CURRICULUM VITAE
Timothy A. Thornton, PhD
May 4, 2016

1. Biographical Information

- Name: Timothy A. Thornton
- Work Address:
  University of Washington
  Department of Biostatistics
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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
- Postdoc, Institute for Human Genetics, University of California, San Francisco, 2008-2009
- Assistant Professor, Department of Biostatistics, University of Washington, 2009-2015
- Associate Professor, Department of Biostatistics, University of Washington, 2015-present
- Affiliate Investigator, Biostat/Biomath, Fred Hutchinson Cancer Research Center, 2010-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 (2006)

- University of California President's Postdoctoral Fellow (2006-2008)
- University of California, San Francisco Lamond Family Postdoctoral Fellow (2008-2009)

6. Professional Activities (outside of UW)

Conference Organizer:

- 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)

Invited Session Organizer:

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

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)

Editorial Service:

- Review Editor, *Frontiers in Genetics* (2010-Present)

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, Frontiers in Genetics, Genetic Epidemiology, Genome Research, Human Heredity, International Journal of Health Geographics, Journal of Medical Genetics, 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)

Professional Memberships:

- American Statistical Association
- Institute of Mathematical Statistics
- American Association for the Advancement of Science
- American Society of Human Genetics

7. Bibliography

Refereed Research Articles

1. Anderson-Cook CM and **Thornton T** (1998) "Measuring Hockey's Special Teams Efficiency." *Chance*, 11: 26-34

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

3. **Thornton T** 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. Manuscript is highlighted in the Editors' Corner of this issue.

4. FitzGerald LM, Patterson B, Thomson R, Polanowski A, Quinn S, Brohede J, **Thornton T**, 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 T** 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. Manuscript is highlighted in the Editors' Corner of this issue.

6. Phasukijwattana N, Kunhapan B, Stankovich J, Chuenkongkaew WL, Thomson R, **Thornton T**, 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 T**, 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. 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

9. **Thornton T**, 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

10. **Thornton T**, 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. Manuscript is highlighted in the Editors' Corner of this issue.

11. 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

12. 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 T**, 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

13. Coram M, Duan Q, Hoffman TJ, **Thornton T**, 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

14. 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

15. 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

16. Fohner A, Muzquiz LI, Austin MA, Gaedigk A, Gordon A, **Thornton T**, 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

17. 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

18. 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

19. Kaklamani VG, Hoffmann TJ, **Thornton T**, 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

20. Perez MV, Hoffmann TJ, Tang H, **Thornton T** , 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

21. 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.

22. 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

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

24. 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, Flannick J, Zhang J, Fuchsberger C, Gaulton K, Lindgren C, Locke A, Manning A, Sim X, Rivas MA, Holmen OL, Gottesman O, Lu Y, Ruderfer D, Stahl EA, Duan Q, Li Y, Durda P, Jiao S, Isaacs A, Hofman A, Bis JC, Correa A, Griswold ME, Jakobsdottir J, Smith AV, Schreiner PJ, Feitosa MF, Zhang Q, Huffman JE, Crosby J, Wassel CL, Do R, Franceschini N, Martin LW, Robinson JG, Assimes TL, Crosslin DR, Rosenthal EA, Tsai M, Rieder MJ, Farlow DN, Folsom AR, Lumley T, Fox ER, Carlson CS, Peters U, Jackson RD, van Duijn CM, Uitterlinden AG, Levy D, Rotter JI, Taylor HA, Gudnason V Jr, Siscovick DS, Fornage M, Borecki IB, Hayward C, Rudan I, Chen YE, Bottinger EP, Loos RJ, Sætrom P, Hveem K, Boehnke M, Groop L, McCarthy M, Meitinger T, Ballantyne CM, Gabriel SB, O'Donnell CJ, Post WS, North KE, Reiner AP, Boerwinkle E, Psaty BM, Altshuler D, Kathiresan S, Lin DY, Jarvik GP, Cupples LA, Kooperberg C, Wilson JG, Nickerson DA, Abecasis GR, Rich SS, Tracy RP, 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

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

26. **Thornton T**, 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

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

28. Hoffman TJ, Tang H, **Thornton T**, 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

29. Alam TM, Petit RA, Crispell EK, **Thornton T**, 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

30. **Thornton T** "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.

31. Hong X, Hao K, Ladd-Acosta C, Hansen KD, Tsai HJ, Liu X, Xu X, **Thornton T**, 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.

32. Conomos MP*, Miller M, **Thornton T** (2015) "Robust Inference of Population Structure for Ancestry Prediction and Correction of Stratification in the Presence of Relatedness" *Genetic Epidemiology* 39 :276-93

33. 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 T**, 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

34. Shirasaka Y, Chaudhry AS, McDonald M, Prasad B, Wong T, Calamia JC, Fohner A, **Thornton T**, 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]

35. Fohner AE, Wang Z, Yracheta J, O'Brien DM, Hopkins SE, Black J, Philip J, Wiener HW, Tiwari HK, Stapleton PL, Tsai JM, **Thornton T**, 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

36. Morrison J, Laurie CC, Marazita ML, Sanders AE, Offenbacher S, Salazar CR, Conomos MP, **Thornton T**, 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

37. Blue EM, Brown LA, Conomos MP, Kirk JL, Nato AQ, Popejoy AB, Raffa J, Ranola J, Wijsman EM, **Thornton T** "Estimating relationships between phenotypes and subjects drawn from admixed families" To appear in *BMC Proceedings*

38. Saad M, Alejandro QN, Grimson FL, Lewis SM, Brown LA, Blue EM, **Thornton T**, Thompson EA, Wijsman "Identity-by-Descent Estimation with Population- and Pedigree-based Imputation in Admixed Family Data" To appear in *BMC Proceedings*

39. Conomos MP*, Reiner AP, Weir BS, **Thornton T** "Model-Free Estimation of Recent Genetic Relatedness" *American Journal of Human Genetics* 98:127–148.

40. 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 T**, Laurie CC "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

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

42. Fohner AE, Wang Z, Yracheta J, O'Brien DM, Hopkins SE, Black J, Philip J, Wiener HW, Tiwari HK, Stapleton PL, Tsai JM, **Thornton T,** 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* pii: jn223388. [Epub ahead of print]

43. Mez J, Mukherjee S, **Thornton T**, 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

44. 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 T**, 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.

45. 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 T**, 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]

** First author is PhD graduate student in Biostatistics with Timothy Thornton as the primary supervisor.*
*** Joint senior authors*

Manuscripts Under Review

46. McHugh CP*, Brown L, **Thornton T** "Detecting Heterogeneity in Population Structure Across the Genome in Admixed Populations" Submitted Revision to *Genetics*

** First author is PhD graduate student in Biostatistics with Timothy Thornton as the primary supervisor.*

Other Refereed Scholarly Publications

47. 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

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

Books and book chapters

49. **Thornton T:** "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 T**, 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 T**, 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 T**, 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 T** (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 T** (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

Current

- K01 CA148958 (Thornton) "Statistical methods for cancer genetic association studies with hidden population structure", NIH/NCI, 9/1/2010-5/31/2016, Total Direct Costs: $686,755, 50% FTE, Role: PI

- P01 HG0099568 (Browning/Gibson/Thompson/Thornton/Visscher/Weir) "Statistical and quantitative genetics", NIH/NIGMS, 6/5/2012-4/30/2017, Total Direct Costs: $6,702,065, 30% FTE, Role: PI of one of 6 component projects

- R01 HL116446 (Reiner) "Leukocyte Telomere Length and Cardiovascular Disease in Jackson Heart Study", NIH/NHLBI, 8/1/2013-5/31/2017, Total Direct Costs: $2,674,085, 5% FTE, Role: Investigator

- HHSN268201300005 (Weir) "Omics in Latinos (Ola) - Genetic Analysis", NIH/NHLBI, 3/18/2013-9/17/2016, Total Direct Costs: $4,283,887, 5% FTE, Role: Investigator

- 5T32GM081062 (Weir/Thornton) "Predoctoral Research Training in Statistical Genetics", NIH/NIGMS, 7/1/2007-6/31/2017, Total Direct Costs (2015-2016): $152,240, Role: Co-PI

Completed

- R13 HG007506 (Thornton) "Impact of large-scale genomic data on statistical and quantitative genetics", NIH/NHGRI/NCI, 9/1/2013-8/31/2014, Total Direct Costs: $15,000, 0% FTE, Role: PI

- N01 WH-2-2110 (Risch/Thornton) "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, Total Direct Costs: $45,131, 20% FTE, Role: PI of subcontract

- CA15704 (Thornton) "Cancer Center Support Grant", NIH/NCI subcontract from FHCRC, 7/1/2009-6/30/2012, Total Direct Costs: $100,000, 0% FTE, Role: PI of subcontract

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. (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. (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)

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-Present)

Departmental of Biostatistics, University of Washington

- Alumni Relations Committee (2009-2010, 2011-2012, 2012-2013)
- Seminar Committee (2009-2010)
- Applied Exam Grader (2009-2010)
- Applied Exam Committee (2010-2011, 2011-2012, 2012-2013,2014-2015)

- Emergency Preparedness Committee (2010-2011, Chair 2012-2013)
- Affiliate/Adjunct Appointments Committee (2011-2012, 2012-2013, Chair 2013-present)
- Diversity Committee (Chair 2014-present)

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: 4.25/5
- Biostatistics 551, Statistical Genetics II: Quantitative Genetics (Fall 2014)
  Enrollment 11; Median evaluations: 4.75/5
- Biostatistics 515/518, Applied Biostatistics II (Winter 2016)
  Enrollment 67; Median evaluations: 3.9/5

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)

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)

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)

Taipei 2015 Summer Institute in Statistical Genetics, Taipei, Taiwan, Co-Instructor:

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

Independent Study:

- Laurel Steinmetz, Genetic Epidemiology MS student (Winter 2012-Winter 2013)
- Matthew Conomos, Biostatistics PhD student (Fall 2011-present)
- Lisa Brown, Biostatistics PhD student (Fall 2013-present)
- Caitlin McHugh, Biostatistics PhD student (Fall 2013-present)
- Jennifer Kirk, Biostatistics PhD student (Fall 2013-present)

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 2016)
- Lisa Brown (co-chair with Sharon Browning), Biostatistics PhD student (2014-present)
- Jennifer Kirk, Biostatistics PhD student (2014-present)
- Anya Tuck, Biostatistics PhD student (2016-present)

Masters Theses, Chair

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

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 (2012-present)
- Mark Hensley, Epidemiology PhD student (2014-present)
- Fiona Grimson, Statistics PhD student (2014-present)
- Charlie Waters, School of Aquatic and Fishery Sciences PhD student (2015-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 2016)
- Lisa Brown, Biostatistics, PhD student (Fall 2014-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-present)
- Jean Morrison, Biostatistics PhD student (2011-present)
- Yingying Zhuang, Biostatistics PhD student (2012-present)
- Anya Tuck, Biostatistics PhD student (2013-present)