CURRICULUM VITAE
Timothy A. Thornton, PhD
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1. Biographical Information

- Name: Timothy A. Thornton
- Work Address:
  University of Washington
  Department of Biostatistics
  HSB F-644, Health Science Building
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2. Education

- Hampton University, Hampton, VA, B.S., Mathematics, 1998
- University of Chicago, Chicago, IL, Ph.D., Statistics, 2005
  Advisor: Professor Mary Sara McPeek
  Dissertation Title: Statistical Inference for Genetic Analysis in Related Individuals

3. Licensure: N/A

4. Professional Positions

- Postdoc, Department of Statistics, University of California, Berkeley, 2006-2008
  Supervisor: Professor Terry Speed
- Postdoc, Institute for Human Genetics, University of California, San Francisco, 2008-2009
  Supervisor: Professor Neil Risch
- Assistant Professor, Department of Biostatistics, University of Washington, 2009-2015
- Associate Professor, Department of Biostatistics, University of Washington, 2015-present
- Adjunct Associate Professor, Department of Statistics, University of Washington, 2018-present
- Affiliate Investigator, Biostat/Biomath, Fred Hutchinson Cancer Research Center, 2010-present
- Chair, UW Graduate School's Interdisciplinary Statistical Genetics Group, 2017-present

5. Honors, Awards, Scholarships

- Office of Naval Research Student Enhancement in Mathematics and Science Scholarship (1994–1998)
- B.A. conferred Magna Cum Laude and with Honors in Mathematics, Salutatorian, Hampton University (1998)
- Graduate Degrees for Minorities in Engineering and Science Fellowship (1998)

- Office of Naval Research-Historically Black Colleges and Universities Graduate Fellowship (1998–2002)
- David and Lucile Packard Foundation Graduate Fellowship (1998–2004)
- University of Chicago Graduate Fellowship (1998–2005)
- FASEB-MARC Travel Award for American Society of Human Genetics Conference (2006)
- University of California President's Postdoctoral Fellow (2006–2008)
- *American Journal of Human Genetics* "Editor's Corner" Article, 2007
- University of California, San Francisco Lamond Family Postdoctoral Fellow (2008–2009)
- *American Journal of Human Genetics* "Editor's Corner" Article, 2010
- *American Journal of Human Genetics* "Editor's Corner" Article, 2012
- Winner of *Genetic Epidemiology* Robert C. Elston Best Paper Award for 2015
- *Genetics* "Editor's Highlight" Article, 2016
- Robert W. Day Endowed Professorship of Public Health (2016–Present)

6. Professional Activities (outside of UW)

Grant Reviewer:

- Reviewer, Medical Research Council, United Kingdom (2010)
- Reviewer, Icelandic Research Fund, Iceland (2012).
- Reviewer, NIH, NHLBI Special Emphasis Panel: X01 TOPMed (2016)
- Standing Member and Reviewer, NIH/NIGMS Training and Workforce Development (TWD) Subcommittee B (2016–Present)
- Standing Member and Reviewer, NIH/NHGRI GNOM-G Committee (2018–Present)
- Standing Member and Reviewer, NIH/NHGRI IGNITE II Protocol Review Committee (2018–Present)

Scientific Conference Leadership:

- Lead organizer (Professor Bruce Weir, co-organizer) for the "Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics" Conference in Seattle, WA (November 2013)

Conference Invited Session Organizer:

- Western North American Region of the International Biometric Society (WNAR) Meeting (June 2013)
- Joint Statistical Meeting (2016)

Conference Session Chair:

- The "Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics" Conference (November 2013)
- Western North American Region of the International Biometric Society Meeting (June 2013)
- Ordered Data Analysis, Models and Health Research Methods Conference at The University of Texas at Dallas (March 2014)

American Statistical Association (ASA) Section on Statistics in Genomics and Genetics

- Chair, 2017 Student Paper Competition (Jan 2017 – Dec 2017)

American Society of Human Genetics

- Member, American Society of Human Genetics Program Committee (2018-Present)

International Genetic Epidemiology Society

- Member, Publications Committee (2017-Present)

Editorial Roles:

- Associate Editor, *American Journal of Human Genetics* (2018-Present)
- Review Editor, *Frontiers in Genetics* (2010–Present)
- Guest Editor, *PLoS Genetics* (2016)
- Guest Editor, *PLoS Genetics* (2017)

Referee Service:

- *Alzheimer's & Dementia*
- *American Journal of Human Genetics*
- *Annals of Human Genetics*
- *Annals of Applied Statistics*
- *Bioinformatics*
- *Biometrics*
- *BioMed Central Genetics*
- *BioMed Central Proceedings*
- *Biostatistics*
- *European Journal of Human Genetics*
- *Frontiers in Genetics*
- *Genetic Epidemiology*
- *Genome Research*
- *Human Heredity*
- *International Journal of Health Geographics*
- *JAMA Neurology*
- *JAMA Open Network*
- *Journal of Medical Genetics*
- *Journal of the Royal Statistical Society*
- *Nature Communications*
- *Nature Reviews Genetics*
- *PLoS Genetics*
- *PLoS One*
- *Proceedings of the National Academy of Sciences*
- *Statistical Applications in Genetics and Molecular Biology*
- *Statistics in Medicine*

Other Professional Service:

- Women's Health Initiative (WHI), Ancillary Studies Committee Member and Grant Reviewer (2012-Present)
- NHGRI-EBI GWAS Catalog Scientific Advisory Board (2018-Present)

Professional Memberships:

- American Statistical Association
- American Society of Human Genetics
- Institute of Mathematical Statistics
- International Genetic Epidemiology Society

7. Bibliography

Refereed Research Articles (highlighted are students* who I supervised, and ** *indicates joint senior authorship*)

1. Anderson-Cook CM and **Thornton TA** (1998) "Measuring Hockey's Special Teams Efficiency." *Chance*, 11: 26-34

2. Anderson-Cook CM and **Thornton TA** (1998) "Response to Letter to the Editor: Shorthanded." *Chance*, 12: 3-5

3. **Thornton TA** and McPeek MS (2007) "Case-Control Association Testing with Related Individuals: A More Powerful Quasi-Likelihood Score Test" *American Journal of Human Genetics* 81: 321-337. [Paper highlighted in the Editors' Corner of this issue]

4. FitzGerald LM, Patterson B, Thomson R, Polanowski A, Quinn S, Brohede J, **Thornton TA**, Challis D, Mackey D, Dwyer T, Foote S, Hannan GN, Stankovich J, McKay JD, Dickinson JL (2009) "Identification of a Prostate Cancer Susceptibility Gene on Chromosome 5p13q12 Associated with Risk of Both Familial and Sporadic Disease" *European Journal of Human Genetics* 17: 368-377

5. **Thornton TA** and McPeek MS (2010) "ROADTRIPS: Case-Control Association Testing with Partially or Completely Unknown Population and Pedigree Structure." *American Journal of Human Genetics* 86: 172-184. [Paper highlighted in the Editors' Corner of this issue.]

6. Phasukijwattana N, Kunhapan B, Stankovich J, Chuenkongkaew WL, Thomson R, **Thornton TA**, Bahlo M, Mushiroda T, Nakamura Y, Mahasirimongkol S, Tun AW, Srisawat C, Limwongse C, Peerapittayamongkol C, Sura T, Suthammarak W, Lertrit P (2010) "Genome-wide Linkage Scan and Association Study of PARL to the Expression of LHON Families in Thailand" *Human Genetics* 128: 39-49

7. Tore S, Casula S, Casu G, Concas MP, Pistidda P, Persico I, Sassu A, Maestrale GM, Caterina Mele C, Caruso MR, Bonerba B, Usai P, Deiana I, **Thornton TA**, Pirastu M, and Forabosco P (2011) "Application of a New Method for GWAS in a Related Case/Control Sample with Known Pedigree Structure: Identification of New Loci for Nephrolithiasis" *PLoS Genetics* 7: e1001281

8. **Thornton TA**, Zhang Q, Cai X, Ober C, and McPeek MS (2012) "XM: Association Testing on the X-Chromosome in Case-Control Samples with Related Individuals" *Genetic Epidemiology* 36: 438-450

9. **Thornton TA**, Tang H, Hoffman TJ, Ochs-Balcom HM, Caan BJ, and Risch NJ (2012) "Estimating Kinship in Admixed Populations" *American Journal of Human Genetics* 91:122-138. [Paper highlighted in the Editors' Corner of this issue.]

10. Ochs-Balcom HM, Preus L, Wactawski-Wende J, Nie J, Johnson NA, Zakharia F, Tang H, Carlson C, Carty C, Chen Z, Hoffman T, Hutter CM, Jackson RD, Kaplan RC, Li L, Liu S, Neuhouser ML, Peters U, Robbins J, Seldin MF, **Thornton TA**, Thompson CL, Kooperberg C, Sucheston LE (2013) "Admixture Mapping of DXA-Derived Phenotypes in WHI SHARe African-Americans" *Journal of Clinical Endocrinology and Metabolism* 98:E713-E717

11. Coram M, Duan Q, Hoffman TJ, **Thornton TA**, Knowles J, Johnson NA, Ochs-Balcom HM, Donlon TA, Martin LW, Eaton CB, Robinson JG, Risch NJ, Zhu X, Kooperberg C, Li Y, Reiner AP, Tang H. (2013) "Genome-wide Characterization of Shared and Distinct Genetic Components that Influence Blood Lipid Levels in Human Populations" *American Journal of Human Genetics* 92:904-916

12. Fohner A, Muzquiz LI, Austin MA, Gaedigk A, Gordon A, **Thornton TA**, Rieder MJ, Pershouse MA, Putnam EA, Howlett K, Beatty P, Thummel KE, Woodahl EL. (2013). "Pharmacogenetics in American Indian Populations: Analysis of CYP2D6, CYP3A4, CYP3A5, and CYP2C9 in the Confederated Salish and Kootenai Tribes" *Pharmacogenetics and Genomics*: 23:403-414

13. Kaklamani VG, Hoffmann TJ, **Thornton TA**, Geoffrey G, Chlebowski R, Horn LV6, Mantzoros C (2013) "Adiponectin pathway polymorphisms and risk of breast cancer in African Americans and Hispanics in the Women's Health Initiative" *Breast Cancer Research and Treatment* 139:461-468

14. Perez MV, Hoffmann TJ, Tang H, **Thornton TA**, Stefanick ML, Larson JC, Kooperberg K, , PhD, Reiner AP, Caan B, DrPH, Iribarren C, Risch N (2013) "African-American race but not genome-wide African ancestry is negatively associated with atrial fibrillation among postmenopausal women" *American Heart Journal* 166:566-572

15. **Thornton TA**, Austin M (2013) "Software and data resources for genetic association studies: Mini Review" *CAB Reviews 8,* 57:1-6

16. **Thornton TA**, Bermejo JL (2014) "Local and Global Ancestry Inference and Applications to Genetic Association Analysis for Admixed Populations" *Genetic Epidemiology 38 (S1): S5-S12*

17. **Thornton TA**, Conomos M, Sverdlov S, Marchani EE, Cheung C, Glazner C, Lewis S, Wijsman EM (2014) "Estimating and Adjusting for Ancestry Admixture in Statistical Methods for Relatedness Inference, Heritability Estimation, and Association Testing" *BMC Proceedings* 8:S5

18. Marchani EE, Cheung CYK, Glazner CG, Conomos MP, Lewis SM, Sverdlov S, **Thornton TA**, Wijsman EM (2014) "Identity-by-Descent Graphs Offer a Flexible Framework for Imputation and both Linkage and Association Analyses" *BMC Proceedings* 8:S19

19. Hoffman TJ, Tang H, **Thornton TA**, Caan BJ, Millen AE, Thomas F, and Risch NJ (2014) "Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative" *Human Molecular Genetics* 23:6634-6643. doi: 10.1093/hmg/ddu364

20. Alam TM, Petit RA, Crispell EK, **Thornton TA**, Conneely KN, Jiang Y, Satola SW, Read TD (2014) "Dissecting Vancomycin-Intermediate Resistance in Staphylococcus aureus Using Genome-Wide Association" *Genome Biology and Evolution* 6:1174-1185

21. **Thornton TA** "Statistical Methods for Genome-Wide and Sequencing Association Studies of Complex Traits in Related Samples" (2015) *Current Protocols in Human Genetics* 84:1.28.1-9. doi: 10.1002/0471142905.hg0128s84

22. Hong X, Hao K, Ladd-Acosta C, Hansen KD, Tsai HJ, Liu X, Xu X, **Thornton TA**, Caruso D, Keet CA, Sun Y, Wang G, Luo W, Kumar R, Fuleihan R, Singh AM, Kim JS, Story RE, Gupta RS, Gao P, Chen Z, Walker S, Bartell TR, Beaty TH, Fallin MD, Schleimer R, Holt PG, Nadeau KC, Wood RA, Pongracic JA, Weeks DE, Wang X (2015) "Genome-wide Association Study of Food Allergy Identifies Peanut Allergy-Specific Susceptibility Loci and Evidence of Epigenetic Mediation in U.S. Children of European Ancestry" *Nature Communications* 6:6304. doi: 10.1038/ncomms7304

23. Conomos MP*, Miller M, **Thornton TA** (2015) "Robust Inference of Population Structure for Ancestry Prediction and Correction of Stratification in the Presence of Relatedness" *Genetic Epidemiology* 39: 276-93. *This paper won the Genetic Epidemiology Robert C. Elston Best Paper Award for original papers published in 2015.*

24. Fohner AE, Robinson R, Yracheta J, Dillard D, Schilling B, Kahn B, Hopkins S, Boyer B, Black J, Gordon A, Nickerson D, Tsai J, Farin F, **Thornton TA**, Rettie AE, Thummel KE (2015) "Variation in Genes Controlling Warfarin Disposition and Response in American Indian and Alaska Native people: CYP2C9, VKORC1, CYP4F2, CYP4F11, GGCX" *Pharmacogenetics and Genomics* 25:343-353

25. Shirasaka Y, Chaudhry AS, McDonald M, Prasad B, Wong T, Calamia JC, Fohner A, **Thornton TA**, Isoherranen N, Unadkat JD, Rettie AE, Schuetz EG, Thummel KE. (2015) "Interindividual variability of CYP2C19-catalyzed drug metabolism due to differences in gene diplotypes and cytochrome P450 oxidoreductase content." *Pharmacogenomics Journal* doi: 10.1038/tpj.2015.58. [Epub ahead of print] [PMID: 26323597]

26. Fohner AE, Wang Z, Yracheta J, O'Brien DM, Hopkins SE, Black J, Philip J, Wiener HW, Tiwari HK, Stapleton PL, Tsai JM, **Thornton TA**, Boyer BB, Thummel KE (2015) "Genetics, Diet, and Season Are Associated with Serum 25-Hydroxylated Cholecalciferol Concentration in a Yup'ik Study Population from Southwestern Alaska" *Journal of Nutrition* doi: 10.3945/jn.115.223388

27. Morrison J, Laurie CC, Marazita ML, Sanders AE, Offenbacher S, Salazar CR, Conomos MP*, **Thornton TA**, Jain D, Laurie CA, Kerr K. (2015) Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). *Human molecular genetics* doi: 10.1093/hmg/ddv506

28. Conomos MP*, Reiner AP, Weir BS, **Thornton TA** (2016) "Model-Free Estimation of Recent Genetic Relatedness" *American Journal of Human Genetics* 98:127–148. *With a shorter version of this paper, Matthew Conomos won the 2014 WNAR student written paper competition.*

29. Conomos MP*, Laurie CA, Stilp AM, Gogarten SM, McHugh CP, Nelson SC, Sofer T, Fernández-Rhodes L, Justice AE, Graff M, Young KL, Seyerle AA, Avery CL, Taylor KD, Rotter JI, Talavera G, Daviglus ML, Wassertheil-Smoller S, Schneiderman N, Heiss G, . Kaplan RC, Franceschini N, Reiner AP, Shaffer JR, Barr RG, Kerr KR, Browning SR, Browning BL, Weir BS, M. Avilés-Santa L, Papanicolaou GJ, Lumley T, Szpiro AA, Rice K**,** **Thornton TA**, Laurie CC (2016)"Genetic Diversity and Association Studies in U.S. Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos" *American Journal of Human Genetics* 98:165–184

30. Schick UM, Jain D, Hodonsky CJ, Morrison JV, Davis JP, Brown L*, Sofer T, Conomos MP*, Schurmann C, McHugh CP*, Nelson SC, Vadlamudi S, Stilp A, Plantinga A, Baier L, Bien SA, Gogarten SM, Laurie CA, Taylor KD, Liu Y, Auer PL, Franceschini N, Szpiro A, Rice K, Kerr KF, Rotter JI, Hanson RL, Papanicolaou G, Rich SS, Loos RJ, Browning BL, Browning SR, Weir BS, Laurie CC, Mohlke KL, North KE**, **Thornton TA****, Reiner AP** (2016) "Genome-wide association study of platelet count identifies ancestry-specific loci in Hispanic/Latino Americans" *American Journal of Human Genetics* 98:229–242

31. Fohner AE, Wang Z, Yracheta J, O'Brien DM, Hopkins SE, Black J, Philip J, Wiener HW, Tiwari HK, Stapleton PL, Tsai JM, **Thornton TA,** Boyer BB, Thummel KE (2016) "Genetics, Diet, and Season Are Associated with Serum 25-Hydroxylated Cholecalciferol Concentration in a Yup'ik Study Population from Southwestern Alaska." *Journal of Nutrition* 146: 318-325

32. Mez J, Mukherjee S, **Thornton TA**, Fardo DW, Trittschuh E, Sutti S, Sherva R, Kauwe JS, Naj AC, Beecham GW, Gross A (2016) "The executive prominent/memory prominent spectrum in Alzheimer's disease are highly heritable" *Neurobiology of Aging* 41:115-21

33. Wheat CL, Clark-Snustad K, Devine B, Grembowski D, **Thornton TA**, Ko CW (2016) "Worldwide Incidence of Colorectal Cancer, Leukemia, and Lymphoma in Inflammatory Bowel Disease: An Updated Systematic Review and Meta-Analysis" *Gastroenterol Res Pract.* 2016:1632439. doi: 10.1155/2016/1632439

34. Chen H, Wang C, Conomos MP*, Stilp AM, Li Z, Sofer T, Szpiro AA, Chen W, Brehm JM, Celedón JC, Redline S, Papanicolaou GJ, **Thornton TA**, Laurie CC, Rice K, Lin X (2016) "Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models" *American Journal of Human Genetics*. 98:653-66

35. Cade BE, Chen H, Stilp AM, Gleason KJ, Sofer T, Ancoli-Israel S, Arens R, Bell GI, Below JE, Bjonnes AC, Chun S, Conomos MP*, Evans DS, Johnson WC, Frazier-Wood AC, Lane JM, Larkin EK, Loredo JS, Post WS, Ramos AR, Rice K, Rotter JI, Shah NA, Stone KL, Taylor KD, **Thornton TA**, Tranah GJ, Wang C, Zee PC, Hanis CL, Sunyaev SR, Patel SR, Laurie CC, Zhu X, Saxena R, Lin X, Redline S. (2016) "Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans." *Am J Respir Crit Care Med* DOI: 10.1164/rccm.201512-2431OC [Epub ahead of print]

36. McHugh CP*, Brown L*, **Thornton TA** (2016) "Detecting Heterogeneity in Population Structure Across the Genome in Admixed Populations." *Genetics* 204: 43-56 [*This paper was chosen by GENETICS Editors as one of the September 2016 Highlights.*]

37. Kramer HJ, Stilp AM, Laurie CC, Reiner AP, Lash J, Daviglus ML, Rosas SE, Ricardo AC, Tayo BO, Flessner MF, Kerr KF, Peralta C, Durazo-Arvizu R, Conomos M, **Thornton TA**, Rotter J, Taylor KD, Cai J, Eckfeldt J, Chen H, Papanicolau G, Franceschini N. (2016) "African Ancestry–Specific Alleles and Kidney Disease Risk in Hispanics/Latinos." *Journal of the American Society of Nephrology*, pp.ASN-2016030357

38. Nelson SC, Stilp AM, Papanicolaou GJ, Taylor KD, Rotter JI, **Thornton TA**, Laurie CC (2016). "Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL)" *Human Molecular Genetics*, ddw174

39. Mahajan A, Rodan AR, Le TH, Gaulton KJ, Haessler J, Stilp AM, Kamatani Y, Zhu G, Sofer T, Puri S, Schellinger JN, Chu PL, Cechova S, van Zuydam N; SUMMIT Consortium.; BioBank Japan Project., Arnlov J, Flessner MF, Giedraitis V, Heath AC, Kubo M, Larsson A, Lindgren CM, Madden PA, Montgomery GW, Papanicolaou GJ, Reiner AP, Sundström J, **Thornton TA**, Lind L, Ingelsson E, Cai J, Martin NG, Kooperberg C, Matsuda K, Whitfield JB, Okada Y, Laurie CC, Morris AP, Franceschini N. (2016) "Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity." *American Journal of Human Genetics* 99: 636-646

40. Saad M, Alejandro QN, Grimson FL, Lewis SM, Brown LA*, Blue EM, **Thornton TA**, Thompson EA, Wijsman (2016) "Identity-by-Descent Estimation with Population- and Pedigree-based Imputation in Admixed Family Data" *BMC Proceedings; 10(Suppl 7):295-301*

41. Blue EM, Brown LA*, Conomos MP*, Kirk JL, Nato AQ, Popejoy AB, Raffa J, Ranola J, Wijsman EM, **Thornton TA** (2016) "Estimating relationships between phenotypes and subjects drawn from admixed families" *BMC Proceedings;10(Suppl 7):357-362*

42. Noordam R, Sitlani CM, Avery CL, Stewart JD, Gogarten SM, Wiggins KL, Trompet S, Warren HR, Sun F, Evans DS, Li X, Li J, Smith AV, Bis JC, Brody JA, Busch EL, Caulfield MJ, Chen YI, Cummings SR, Cupples LA,…, **Thornton TA**,… Rotter JI, Vasan RS, Psaty BM, Stricker BH, Whitsel EA (2016). A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Journal of Medical Genetics*, jmedgenet-2016

43. Sofer T, Heller R, Bogomolov M, Avery CL, Graff M, North KE, Reiner AP, **Thornton TA**, Rice K, Benjamini Y, Laurie CC, Kerr KF (2017) A Powerful Statistical Framework for Generalization Testing in GWAS, with Application to the HCHS/SOL. *Genet Epidemiol*, doi: 10.1002/gepi.22029

44. Brown LA*, Sofer T, Stilp AM, Baier LJ, Kramer HJ, Masindova I, Levy D, Hanson RL, Moncrieft AE, Redline S, Rosas SE, Lash JP, Cai J, Laurie CC, Browning S, **Thornton TA**, Franceschini N (2017) Admixture Mapping Identifies an Amerindian Ancestry Locus Associated with Albuminuria in Hispanics in the United States. *Journal of the American Society of Nephrology*, 30:ASN-2016091010

45. Jain D, Hodonsky CJ, Schick UM, Morrison JV, Minnerath S, Brown LA*, Schurmann C, Liu Y, Auer PL, Laurie CA, Taylor KD, Browning BL, Papanicolaou G, Browning SR, Loos RJF, North KE, Thyagarajan B, Laurie CC, **Thornton TA**, Sofer T, Reiner AP. (2017). Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. *Human Molecular Genetics*, 26(6), 1193-1204

46. Jun GR, Chung J, Mez J, Barber R, Beecham GW, Bennett DA, ..., **Thornton TA**, Younkin SG, Vardarajan BN, Wang LS, Wendlund JR, Winslow AR; Alzheimer's Disease Genetics Consortium, Haines J, Mayeux R, Pericak-Vance MA, Schellenberg G, Lunetta KL, Farrer LA (2017) Transethnic genome-wide scan identifies novel Alzheimer's disease loci. *Alzheimers Dement*. 13(7):727-738. doi: 10.1016/j.jalz.2016.12.012

47. Raffield LM, Louie T, Sofer T, Jain D, Ipp E, Taylor KD, Papanicolaou GJ, Avilés-Santa L, Lange LA, Laurie CC, Conomos MP*, **Thornton TA**, Chen YI, Qi Q, Cotler S, Thyagarajan B, Schneiderman N, Rotter JI, Reiner AP, Lin HJ (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 Gene*, 26(10):1966-1978. doi: 10.1093/hmg/ddx082

48. Au NT, Reyes M, Boyer BB, Hopkins SE, Black J, O'Brien D, Fohner AE, Yracheta J, **Thornton TA**, Austin MA, Burke W, Thummel KE, Rettie AE (2017) Dietary and genetic influences on hemostasis in a Yup'ik Alaska Native population. PLoS One, 12(4):e0173616. doi: 10.1371/journal.pone.0173616. eCollection 2017

49. Wheat CL, Ko CW, Clark-Snustad K, Grembowski D, **Thornton TA**, Devine B (2017) Inflammatory Bowel Disease (IBD) pharmacotherapy and the risk of serious infection: a systematic review and network meta-analysis. *BMC Gastroenterol*, 17(1):52. doi: 10.1186/s12876-017-0602-0

50. Hodonsky CJ, Jain D, Schick UM, Morrison JV, Brown L, McHugh CP, Schurmann C, Chen DD, Liu YM, Auer PL, Laurie CA, Taylor KD, Browning BL, Li Y, Papanicolaou G, Rotter JI, Kurita R, Nakamura Y, Browning SR, Loos RJF, North KE, Laurie CC, **Thornton TA**, Pankratz N, Bauer DE, Sofer T, Reiner AP (2017) Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. *PLoS Genetics*, 13(4):e1006760. doi: 10.1371/journal.pgen.1006760

51. Kerr KF, Avery CL, Lin HJ, Raffield LM, Zhang QS, Browning BL, Browning SR, Conomos MP*, Gogarten SM, Laurie CC, Sofer T, **Thornton TA**, Hohensee C, Jackson RD, Kooperberg C, Li Y, Méndez-Giráldez R, Perez MV, Peters U, Reiner AP, Zhang ZM, Yao J, Sotoodehnia N, Taylor KD, Guo X, Lange LA, Soliman EZ, Wilson JG, Rotter JI, Heckbert SR, Jain D, Whitsel EA. (2017) Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. *Heart Rhythm*, 14(11):1675-1684. doi: 10.1016/j.hrthm.2017.06.018

52. Nolte IM, Munoz ML, Tragante V, Amare AT, Jansen R, Vaez A, von der Heyde B, Avery CL, Bis JC, Dierckx B, van Dongen J, Gogarten SM, Goyette P, ..., **Thornton TA**, ..., Brundel BJJM, Heckbert SR, Whitsel EA, den Hoed M, Snieder H, de Geus EJC (2017) Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, 8:15805. doi: 10.1038/ncomms15805

53. Zhan X, Zhao N, Plantinga A, **Thornton TA**, Conneely KN, Epstein MP, Wu MC (2017) Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. *Genetics*, 206(4):1779-1790. doi: 10.1534/genetics.116.199646

54. Chen H, Cade BE, Gleason KJ, Bjonnes AC, Stilp AM, Sofer T, Conomos MP*, Ancoli-Israel S, Arens R, Azarbarzin A, Bell GI, Below JE, ..., **Thornton TA**, Tranah GJ, Wang C,..., Lin X, Redline S. (2017) Multi-ethnic Meta-analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea Related Quantitative Trait Locus in Men. *Am J Respir Cell Mol Bio*, doi: 10.1165/rcmb.2017-0237OC

55. Au NT, Ryman T, Rettie AE, Hopkins SE, Boyer BB, Black J, Philip J, Yracheta J, Fohner AE, Reyes M, **Thornton TA**, Austin MA, Thummel KE (2017) Dietary Vitamin K and Association with Hepatic Vitamin K Status in a Yup'ik Study Population from Southwestern Alaska. *Mol Nutr Food Res*, doi: 10.1002/mnfr.201700746

56. Sofer T, Baier LJ, Browning SR, **Thornton TA**, Talavera GA, Wassertheil-Smoller S, Daviglus ML, Hanson R, Kobes S, Cooper RS, Cai J, Levy D, Reiner AP, Franceschini N (2017) Admixture mapping in the Hispanic Community Health Study/Study of Latinos reveals regions of genetic associations with blood pressure traits. *PLoS One*, 12(11):e0188400. doi: 10.1371/journal.pone.0188400

57. Khan BA, Robinson R, Fohner AE, Muzquiz LI, Schilling BD, Beans JA, Olnes MJ, Trawicki L, Frydenlund H, Laukes C, Beatty P, Phillips B, Nickerson D, Howlett K, Dillard DA, **Thornton TA**, Thummel KE, Woodahl EL (2018) Cytochrome P450 Genetic Variation Associated with Tamoxifen Biotransformation in American Indian and Alaska Native People. *Clin Transl Sci*. doi: 10.1111/cts.12542

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59. Blue EE, Bis JC, Dorschner MO, Tsuang DW, Barral SM, Beecham G, Below JE, Bush WS, Butkiewicz M, Cruchaga C, DeStefano A, Farrer LA, Goate A, Haines J, Jaworski J, Jun G, Kunkle B, Kuzma A, Lee JJ, Lunetta KL, Ma Y, Martin E, Naj A, Nato AQ, Navas P, Nguyen H, Reitz C, Reyes D, Salerno W, Schellenberg GD, Seshadri S, Sohi H, **Thornton TA**, Valadares O, van Duijn C, Vardarajan BN, Wang LS, Boerwinkle E, Dupuis J, Pericak-Vance MA, Mayeux R, Wijsman EM; on behalf of the Alzheimer's Disease Sequencing Project (2018) Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimer's Disease Sequencing Project. *Dement Geriatr Cogn Disord* 45(1-2):1-17. doi: 10.1159/000485503

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64. Nafikov RA, Nato AQ Jr, Sohi H, Wang B, Brown L, Horimoto AR, Vardarajan BN, Barral SM, Tosto G, Mayeux RP, **Thornton TA**, Blue E, Wijsman EM (2018) Analysis of pedigree data in populations with multiple ancestries: Strategies for dealing with admixture in Caribbean Hispanic families from the ADSP. *Genet Epidemiol* 42(6):500-515. doi: 10.1002/gepi.22133

65. Workalemahu T, Enquobahrie DA, Gelaye B, Sanchez SE, Garcia PJ, Tekola-Ayele F, Hajat A, **Thornton TA**, Ananth CV, Williams MA (2018) Genetic variations and risk of placental abruption: A genome-wide association study and meta-analysis of genome-wide association studies. *Placenta* 66:8-16. doi: 10.1016/j.placenta.2018.04.008

66. Bis JC, Jian X, Kunkle BW, Chen Y, Hamilton-Nelson KL, Bush WS, Salerno WJ, Lancour D, Ma Y, Renton AE, Marcora E, Farrell JJ, Zhao Y, Qu L, Ahmad S, Amin N, Amouyel P, Beecham GW, Below JE, Campion D, Charbonnier C, …, Soininen H, **Thornton TA**, …, Boerwinkle E, Lunetta KL, Destefano AL, Dupuis J, Martin ER, Schellenberg GD, Seshadri S, Naj AC, Fornage M, Farrer LA (2018) Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. *Mol Psychiatry* doi: 10.1038/s41380-018-0112-7

67. Workalemahu T, Enquobahrie DA, Gelaye B, **Thornton TA**, Tekola-Ayele F, Sanchez SE, Garcia PJ, Palomino HG, Hajat A, Romero R, Ananth CV, Williams MA (2018) Abruptio placentae risk and genetic variations in mitochondrial biogenesis and oxidative phosphorylation: replication of a candidate gene association study. *Am J Obstet Gynecol* 219(6):617.e1-617.e17. doi: 10.1016/j.ajog.2018.08.042

68. Grinde KE, Qi Q, **Thornton TA**, Liu S, Shadyab AH, Chan KHK, Reiner AP, Sofer T (2018) Generalizing polygenic risk scores from Europeans to Hispanics/Latinos. *Genet Epidemiol* doi: 10.1002/gepi.22166

69. Wang H, Cade BE, Sofer T, Sands SA, Chen H, Browning S, Stilp AM, Louie TL, **Thornton TA**, Craig Johnson W, Below JE, Conomos MP, Evans DS, Gharib SA, Guo X, Frazier-Wood AC, Mei H, Yaffe K, Loredo JS, Ramos AR, Barrett-Connor E, Ancoli-Israel S, Zee PC, Arens R, Shah NA, Taylor KD, Tranah GJ, Stone KL, Hanis CL, Wilson JG, Gottlieb DJ, Patel SR, Rice K, Post WS, Rotter JI, Sunyaev SR, Cai J, Lin X, Purcell SM, Laurie CC, Saxena R, Redline S, Zhu X. (2018) Admixture mapping identifies novel loci for obstructive sleep apnea in hispanic/latino americans. *Hum Mol Genet* doi: 10.1093/hmg/ddy387

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72. Mikhaylova A*, **Thornton TA** (2019) Accuracy of gene expression prediction from genotype data with PrediXcan varies across and within continental populations. *Frontiers in Genetics*. doi: 10.3389/fgene.2019.00261

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74. Thomson RJ, McMorran B, Hoy W, Jose M, Whittock L, **Thornton TA**, Burgio G, Mathews JD, Foote S (2019) New Genetic Loci Associated With Chronic Kidney Disease in an Indigenous Australian Population. doi: 10.3389/fgene.2019.00330.

75. Wojcik G, Graff M, Nishimura KK, Tao R, Haessler J, Gignoux CR, Highland HM, Patel YM, Sorokin EP, Avery CL, Belbin GM, Bien SA, Iona Cheng, 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 VS, Sockell A, Vahi K, Vishnu A, Verbanck M, Walker R, Young KJ, Zubair N, Acuna-Alonso V, Ambite JL, Barnes KC, Boerwinkle E, Bottinger E, Bustamante CD, Caberto C, Canizales-Quinteros S, Conomos MP*, Deelman E, Do R, Doheny K, Fernandez-Rhodes L, Fornage M, Heiss G, Henn BM, Hindorff LA, Jackson RD, Hailu B, Laurie CA, Laurie CC, Li Y, Lin DY, Moreno-Estrada A, Nadkarni G, Norman PJ, Pooler LC, Reiner AP, Romm J, Sabati C, Sandoval K, Sheng X, Stahl EA, Stram DO, **Thornton TA**, Wassel CL, Wilkens LR, Winkler CA, Yoneyama S, Buyske S, Haiman C, Kooperberg C, Marchand LL, Loos RJF, Matise TC, North KE, Peters U, Kenny EE, Carlson CC (2019) The PAGE Study: How Genetic Diversity Improves Our Understanding of the Architecture of Complex Traits. *Nature* 70:514-518. doi: 10.1038/s41586-019-1310-4.

76. Swenson BR, Louie T, Lin HJ, Méndez-Giráldez R, Below JE, Laurie CC, Kerr KF, Highland H, **Thornton TA**, Ryckman KK, Kooperberg C, Soliman EZ, Seyerle AA, Guo X, Taylor KD, Yao J, Heckbert SR, Darbar D, Petty LE, McKnight B, Cheng S, Bello NA, Whitsel EA, Hanis CL, Nalls MA, Evans DS, Rotter JI, Sofer T, Avery CL, Sotoodehnia N (2019) GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. *PLoS One* 14:e0217796. doi: 10.1371/journal.pone.0217796.

Submitted Manuscripts Currently Under Review/Revision

1. Conomos MA*, Reiner AP, McPeek MS, **Thornton TA.** "Genome-wide Control of Population Structure via Linear Mixed Models with Orthogonally Partitioned Structure" (Under Revision)

2. JL Kirk*, **Thornton TA**. "Principal components analysis with sensible weighting of rare variants: Improved inference of fine-scale population structure" (Under Revision)

3. Blue EE, Horimoto AR, Wijsman EM, **Thornton TA**. "Local ancestry at *APOE* modifies Alzheimer's disease risk in Caribbean Hispanics" (Under Revision)

4. McHugh CP*, Conomos MP, Gogarten SM, Jain D, Laurie CC, North K, Reiner AP, **Thornton TA**. "UMMAX: A Unified Mixed Model Framework for Autosomal and X Chromosome Association Testing in Samples with Population Structure and Relatedness" (Under Review)

5. Gogarten SM, Sofer T, Chen H, Yu C, Brody JA, **Thornton TA**, Rice KM, Conomos MP*. "Genetic association testing using the GENESIS R/Bioconductor package" (Under Second Round of Review)

Refereed Consortium Member Publications

1. Emond MJ, Louie T, Emerson J, Zhao W, Mathias RA, Knowles MR, Wright FA, Rieder MJ, Tabor HK, Nickerson DA, Barnes KC; **NHLBI GO Exome Sequencing Project**; Lung GO, Gibson RL, Bamshad MJ (2012) "Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic Pseudomonas aeruginosa infection in cystic fibrosis" *Nature Genetics* 44: 886-889

2. Boileau C, Guo DC, Hanna N, Regalado ES, Detaint D, Gong L, Varret M, Prakash SK, Li AH, d'Indy H, Braverman AC, Grandchamp B, Kwartler CS, Gouya L, Santos-Cortez RL, Abifadel M, Leal SM, Muti C, Shendure J, Gross MS, Rieder MJ, Vahanian A, Nickerson DA, Michel JB; **NHLBIGO Exome Sequencing Project**, Jondeau G, Milewicz DM (2012) "TGFB2 mutations cause familial thoracic aortic aneurysms and dissections associated with mild systemic features of Marfan syndrome" *Nature Genetics* 44:916-921

3. Fu W, O'Connor TD, Jun G, Kang HM, Abecasis G, Leal SM, Gabriel S, Rieder MJ, Altshuler D, Shendure J, Nickerson DA, Bamshad MJ; **NHLBI Exome Sequencing Project**, Akey JM. (2013). "Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants" *Nature* 493:216-220

4. Rosenthal EA, Ranchalis J, Crosslin DR, Burt A, Brunzell JD, Motulsky AG, Nickerson DA; **NHLBIGO Exome Sequencing Project**, Wijsman EM, Jarvik GP (2013) "Joint Linkage and Association Analysis with Exome Sequence Data Implicates SLC25A40 in Hypertriglyceridemia" *American Journal of Human Genetics* 93:1035-1045

5. Guo DC, Regalado E, Casteel DE, Santos-Cortez RL, Gong L, Kim JJ, Dyack S, Horne SG, Chang G, Jondeau G, Boileau C, Coselli JS, Li Z, Leal SM, Shendure J, Rieder MJ, Bamshad MJ, Nickerson DA; GenTAC Registry Consortium; **NHLBIGO Exome Sequencing Project**, Kim C, Milewicz DM (2013) "Recurrent Gain-of-Function Mutation in PRKG1 Causes Thoracic Aortic Aneurysms and Acute Aortic Dissections" *American Journal of Human Genetics* 93:398-404

6. O'Connor TD, Kiezun A, Bamshad M, Rich SS, Smith JD, Turner E; **NHLBIGO Exome Sequencing Project**; ESP Population Genetics, Statistical Analysis Working Group, Leal SM, Akey JM (2013) "Fine-scale patterns of population stratification confound rare variant association tests" *PloS One* 8:e65834

7. Johnsen JM, Auer PL, Morrison AC, Jiao S, Wei P, Haessler J, Fox K, McGee SR, Smith JD, Carlson CS, Smith N, Boerwinkle E, Kooperberg C, Nickerson DA, Rich SS, Green D, Peters U, Cushman M, Reiner AP; **NHLBI Exome Sequencing Project** (2013) "Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project" *Blood* 122:590-597

8. Norton N, Li D, Rampersaud E, Morales A, Martin ER, Zuchner S, Guo S, Gonzalez M, Hedges DJ, Robertson PD, Krumm N, Nickerson DA, Hershberger RE; **NHLBI Exome Sequencing Project** and the Exome Sequencing Project Family Studies Project Team (2013) "Exome sequencing and genome-wide linkage analysis in 17 families illustrate the complex contribution of TTN truncating variants to dilated cardiomyopathy" *Circulation Cardiovascular Genetics* 6:144-153.

9. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, Tang ZZ, Bizon C, Lange EM, Smith JD, Turner EH, Jun G, Kang HM, Peloso G, Auer P, Li KP, …, Willer CJ; **NHLBIGO Exome Sequencing Project** (2014) "Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol" *American Journal of Human Genetics* 94:233-245

10. Zekavat SM, Ruotsalainen S, Handsaker RE, Alver M, Bloom J, Poterba T, Seed C, Ernst J, Chaffin M, Engreitz J, Peloso GM, Manichaikul A, Yang C, Ryan KA, Fu M, Johnson WC, Tsai M, Budoff M, Vasan RS, Cupples LA, Rotter JI, Rich SS, Post W, Mitchell BD, Correa A, Metspalu A, Wilson JG, Salomaa V, Kellis M, Daly MJ, Neale BM, McCarroll S, Surakka I, Esko T, Ganna A, Ripatti S, Kathiresan S, Natarajan P; **NHLBI TOPMed Lipids Working Group** (2018). Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nat Commun* 9(1):2606. doi: 10.1038/s41467-018-04668

11. Natarajan P, Peloso GM, Zekavat SM, Montasser M, Ganna A, Chaffin M, Khera AV, Zhou W, Bloom JM, Engreitz JM, Ernst J, O'Connell JR, Ruotsalainen SE, Alver M, Manichaikul A, Johnson WC, Perry JA, Poterba T, Seed C, Surakka IL, Esko T, Ripatti S, Salomaa V, Correa A, Vasan RS, Kellis M, Neale BM, Lander ES, Abecasis G, Mitchell B, Rich SS, Wilson JG, Cupples LA, Rotter JI, Willer CJ, Kathiresan S; **NHLBI TOPMed Lipids Working Group**. (2018) Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nat Commun* 9(1):3391. doi: 10.1038/s41467-018-05747-8

12. Rosenthal EA, Shirts BH, Amendola LM, Horike-Pyne M, Robertson PD, Hisama FM, Bennett RL, Dorschner MO, Nickerson DA, Stanaway IB, Nassir R, Vickers KT, Li C, Grady WM, Peters U, Jarvik GP; **NHLBI GO Exome Sequencing Project**. (2018) Rare loss of function variants in candidate genes and risk of colorectal cancer. *Hum Genet* 37(10):795-806. doi: 10.1007/s00439-018-1938-4

13. Zhang X, Zhu C, Beecham G, Vardarajan BN, Ma Y, Lancour D, Farrell JJ, Chung J; **Alzheimer's Disease Sequencing Project**, Mayeux R, Haines JL, Schellenberg GD, Pericak-Vance MA, Lunetta KL, Farrer LA. (2019) A rare missense variant of CASP7 is associated with familial late-onset Alzheimer's disease. Alzheimers & Dement 15(3):441-452. doi: 10.1016/j.jalz.2018.10.005

Other Refereed Scholarly Publications

1. Anderson-Cook CM, **Thornton, T**, Robles, R (1997), "Measuring Hockey Powerplay and Penalty Killing Efficiency", *Proceedings of the American Statistical Association Section on Statistics in Sports*, Alexandria, VA: American Statistical Association, 11-14.

Other Non-Refereed Scholarly Publications

1. **Thornton TA** (2005) Statistical Inference for Genetic Analysis in Related Individuals. PhD Dissertation, Department of Statistics, University of Chicago

Books and book chapters

1. **Thornton TA:** "Software and Data Resources for Genetic Epidemiology Studies," **In** : Genetic Epidemiology: Methods and Applications (authors: Austin MA, Beaty TH, Dotson WD, Edwards K, Fullerton SM, Gwinn M, Khoury M, Mcknight B, Ottman R, Psaty B, Schwartz SM, Stanford J, Thornton T). Wallingford, Oxfordshire, UK: CAB International Publishing, 2013.

8. Patents and Other Intellectual Property

Publically Available Software

1. **Thornton TA**, McPeek M (2007) MQLS – software written in C for case-control genetic association testing in samples that contain related individuals with known pedigrees, available at http://galton.uchicago.edu/~mcpeek/software/MQLS/index.html

2. **Thornton TA**, McPeek M (2010) ROADTRIPS - software written in C for case-control genetic association testing in samples with partially or completely unknown population and pedigree structure, available at http://galton.uchicago.edu/~mcpeek/software/ROADTRIPS/index.html

3. **Thornton TA**, McPeek M (2012) MQLS-XM – software written in C for performing single-SNP, case-control association testing for the autosomal chromosomes and the X-chromosome in samples with known relatedness, available at http://galton.uchicago.edu/~mcpeek/software/MQLX_XM/index.html

4. **Thornton TA** (2012) REAP - software written in C for estimating autosomal kinship coefficients and identity-by-descent (IBD) sharing probabilities using SNP genotype data in

samples with admixed ancestry, available at
http://faculty.washington.edu/tathornt/software/REAP/index.html

5. Conomos MP, **Thornton TA**, Gogarten SM (2015-) GENESIS: GENetic EStimation and Inference in Structured samples (GENESIS) – R Software package for a variety of statistical analyses with genetic data from samples with population structure and/or relatedness. Available from Bioconductor at
http://bioconductor.org/packages/release/bioc/html/GENESIS.html

9. Funding History

Active Funded Projects

- Principal Investigator and Program Director, T32GM081062 (Thornton) "Predoctoral Research Training in Statistical Genetics", NIH/NIGMS, 7/01/2017-6/31/2022, 5% FTE.
- Principal Investigator of Subcontract and Co-Investigator (Haines/subc-Thornton) U01 AG058654 "The Alzheimer Disease Sequence Analysis Collaborative",NIH/NIA, 09/30/2018-08/31/2023, 5% FTE
- Principal Investigator of Subcontract and Co-Investigator, RF1 AG054074 (Pericak-Vance/sub-Thornton) "Genomic Characterization of Alzheimer's Disease Risk in the Puerto Rican population", NIH/NIA, 7/1/2016-6/30/2021, 10% FTE
- Principal Investigator of Subcontract and Co-Investigator, R01 MD012765 (N Franceschini/sub-Thornton) "Leveraging ancestry to map kidney loci", NIMHD, 09/24/2017 - 04/30/2022, 10% FTE
- Investigator HHSN268201800001I (Rice, Psaty, Weir) "Trans-Omics for Precision Medicine (TOPMed) Data Coordinating Center (DCC) NIH/NHLBI 5/1/2018-5/16/2020, 10% FTE
- Investigator, R01 AG059737 (E Blue) "Identification of genetic modifiers of Alzheimer's disease in multiethnic cohorts" NIA, 06/01/2016 - 05/31/2019, 10% FTE
- Investigator, U01 HL137162-01 (Rice/Weir), " From gene regions to whole chromosomes: scaling up association-finding for disease and omics outcomes in TOPMed", NIH/NHLBI, 04/01/2017-3/31/2020, 7.5% FTE
- Investigator, U01 AG049507 (Wijsman), "Sequence-based discovery of AD Risk & Protective Alleles" NIH/NIA, 6/15/2016-5/31/2019, 5% FTE.
- Investigator, R01 HL130733 (Lange/Reiner), "Sequence analysis of hematological traits in African Americans", NIH/NHLBI, 8/1/2016-4/20/2020, 5% FTE
- Investigator, P01 GM116691 (Burke/Thummel) "Program on Genetic and Dietary Predictors of Drug Response in Rural and AI/AN Populations", NIH/NIGMS, 08/01/2016- 07/31/2021, 10% FTE
- Investigator, R01 HL071862 (Reiner), "Thrombosis genetics in African Americans", NIH/NHLBI, 5/1/2017-4/30/2021, 5% FTE

Completed Funded Projects

- Principal Investigator of component project, P01 HG0099568 (Weir) "Statistical and quantitative genetics", NIH/NIGMS, 6/5/2012-4/30/2017, 30% FTE
- Investigator, R01 HL120393-02A1S1 (Psaty/Rice/Weir), "DCC supplement for rare variants and NHLBI traits", NIH/NHLBI, 06/01/2016-3/31/2018, 5% FTE
- Investigator, R01 AG04237 (P Crane), "Genetic architecture of memory and executive functioning in Alzheimer's disease", NIH/NIA 9/1/2014-5/31/2018, 5% FTE
- Investigator, U01 (Seshadri/sub-Psaty), "Identifying Risk & Protective SNV for AD in ADSP Case-control Sample", NIH/NIA, 6/15/2014-5/31/2018, 5% FTE.
- Principal Investigator of Subcontract and Co-Investigator, R01 HL116446 (Reiner) "Leukocyte Telomere Length and Cardiovascular Disease in Jackson Heart Study", NIH/NHLBI, 8/1/2013-5/31/2017, 10% FTE
- Principal Investigator, K01 CA148958 (Thornton) "Statistical methods for cancer genetic association studies with hidden population structure", NIH/NCI, 9/1/2010-5/31/2016, 50% FTE

- Investigator, HHSN268201300005 (Weir) "Omics in Latinos (Ola) - Genetic Analysis", NIH/NHLBI, 3/18/2013-9/17/2016, 5% FTE, Role: Investigator
- Principal Investigator, R13 HG007506 (Thornton) "Impact of large-scale genomic data on statistical and quantitative genetics", NIH/NHGRI/NCI, 9/1/2013-8/31/2014, 0% FTE, Role: PI
- Principal Investigator of Subcontract N01 WH-2-2110 (Risch) "Women's Health Initiative SNP Health Association Resource Analytic Center (SHARe Analytic Centers)", NIH/NHLBI with subcontract from UCSF, 8/1/2009-3/31/2011, 20% FTE
- Principal Investigator of Subcontract, CA15704 (Prentice) "Cancer Center Support Grant", NIH/NCI subcontract from FHCRC, 7/1/2009-6/30/2012

10. Public Health Practice Activities

N/A

11. Conferences and Symposiums

Invited Oral Presentations and Seminars

1. Loyola University, Department of Preventive Medicine & Epidemiology, Chicago, IL (Sep 2005)
2. Mayo Clinic, Division of Biostatistics, Rochester, MN (Dec 2005)
3. University of Chicago, Department of Statistics, Chicago, IL. (Dec 2005)
4. North Carolina State University, Department of Statistics, Raleigh, NC. (Apr 2006)
5. Walter and Eliza Hall Institute of Medicine, Melbourne, Australia. (Nov 2006)
6. University of California at Irvine, Department of Statistics, Irvine, CA. (Jan 2007)
7. Tulane University, Department of Mathematics, New Orleans, LA. (Sep 2007)
8. Walter and Eliza Hall Institute of Medicine, Melbourne, Australia. (Oct 2007)
9. Joint Mathematics Meetings, San Diego, CA. (Jan 2008)
10. University of California at Riverside, Department of Statistics, Riverside, CA. (Feb 2008)
11. University of California at Berkeley, Department of Statistics, Berkeley, CA. (Feb 2008)
12. University of Washington, Department of Biostatistics, Seattle, WA.(Apr 2008)
13. Menzies Research Institute, Hobart, Tasmania. (Jun 2008)
14. Walter and Eliza Hall Institute of Medicine, Melbourne, Australia. (Jun 2008)
15. Conference for African American Researchers in Mathematical Sciences (CAARMS), Atlanta, GA (Jul 2008)
16. Blackwell-Tapia Conference, Statistical and Applied Mathematical Sciences Institute, Research Triangle Park, NC. (Nov 2008)
17. Georgia Institute of Technology, School of Industrial & Systems Engineering, Atlanta, GA (Dec 2008)
18. Fred Hutchinson Cancer Research Center, Biostatistics, Seattle, WA. (Oct 2009)
19. University of Washington, Northwest Institute of Genetic Medicine, Seattle, WA. (Jun 2010)
20. University of Washington, Institute for Public Health Genetics, Seattle, WA. (Nov 2010)
21. Joint Statistical Meetings, Miami, FL. (Aug 2011)
22. Northwest/Alaska Pharmacogenomics Research Network Conference, University of Washington. Seattle, WA. (Aug 2011)
23. University of Pennsylvania, Department of Biostatistics. Philadelphia, PA (April 2012)
24. Northwest/Alaska Pharmacogenomics Research Network All-Investigator Meeting, University of Montana, Missoula, MO. (July 2012)
25. Joint Statistical Meetings, San Diego, CA. (Aug 2012)
26. Society for Advancements of Chicanos and Native Americans in Science (SACNAS) National

27. Conference, Seattle, WA. (Oct 2012)
28. Yale University, Department of Biostatistics, New Haven, CT. (May 2013)
29. WNAR/IMS Conference, University of California at Los Angeles. Los Angeles, CA (Jun 2013)
30. Impact of Large Scale Genomic Data on Statistical and Quantitative Genetic Conference, Seattle, WA. (November 2013)
31. Vanderbilt University, Department of Biostatistics, Nashville, TN (Jan 2014)
32. Ordered Data Analysis, Models and Health Research Methods Conference, The University of Texas at Dallas, Dallas, TX. (Mar 2014)
33. Conference for African American Researchers in Mathematical Sciences (CAARMS), Princeton University. Princeton, NJ. (Jun 2014)
34. Emerging Statistical Challenges and Methods for Analysis of Massive Genomic Data in Complex Human Disease Studies Workshop, Banff International Research Station, Banff, AB Canada. (Jun 2014)
35. StatFest 2014 Minority Outreach Conference, North Carolina State University, Raleigh, NC. (Sep 2014)
36. Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Investigators Meeting, Washington, D.C. (Nov 2014)
37. StatFest 2015 Minority Outreach Conference, University of Chicago, Chicago, IL. (Sep 2015)
38. International Genetic Epidemiology Society Meeting, Baltimore, MD. (Oct 2015)
39. Annual Biomedical Research Conference for Minority Students (ABRCMS), Seattle, WA. (Nov 2015)
40. Emory University, Department of Human Genetics, Atlanta, GA (Dec 2015)
41. Fred Hutchinson Cancer Research Center, Biostatistics and Biomathematics. Seattle, WA. (Dec 2015)
42. ENAR 2016 Meeting, Austin, TX (March 2016)
43. Wellcome Trust Genome Center, Hinxton/Cambridge, United Kingdom (July 2016)
44. Joint Statistical Meetings, Chicago, IL (August 2016)
45. Washington University, Department of Genetics, St. Louis, MS (September 2016)
46. Case Western Reserve University, Institute for Computational Biology, Cleveland, OH (September 2016)
47. Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Investigators Meeting, New York City, NY. (March 2017)
48. Duke University, Duke Molecular Physiology Institute. Durham, NC (April 2017)
49. Joint Statistical Meetings, Baltimore, MD (Aug 2017)
50. University of Miami, Department of Human Genetics, Miami, FL (April 2018)
51. University of Michigan, Department of Biostatistics, Ann Arbor, MI (May 2018)
52. University of Washington, Division of Medical Genomics, Seattle, WA (May 2018)
53. Clinical Sequencing Evidence-Generating Research (CSER) Meeting, Seattle, WA (September 2018)
54. Stanford University, Department of Biomedical Data Science, Stanford, CA (November 2018)
55. University of Michigan, Department of Biostatistics, Ann Arbor, MI (February 2019)
56. University of Toronto, Department of Statistical Sciences, Toronto, Ontario, Canada (June 2019)

12. University Service

University of Washington

- Reviewer for Royalty Research Fund (2011)
- School of Public Health Grayston-Day Fellowship Selection Committee (2013)
- Co-faculty facilitator for Graduate Opportunities & Minority Achievement Program (GO-MAP) Dissertation Writing Group (2015-2016)

- School of Public Heath Dean Search Committee (2017-2018)

Departmental of Biostatistics, University of Washington

- Alumni Relations Committee (2009-2010, 2011-2012, 2012-2013)
- Seminar Committee (2009-2010)
- Applied Exam Grader (2009-2010)
- Emergency Preparedness Committee (2010-2011, Chair 2012-2013)
- Applied Exam Committee (2010-2011, 2011-2012, 2012-2013,2014-2015, 2015-2016,2016-2017)
- Affiliate/Adjunct Appointments Committee (2011-2012, 2012-2013, Chair 2013-present)
- Diversity Committee (Chair 2014-2016, 2016-)

Institute for Public Health, University of Washington

- Admissions Committee for MS in Genetic Epidemiology (MSGE) program (2009-2012)

13. Professionally-Related Community Service

- Research Grant Reviewer for Medical Research Council (UK) (2010)
- Research Grant Reviewer for Icelandic Research Fund (2012)
- Invited Participant for National Human Genome Research Institute (NHGRI) "Inclusion and Engagement of Underrepresented Populations in Genomics" Roundtable (Sep 2015)
- Tenure-Track Review Committee Member for National Institute of Child Health and Human Development (NICHD), Board of Scientific Counselors (Dec 2015)

14. Other Pertinent Information As Needed

N/A

15. Teaching History (100% responsibility unless otherwise noted)

Formal Teaching at University of Chicago:

- Statistics 200, Introductory Statistics (Fall 1999)
- Statistics 200, Introductory Statistics (Spring 2000)

Formal Teaching at University of California at Berkeley:

- Statistics 20, Introduction to Probability and Statistics (Summer 2006)
- Statistics 20, Introduction to Probability and Statistics (Summer 2007)

Formal Teaching at University of Washington:

- Biostatistics 516, Statistical Methods in Genetic Epidemiology (Fall 2009)
  Enrollment 15; Median evaluations: 3.3/5
- Biostatistics 516, Statistical Methods in Genetic Epidemiology (Fall 2010)
  Enrollment 8; Median evaluations: 3.8/5
- Biostatistics 516, Statistical Methods in Genetic Epidemiology (Fall 2011)
  Enrollment 8; Median evaluations: 4.2/5
- Biostatistics 551, Statistical Genetics II: Quantitative Genetics (Fall 2012)
  Enrollment 7; Median evaluations: 4.5/5
- Biostatistics 551, Statistical Genetics II: Quantitative Genetics (Fall 2013)
  Enrollment 17; Median evaluations: 4.3/5
- Biostatistics 551, Statistical Genetics II: Quantitative Genetics (Fall 2014)
  Enrollment 11; Median evaluations: 4.8/5
- Biostatistics 515/518, Applied Biostatistics II (Winter 2016)
  Enrollment 67; Median evaluations: 3.9/5
- Biostatistics 509, Introduction to R for Data Analysis in Health Sciences (Fall 2016)
  Enrollment 50; Median evaluations: 3.9/5
- Biostatistics 515/518, Applied Biostatistics II (Winter 2017)
  Enrollment 66; Median evaluations: 4.3/5
- Biostatistics 562, Computational Skills for Biostatistics II (Winter 2017)
  Enrollment 15; Median evaluations: 4.0/5
- Biostatistics 509, Introduction to R for Data Analysis in Health Sciences (Fall 2017)
  Enrollment 54; Median evaluations: 4.5/5
- Biostatistics 515/518, Applied Biostatistics II (Winter 2018)
  Enrollment 66; Median evaluations: 4.3/5

Biostatistics Seminar Courses at University of Washington:

- Biostatistics 581, Statistical Genetics Seminar (Winter 2013)
- Biostatistics 581, Statistical Genetics Seminar (Spring 2014)
- Biostatistics 581, Statistical Genetics Seminar (Spring 2015)
- Biostatistics 581, Statistical Genetics Seminar (Spring 2016)
- Biostatistics 581, Statistical Genetics Seminar (Spring 2017)
- Biostatistics 581, Statistical Genetics Seminar (Spring 2018)

Guest Lectures at University of Washington:

- Epidemiology 517, Genetic Epidemiology (Spring 2011)
- Epidemiology 517, Genetic Epidemiology (Spring 2012)
- Biostatistics 516, Statistical Methods in Genetic (Fall 2012)
- Epidemiology 517, Genetic Epidemiology (Spring 2013)
- Biostatistics 111, Lectures in Applied Statistics (Spring 2013)
- Biostatistics 111, Lectures in Applied Statistics (Spring 2014)
- Epidemiology 517, Genetic Epidemiology (Spring 2014)

- Biostatistics 111, Lectures in Applied Statistics (Spring 2015)
- Biostatistics 111, Lectures in Applied Statistics (Spring 2016)
- Biostatistics 111, Lectures in Applied Statistics (Spring 2017)
- Biostatistics 514/517, Applied Biostatistics I (Fall 2017)
- Biostatistics 111, Lectures in Applied Statistics (Spring 2018)

Other Teaching:

Summer Institute in Statistical Genetics, Seattle, WA; Co-Instructor:

- Population Genetics: Theory and Methods (Summer 2009)
- Population Genetics: Theory and Methods (Summer 2010)
- Population Genetics: Theory and Methods (Summer 2011)
- Population Genetics and Association Mapping (Summer 2012)
- Population Genetics and Association Mapping (Summer 2013)
- Introduction to R (Summer 2013)
- Population Genetics and Association Mapping (Summer 2014)
- Introduction to R (Summer 2014)
- Association Mapping: GWAS and Sequencing Data (Summer 2015)
- Introduction to R (Summer 2015)
- Association Mapping: GWAS and Sequencing Data (Summer 2016)
- Introduction to R (Summer 2016)
- Association Mapping: GWAS and Sequencing Data (Summer 2017)
- Introduction to R (Summer 2017)
- Association Mapping: GWAS and Sequencing Data (Summer 2018)
- Introduction to R (Summer 2018)
- Computational Pipeline for Whole Genome Sequencing Data (Summer 2018)
- Association Mapping: GWAS and Sequencing Data (Summer 2019)
- Introduction to R (Summer 2019)
- Computational Pipeline for Whole Genome Sequencing Data (Summer 2019)

Summer Institute in Statistical Genetics (SISG) Taipei 2015, Taipei, Taiwan; Co-Instructor:

- Association Mapping: GWAS and Sequencing Data (Summer 2015)

Summer Institute in Statistical Genetics (SISG) Brisbane 2017, Brisbane, Australia; Co-Instructor:

- Association Mapping: GWAS and Sequencing Data (July 2017)

Winter Institute in Statistical Genetics (WISG) NYU Abu Dhabi 2019, Abu Dhabi, United Arab Emirates; Co-Instructor:

- Computational Pipeline for Whole Genome Sequencing Data (January 2019)

Summer Health Professions Education Program, University of Washington; Instructor:

- Introduction to Biostatistics (Summer 2017)
- Introduction to Biostatistics (Summer 2018)
- Introduction to Biostatistics (Summer 2019)

Independent Study:

- Laurel Steinmetz, Genetic Epidemiology MS student (Winter 2012–Winter 2013)
- Matthew Conomos, Biostatistics PhD student (Fall 2011–Present)
- Caitlin McHugh, Biostatistics PhD student (Fall 2013–Fall 2015)
- Lisa Brown, Biostatistics PhD student (Fall 2013–Summer 2016)
- Jennifer Kirk, Biostatistics PhD student (Fall 2013–Fall 2016)
- Anya Mikhaylova, Biostatistics PhD student (Fall 2015–Present)
- Yichen Jia, Biostatistics MS student (Fall 2016–Summer 2017)
- Edward Zhao, Biostatistics PhD Student (Fall 2017)

16. Advising and Formal Mentoring

PhD Dissertations, Chair

- Matthew Conomos (co-chair with Bruce Weir), Biostatistics PhD student (Completed 2014)
    - Winner of Student Paper Competition at the 2014 Meeting of the Western North American Region of the International Biometric Society (WNAR)
- Caitlin McHugh, Biostatistics PhD student (Completed 2015)
- Lisa Brown (co-chair with Sharon Browning), Biostatistics PhD student (Completed 2016)
- Jennifer Kirk, Biostatistics PhD student (Completed 2016)
- Anya Mikhaylova, Biostatistics PhD student (2016–Present)
- Amarise Little, Biostatistics PhD student (2018–Present)

Masters Theses, Chair

- Laurel Steinmetz, Genetic Epidemiology MS student (Completed 2013)
- Mingdong Liu, Biostatistics MS student (Completed 2015)
- Yichen Jia, Biostatistics MS student (Completed 2017)

Postdoctoral Fellows (Mentor)

- Shizhen Wang, Biostatistics postdoc (2010-2011)

MS Committees in Non-Chair Role

- Saee Hamine, Genetic Epidemiology MS student (Completed 2009)
- Nora Kozloff, Genetic Epidemiology MS student (Completed 2010)
- Nicholas Mosely, Genetic Epidemiology MS student (Completed 2011)
- Sukh Makhnoon, Genetic Epidemiology MS student (Completed 2014)

PhD Committees in Non-Chair Role

- Rora Rohlfs, Genome Sciences PhD student (Completed 2010)
- Ursula Schick, Public Health Genetics PhD student (Completed 2014)
- Chelle Lorraine Wheat, Health Services PhD student (Completed 2015)
- Elizabeth Dorfman, Public Health Genetics PhD student (Completed 2015)
- Alie Fohner, Public Health Genetics PhD student (Completed 2015)
- Elizabeth Hom, Epidemiology PhD student (Completed 2018)
- Fiona Grimson, Statistics PhD student (Completed 2016)
- Charlie Waters, School of Aquatic and Fishery Sciences PhD student (Completed 2018)
- Tsegaselassie Workalemahu, Epidemiology PhD student (Completed 2018)
- Mark Hensley, Epidemiology PhD student (2014–Present)
- Bowen Wang, Statistics PhD student (2016–Present)
- Kesley Grinde, Biostatistics PhD student (2016-Present)
- Xiaowen Tian, Biostatistics PhD student (2016-Present)
- Lindsay Henderson, Pharmaceutics PhD student (2017-Present)
- Tom Austin, Epidemiology PhD student (2018-Present)
- Hongjie Chen, Epidemiology PhD student (2018-Present)
- Arthur Sillah, Epidemiology PhD student (2018-Present)

Research Assistants Supervised

- Mike Garcia, Biostatistics MS student (Fall 2011–Summer 2012)
- Scott Coggeshall, Biostatistics PhD student (Fall 2012–Summer 2013)
- Brayan Ortiz, Biostatistics PhD student (Fall 2013–Fall 2015)
- Matthew Conomos, Biostatistics PhD student (Fall 2013–Fall 2014)
- Caitlin McHugh, Biostatistics, PhD student (Winter 2014–Winter 2015)
- Lisa Brown, Biostatistics, PhD student (Fall 2014–Summer 2016)
- Jennifer Kirk, Biostatistics PhD student (Fall 2015–Fall 2016)
- Yichen Jia, Biostatistics MS student (Fall 2016- Summer 2017)
- Anya Mikhaylova, Biostatistics PhD student (Summer 2016–Present)
- Amarise Little, Biostatistics PhD student (Fall 2016–Present)
- Edward Zhao, Biostatistics PhD Student (StatGen Training Grant; Fall 2017–Present)
- Kaleigh Ervin, Biostatistics PhD Student (StatGen Training Grant; Fall 2017–Summer 2018)
- Charles Wolock, Biostatistics PhD Student (StatGen Training Grant; Fall 2018–Present)
- Michael Goldber, Genome Sciences PhD Student (StatGen Training Grant; Fall 2018–Present)
- Alan Min, Statistics PhD Student (StatGen Training Grant; Fall 2018–Present)

Other Mentoring

- Jean Morrison, Biostatistics PhD student, Poster project mentoring (Summer 2012)
    - Winner of Student Poster Award (chosen by the Biostatistics Faculty) (Summer 2012)
- Scott Coggeshall, Poster project mentoring (Summer 2012)
- Jia Jen Kee, Poster project mentoring (Summer 2013)

Academic Advising

- Lisa Brown, Biostatistics PhD student (2010-2013)
- Jean Morrison, Biostatistics PhD student (2011-2013)
- Yingying Zhuang, Biostatistics PhD student (2012-2014)
- Anya Mikhaylova, Biostatistics PhD student (2013-2016)
- Nick Etzel, Biostatistics PhD student (2017-Present)
- Tianyu Zhang, Biostatistics MS student (2017-Present)