K., Kachroo, P., Huan, T., Van Den Berg, D., Lee, G. Y., Bui, H., ... & Graw, S. (2023). Epigenome-wide DNA methylation association study of circulating IgE levels identifies novel targets for asthma. *EBioMedicine*, *95*.

2. Ngo, D., Pratte, K. A., Flexeder, C., Petersen, H., Dang, H., Ma, Y., ... & Bowler, R. P. (2023). Systemic markers of lung function and forced expiratory volume in 1 second decline across diverse cohorts. *Annals of the American Thoracic Society*, *20*(8), 1124-1135.
3. Ahalt, S., Avillach, P., Boyles, R., Bradford, K., Cox, S., Davis-Dusenbery, B., ... & Asare, J. (2023). Building a collaborative cloud platform to accelerate heart, lung, blood, and sleep research. *Journal of the American Medical Informatics Association*, *30*(7), 1293-1300.
4. Seyerle, A. A., Laurie, C. A., Coombes, B. J., Jain, D., **Conomos, M. P.**, Brody, J., ... & Pankratz, N. (2023). Whole Genome Analysis of Venous Thromboembolism: the Trans-Omics for Precision Medicine Program. *Circulation: Genomic and Precision Medicine*, *16*(2), e003532.
5. Sarnowski, C., **Conomos, M. P.**, Vasan, R. S., Meigs, J. B., Dupuis, J., Liu, C. T., & Leong, A. (2023). Genetic Effect on Body Mass Index and Cardiovascular Disease Across Generations. *Circulation: Genomic and Precision Medicine*, *16*(1), e003858.
6. Wheeler, M. M., Stilp, A. M., Rao, S., Halldórsson, B. V., Beyter, D., Wen, J., ... & Reiner, A. P. (2022). Whole genome sequencing identifies structural variants contributing to hematologic traits in the NHLBI TOPMed program. *Nature communications*, *13*(1), 7592.
7. Li, Z., Li, X., Zhou, H., Gaynor, S. M., Selvaraj, M. S., Arapoglou, T., ... & Lin, X. (2022). A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. *Nature methods*, *19*(12), 1599-1611.
8. Khan, A. T., Gogarten, S. M., McHugh, C. P., Stilp, A. M., Sofer, T., Bowers, M. L., ... & **Conomos, M. P.**, Nelson, S. C. (2022). Recommendations on the use and reporting of race, ethnicity, and ancestry in genetic research: Experiences from the NHLBI TOPMed program. *Cell Genomics*, 100155.
9. Huang, L., Rosen, J. D., Sun, Q., Chen, J., Wheeler, M. M., Zhou, Y., ... & Li, Y. (2022). TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. *The American Journal of Human Genetics*, *109*(6), 1175-1181.
10. Wilmanski, T., Kornilov, S. A., Diener, C., **Conomos, M. P.**, Lovejoy, J. C., Sebastiani, P., ... & Gibbons, S. M. (2022). Heterogeneity in statin responses explained by variation in the human gut microbiome. *Med*.
11. Manichaikul, A., Lin, H., Kang, C., Yang, C., Rich, S. S., Taylor, K. D., ... & Rodriguez, A. (2022). Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. *Communications biology*, *5*(1), 1-11.
12. Schubert, R., Geoffroy, E., Gregga, I., Mulford, A. J., Aguet, F., Ardlie, K., ... & Wheeler, H. E. (2022). Protein prediction for trait mapping in diverse populations. *PloS one*, *17*(2), e0264341.
13. Little, A., Hu, Y., Sun, Q., Jain, D., Broome, J., Chen, M. H., ... & Raffield, L. M. (2022). Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. *Human molecular genetics*, *31*(3), 347-361.
14. Taub, M. A., **Conomos, M. P.**, Keener, R., Iyer, K. R., Weinstock, J. S., Yanek, L. R., ... & TOPMed Structural Variation Working Group. (2022). Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. *Cell Genomics*, *2*(1), 100084.
15. Lin, E., Tsai, S. J., Kuo, P. H., Liu, Y. L., Yang, A. C., **Conomos, M. P.**, & Thornton, T. A. (2021). Genome-wide association study in the Taiwan biobank identifies four novel genes for human height: NABP2, RASA2, RNF41 and SLC39A5. *Human Molecular Genetics*.
16. Mikhaylova, A. V., McHugh, C. P., Polfus, L. M., Raffield, L. M., Boorgula, M. P., Blackwell, T. W., ... & Auer, P. L. (2021). Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *The American Journal of Human Genetics*, *108*(10), 1836-1851.
17. Sofer, T., Lee, J., Kurniansyah, N., Jain, D., Laurie, C. A., Gogarten, S. M., ... & Schifano, E. D. (2021). BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. *Human Genetics and Genomics Advances*, 100040.

18. Sofer, T., Zheng, X., Laurie, C. A., Gogarten, S. M., Brody, J. A., **Conomos, M. P**., ... & Rice, K. M. (2021). Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. *Nature Communications*, 12(1), 1-14.
19. Hu, Y., Stilp, A. M., McHugh, C. P., Rao, S., Jain, D., Zheng, X., ... & **Conomos, M.P.**, Reiner, A. P. (2021). Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *The American Journal of Human Genetics*, 108(5), 874-893.
20. Grasberger, H., Magis, A. T., Sheng, E., **Conomos, M. P.**, Zhang, M., Garzotto, L. S., ... & Kao, J. Y. (2021). DUOX2 variants associate with preclinical disturbances in microbiota-immune homeostasis and increased inflammatory bowel disease risk. *The Journal of clinical investigation*, 131(9).
21. Kwong, A. M., Blackwell, T. W., LeFaive, J., de Andrade, M., Barnard, J., Barnes, K. C., ... & Kang, H. M. (2021). Robust, flexible, and scalable tests for Hardy–Weinberg equilibrium across diverse ancestries. *Genetics*, 218(1), iyab044.
22. Taliun, D., et al. (2021). Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*, 590(7845), 290-299.
23. Magis, A. T., Rappaport, N., **Conomos, M. P.**, Omenn, G. S., Lovejoy, J. C., Hood, L., & Price, N. D. (2020). Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. *Scientific reports*, 10(1), 1-6.
24. Li, X., Li, Z., Zhou, H., Gaynor, S. M., Liu, Y., Chen, H., ... & Lin, X. (2020). Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nature genetics*, 52(9), 969-983.
25. Gogarten, S. M., Sofer, T., Chen, H., Yu, C., Brody, J. A., Thornton, T. A., ... & **Conomos, M. P.** (2019). Genetic association testing using the GENESIS R/Bioconductor package. *Bioinformatics*, 35(24), 5346-5348.
26. Wojcik, G. L., Graff, M., Nishimura, K. K., Tao, R., Haessler, J., Gignoux, C. R., ... & Belbin, G. M. (2019). Genetic analyses of diverse populations improves discovery for complex traits. *Nature*, 570(7762), 514-518.
27. Zubair, N., **Conomos, M. P.**, Hood, L., Omenn, G. S., Price, N. D., Spring, B. J., ... & Lovejoy, J. C. (2019). Genetic predisposition impacts clinical changes in a lifestyle coaching program. *Scientific reports*, 9(1), 1-11.
28. Cade, B. E., Chen, H., Stilp, A. M., Louie, T., Ancoli-Israel, S., Arens, R., ... & Evans, D. S. (2019). Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. *PLoS genetics*, 15(4), e1007739.
29. Wang, H., Cade, B. E., Sofer, T., Sands, S. A., Chen, H., Browning, S. R., ... & Below, J. E. (2019). Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. *Human molecular genetics*, 28(4), 675-687.
30. Manor, O., Zubair, N., **Conomos, M. P.**, Xu, X., Rohwer, J. E., Krafft, C. E., ... & Magis, A. T. (2018). A multi-omic association study of trimethylamine N-oxide. *Cell reports*, 24(4), 935-946.
31. Xu, X., **Conomos, M. P.**, Manor, O., Rohwer, J. E., Magis, A. T., & Lovejoy, J. C. (2018). Habitual sleep duration and sleep duration variation are independently associated with body mass index. *International Journal of Obesity*, *42*(4), 794.
32. Chen, H., Cade, B. E., Gleason, K. J., Bjonnes, A. C., Stilp, A. M., Sofer, T., ... & Redline, S. (2018). Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea–related Quantitative Trait Locus in Men. *American journal of respiratory cell and molecular biology*, *58*(3), 391-401.
33. Méndez-Giráldez, R., Gogarten, S. M., Below, J. E., Yao, J., Seyerle, A. A., Highland, H. M., ... & Avery, C. L. (2017). GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. *Scientific reports*, *7*(1), 17075.
34. Brody, J. A., Morrison, A. C., Bis, J. C., O'Connell, J. R., Brown, M. R., Huffman, J. E., ... & Cupples, L. A. (2017). Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. *Nature genetics*, *49*(11), 1560.

35. Kerr, K. F., Avery, C. L., Lin, H. J., Raffield, L. M., Zhang, Q. S., Browning, B. L., ... & Whitsel, E. A. (2017). Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart rhythm*, *14*(11), 1675-1684.
36. Chen, H., Cade, B. E., Gleason, K. J., Bjonnes, A. C., Stilp, A. M., Sofer, T., ... & Redline, S. (2018). Multiethnic meta-analysis identifies RAI1 as a possible obstructive sleep apnea–related quantitative trait locus in men. *American journal of respiratory cell and molecular biology*, 58(3), 391-401.
37. Raffield, L. M., Louie, T., Sofer, T., Jain, D., Ipp, E., Taylor, K. D., ... & Lin, H. J. (2017). Genome-wide association study of iron traits and relation to diabetes in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL): potential genomic intersection of iron and glucose regulation?. *Human molecular genetics*, 26(10), 1966-1978.
38. Yan, Q., Brehm, J., Pino-Yanes, M., Forno, E., Lin, J., Oh, S. S., ... & Celedon, J. C. (2017). A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *European Respiratory Journal*, 49(5), 1601505.
39. Zheng, X., Gogarten, S. M., Lawrence, M., Stilp, A., Conomos, M. P., Weir, B. S., ... & Levine, D. (2017). SeqArray—a storage-efficient high-performance data format for WGS variant calls. *Bioinformatics*, 33(15), 2251-2257.
40. Blue, E. M., Brown, L. A., **Conomos, M. P.,** Kirk, J. L., Nato, A. Q., Popejoy, A. B., ... & Thornton, T. (2016, October). Estimating relationships between phenotypes and subjects drawn from admixed families. In *BMC proceedings* (Vol. 10, No. 7, p. 42). BioMed Central.
41. Cade, B. E., Chen, H., Stilp, A. M., Gleason, K. J., Sofer, T., Ancoli-Israel, S., ... & Redline, S. (2016). Genetic associations with obstructive sleep apnea traits in Hispanic/Latino Americans. *American journal of respiratory and critical care medicine*, 194(7), 886-897.
42. Chen, H., Wang, C., **Conomos, M. P.,** Stilp, A. M., Li, Z., Sofer, T., ... & Lin, X. (2016). Control for population structure and relatedness for binary traits in genetic association studies via logistic mixed models. *The American Journal of Human Genetics*, *98*(4), 653-666.
43. Morrison, J., Laurie, C. C., Marazita, M. L., Sanders, A. E., Offenbacher, S., Salazar, C. R., ... & Shaffer, J. R. (2016). Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). *Human molecular genetics*, 25(4), 807-816.
44. Schick, U. M., Jain, D., Hodonsky, C. J., Morrison, J. V., Davis, J. P., Brown, L., ... & Reiner, A. P. (2016). Genome-wide association study of platelet count identifies ancestry-specific loci in Hispanic/Latino Americans. *The American Journal of Human Genetics*, 98(2), 229-242.
45. **Conomos, M. P.**, Reiner, A. P., Weir, B. S., & Thornton, T. A. (2016). Model-free estimation of recent genetic relatedness. *The American Journal of Human Genetics*, *98*(1), 127-148.
46. **Conomos, M. P.**, Laurie, C. A., Stilp, A. M., Gogarten, S. M., McHugh, C. P., Nelson, S. C., ... & Laurie, C. C. (2016). Genetic diversity and association studies in US Hispanic/Latino populations: applications in the Hispanic Community Health Study/Study of Latinos. *The American Journal of Human Genetics*, *98*(1), 165-184.
47. **Conomos, M. P.**, Miller, M. B., & Thornton, T. A. (2015). Robust inference of population structure for ancestry prediction and correction of stratification in the presence of relatedness. *Genetic epidemiology*, *39*(4), 276-293.
48. Blue, E. M., Cheung, C. Y., Glazner, C. G., **Conomos, M. P.,** Lewis, S. M., Sverdlov, S., ... & Wijsman, E. M. (2014, June). Identity-by-descent graphs offer a flexible framework for imputation and both linkage and association analyses. In *BMC proceedings* (Vol. 8, No. 1, p. S19). BioMed Central.
49. Thornton, T., **Conomos, M. P.**, Sverdlov, S., Blue, E. M., Cheung, C. Y., Glazner, C. G., ... & Wijsman, E. M. (2014, June). Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. In *BMC proceedings* (Vol. 8, No. 1, p. S5). BioMed Central.
50. Gogarten, S. M., Bhangale, T., **Conomos, M. P.**, Laurie, C. A., McHugh, C. P., Painter, I., ... & Laurie, C. C. (2012). GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. *Bioinformatics*, *28*(24), 3329-3331.

51. Laurie, C. C., Laurie, C. A., Rice, K., Doheny, K. F., Zelnick, L. R., McHugh, C. P., ... & Weir, B. S. (2012). Detectable clonal mosaicism from birth to old age and its relationship to cancer. *Nature genetics*, *44*(6), 642.
52. FitzGerald, L. M., Kwon, E. M., **Conomos, M. P.,** Kolb, S., Holt, S. K., Levine, D., ... & Stanford, J. L. (2011). Genome-wide association study identifies a genetic variant associated with risk for more aggressive prostate cancer. *Cancer Epidemiology and Prevention Biomarkers*.
53. Starr, S., & **Conomos, M. P.** (2011). Asymptotics of the spectral gap for the interchange process on large hypercubes. *Journal of Statistical Mechanics: Theory and Experiment*, *2011*(10), P10018.

b) Other non-refereed published scholarly publications

1. **Conomos, M. P.** (2014). Inferring, estimating, and accounting for population and pedigree structure in genetic analyses. Ph.D. Dissertation, Department of Biostatistics, University of Washington.

8. Patents and Other Intellectual Property

- None

9. Funding History

a) Funded Projects

Ongoing Research Support

U01 HG011697 (Rice) 06/08/2021-03/31/2026 6.0 CM
NIH $8,546,016
Polygenic Risk Score Diversity Consortium Coordinating Center *(A157210 PRS CC)*
Polygenic Risk Scores (PRS) combine information across numerous genetic variants to improve disease prediction; however, lack of diversity in PRS research to date threatens applicability in non-European ancestry individuals. The NHGRI Polygenic Risk Score Diversity Consortium will conduct collaborative data integration, analysis, and methods development in existing research cohorts to improve PRS prediction across diverse populations. As Coordinating Center for the Consortium, we will perform genotype and phenotype data harmonization, lead collaborative analysis, contribute to methods development, help identify Ethical, Legal, and Social Implications (ELSI) of PRS, facilitate data sharing, and coordinate program logistics and outreach.

U24 HG011746 (May) 06/01/2021-03/31/2026 3.3 CM
NIH $14,235,209
University of Washington (UW) Mendelian Genomics Data Coordinating Center *(A155208 Mendelian Genomics DCC)*
As the Data Coordinating Center for the Mendelian Genomics Research Consortium, we will lead efforts to establish Consortium-wide data standards, utilize cloud-based resources to enable rapid data sharing among Consortium members and timely release to the broader scientific community, manage the opportunity fund supporting scalable functional studies of candidate genes and variants, and coordinate program logistics and outreach.

R01 HL15385 (N Smith) 8/15/2020-6/30/2024 1.8 CM
NIH $2,979,909
Structural and Nucleotide Variation as Genomic Risks for Venous Thrombosis: TOPMED and INVENT Collaboration *(A149939 TOPMED VTE)*
Venous thrombosis (blood clots in the legs and/or lungs) is a cardiovascular condition that is influenced by a person's DNA characteristics. Human DNA differs among people in many ways, and this project will look at 2 ways in which DNA differs among adults to see if these differences are associated with the risk of developing clots in the legs or lungs. We will first determine if the insertions of extra DNA material or deletions of DNA

material are associated with risk; we will then determine if substitutions in DNA material are associated with risk.

R01 HL147894 (N Smith and A Wolberg) 06/2021-02/2025 0.6 CM
NIH $2,784,530
Genetic Discovery and Functional Validation to Identify Precursors of Clot Embolization in those with a Deep Vein Thrombosis *(A175300 DVT PE)*
The aim of this proposal is to better understand why venous clots in the legs sometimes dislodge and travel to the lungs. These clots block circulation to the lungs and are life-threatening. We are interested in identifying inherited factors that lead to clots traveling to the lung and learning how the inherited factors change the biologic function that causes a clot to dislodge.

R01 HL146500 (A Reiner) 02/2020-01/2024 0.15 CM
NIH $3,397,630
Next generation functional genomics of hematology traits *(C19 HEMENET)*
This project will lead to improved insight into the genetic basis of hematologic traits and red blood cell disorders.

R01 HL165061 (A Reiner) 0.15 CM
NIH $3,279,441
Structural Variation and Hematologic Traits *(A172457 R01 SVHT)*
Blood cells are derived from bone marrow progenitor cells and released into circulation, where they play key roles in oxygen transport, immune response, and blood clotting. In the proposed research, we assemble the largest collection of participants with blood cell traits and whole genome sequencing and apply rigorous scientific methods to interrogate genome-wide structural variation and functional characterization of the blood cell associated structural variants. Results generated from this research may contribute to a better understanding of blood cell biology and pave the way for new research into precision medicine for blood diseases.

Completed Research Support

OT3 HL142478 (B Davis-Dusenbery/sub-Jain)11/12/2019-08/31/2022 0.3 CM
Seven Bridges Genomics Inc $1,117,632
Development of scalable and user friendly engine to support genotype-phenotype association testing *(A149951 TopMed Seven Bridges 3)*
In this project, Seven Bridges Genomics and the TOPMed Data Coordinating Center will collaborate to develop a highly scalable, performant, and reliable system to enable all steps of the association testing process.

U01 HL137162 (K Rice & B Weir) 4/21/2017 - 03/31/2022 NCE
NIH $1,598,130
From gene regions to whole chromosomes: scaling up association-finding for disease and omics outcomes in TOPMed *(A114244, TOPMed U01)*
This application will bring unprecedented forms of analysis to the Trans-Omics for Precision Medicine (TOPMed) already-rich data resources. By using new computational methods, and collaborating with TOPMeds Working Groups, it will address scientific questions that are currently out of reach. The application's investigators are already known in TOPMed for their wealth of technical skill and commitment to the overall project.

HHSN268201800001I (May) 05/01/2018-09/30/2021
HHSN26800001

NIH/NHLBI $12,356,586
"Trans-Omics for Precision Medicine (TOPMed) Data Coordinating Center (DCC)" Task Order 1 *(A1664037 TOPMed TO1-TO2 9 mo)*
The DCC will provide administrative and technical support for the TOPMed program. Administrative tasks include program coordination, publications and data sharing, working group support, in-person meeting coordination, progress reporting, and website maintenance. Technical tasks include facilitating release, quality control, and documentation of molecular data.

b) Pending Applications
None

10. Public Health Practice Activities
- None

11. Conferences and Symposiums
a) Oral Presentations
1. "Sparse kinship matrices enable computationally efficient, accurate, association tests", NHLBI TOPMed in-person Meeting, Tysons, VA, December 2019.
2. "Genetic Association Testing with Linear Mixed Models in Samples with Complex Structure," The Western North American Region of The International Biometric Society (WNAR) Meeting, Boise State University, Boise, ID, June 2015
3. "Genetic Association Testing with Linear Mixed Models in Admixed Populations with Familial Relatives," The Western North American Region of The International Biometric Society (WNAR) Meeting, University of Hawaii at Manoa, Honolulu, HI, June 2014
4. "About a Conjecture of Aldous and Diaconis," Young Mathematicians' Conference, Ohio State University, August 2007

b) Poster Presentations
1. "Sparse empirical kinship matrices enable computationally efficient and accurate association tests in large samples." 69th Annual Meeting of The American Society of Human Genetics (ASHG), Houston, TX, USA, October 2019
2. "Impact of polygenic risk on changes in biomarkers over time due to lifestyle intervention and aging," 67th Annual Meeting of The American Society of Human Genetics (ASHG), Orlando, FL, USA, October 2017
3. "The Impact of Genetic Risk on Effectiveness of Lifestyle Intervention in a General Population," 66th Annual Meeting of The American Society of Human Genetics (ASHG), Vancouver, Canada, October 2016
4. "Improved Association Testing with Linear Mixed Models by Modeling Non-Genetic Phenotypic Covariance Structures," 65th Annual Meeting of the American Society of Human Genetics (ASHG), Baltimore, MD, USA, October 2015
5. "Overcoming Systematic Miscalibration of Linear Mixed Model Test Statistics in Genetic Association Studies by Leveraging Ancestry Representative Principal Components," 64th Annual Meeting of the American Society of Human Genetics (ASHG), San Diego, CA, USA, October 2014
6. "Model-free Estimation of IBD Sharing Probabilities in Admixed Populations," 63rd Annual Meeting of the American Society of Human Genetics (ASHG), Boston, MA, USA, October 2013
7. "Ancestry Informative Principal Components Analysis in Structured Samples with Known or Cryptic Relatedness," 62nd Annual Meeting of the American Society of Human Genetics (ASHG), San Francisco, CA, USA, November 2012
8. "Whole Genome Searching for Non-Additive Genetic Variance," 4th International Conference of Quantitative Genetics, Edinburgh, Scotland, June 2012

12. University Service

- None

13. Professionally-Related Community Service

- Program Committees: GSP-TOPMed Analysis Workshop, 2020 and 2021. NHLBI TOPMed Virtual Meeting, 2020.

14. Publicly Available Software

- GENESIS R/Bioconductor package, maintainer – Genetic Estimation and Inference in Structured Samples: Statistical methods for analyzing genetic data from samples with population structure and/or relatedness, available at: https://www.bioconductor.org/packages/release/bioc/html/GENESIS.html and https://github.com/UW-GAC/GENESIS
- GWASTools R/Bioconductor package, contributor – Tools for Genome-Wide Association Studies, available at: https://www.bioconductor.org/packages/release/bioc/html/GWASTools.html

15. Teaching History

a) Formal Courses

- Biostatistics 551, Statistical Genetics II: Quantitative Traits, Autumn 2022
- Biostatistics 551, Statistical Genetics II: Quantitative Traits, Autumn 2021

b) Other Teaching

- Computational Pipeline for WGS Data, Co-instructor 33%, SISG, July 26-28, 2023
- Computational Pipeline for WGS Data, Co-instructor 33%, SISG, July 27-29, 2022
- Computational Pipeline for WGS Data, Co-instructor 33%, SISG, July 21-23, 2021
- Advanced Regression Methods for Independent Data, Teaching Assistant and Guest Lecturer, University of Washington Department of Biostatistics, Fall 2011

c) Independent Study

- None

16. Advising and Formal Mentoring

- None