10/05/2018

# Han Chen, Ph.D.

Human Genetics Center
Department of Epidemiology, Human Genetics and Environmental Sciences
Center for Precision Health
School of Public Health
School of Biomedical Informatics
The University of Texas Health Science Center at Houston
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## Research Interests

Statistical genetics and genomics; population structure and admixture; gene-environment interactions; sleep genetic epidemiology; computational methods for big data; mixed model theory and application; high-dimensional data analysis; rare genetic variant association analysis; meta-analysis; survival analysis; collaborative research on genetic studies of complex human disease.

## Academic Positions

2016 – : **Assistant Professor**
Human Genetics Center
Department of Epidemiology, Human Genetics and Environmental Sciences
School of Public Health
The University of Texas Health Science Center at Houston, Houston, Texas, USA.

2016 – : **Assistant Professor**
Center for Precision Health
School of Public Health
School of Biomedical Informatics
The University of Texas Health Science Center at Houston, Houston, Texas, USA.

2013 – 2016: **Postdoctoral Research Fellow**
Department of Biostatistics
Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA.

## Education

2009 – 2013: **Ph.D.** in Biostatistics
Dissertation: Statistical Methods for Genetic Association Studies: Multi-Cohort and Rare Genetic Variants Approaches
Boston University, Boston, Massachusetts, USA.

2008 – 2009: **M.A.** in Statistics
Columbia University, New York, New York, USA.

2003 – 2007: **B.S.** in Biological Sciences
Tsinghua University, Beijing, China.

## Teaching Experience

Fall 2018: Introduction to R Programming for Epidemiologic Research (2183PH-2998L125)
The University of Texas Health Science Center at Houston, Houston, Texas, USA.
Fall 2017: Principles and Foundations of Public Health Informatics (BMI5380, Guest Lecture)
The University of Texas Health Science Center at Houston, Houston, Texas, USA.
Spring 2014: Introduction to R Programming (Short Course)
Massachusetts Department of Public Health, Boston, Massachusetts, USA.
Spring 2013: Introduction to Statistical Computing (SPH BS723)
Boston University, Boston, Massachusetts, USA.
Fall 2012: Introduction to Statistical Computing (SPH BS723)
Boston University, Boston, Massachusetts, USA.

## Student Mentoring

Graduated Students

| | | | |
|---|---|---|---|
| Tianzhong Yang | Ph.D. | Biostatistics (2018) | Dissertation Committee Member |
| Weiwei Shan | M.S. | Biostatistics (2018) | Minor Advisor |

Current Students

| | | | |
|---|---|---|---|
| Zhe Wang | Ph.D. | Epidemiology | Dissertation Committee Member |
| Elena V. Feofanova | Ph.D. | Epidemiology | Dissertation Committee Member |
| Priyadarshani P. Dharia | Ph.D. | Epidemiology | Dissertation Committee Member |
| Jun Yu | Ph.D. | Biostatistics | Dissertation Committee Member |
| Kirsten Bevan | M.S. | Epidemiology | Academic Advisor |
| Arlene Cortez | M.P.H. | Epidemiology | Academic Advisor |
| Tara M. Prezioso | M.P.H. | Epidemiology | Academic Advisor |
| Pilar Zaibaq | M.P.H. | Epidemiology | Academic Advisor |
| Sofia Siddiq | M.P.H. | Epidemiology | Academic Advisor |
| Xiangyu Liu | Ph.D. | Biostatistics | Minor Advisor |

## Current Research Support

R00 HL130593 (Chen) 12/19/2016 – 11/30/2019
NIH/NHLBI $165,310
**Statistical and Computational Methods for Large-Scale Sequencing Studies**
Role: PI

U01 HL120393 (Psaty) 04/01/2017 – 03/31/2019
NIH/NHLBI $653,465

**Rare Variants and NHLBI Traits in Deeply Phenotyped Cohorts**
Role: Consortium PI

R01 HL142003 (Yu) 05/01/2018 – 04/30/2020
NIH/NHLBI $360,474
**Trans-Omics Analysis to Unravel Molecular Underpinnings of Heart, Lung and Blood Disease Risk Factors**
Role: Co-Investigator

**Completed Research Support**

K99 HL130593 (Chen) 12/15/2015 – 11/30/2016
NIH/NHLBI $96,000
**Statistical and Computational Methods for Large-Scale Sequencing Studies**
Role: PI

## Awards and Honors

2018 Travel Award, The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Fall 2018 Meeting
2016 Stellar Abstract Award, 2016 Program in Quantitative Genomics (PQG) Conference
2015 NIH Pathway to Independence Award (K99/R00), NIH/NHLBI
2014 PQG Travel Award, Harvard T.H. Chan School of Public Health
2012 Travel Award, Genetic Analysis Workshop 18
2011 Inducted into Mu Sigma Rho, The National Statistics Honor Society
2006 China Construction Bank Scholarship, Tsinghua University
2005 Moutai Scholarship, Tsinghua University
2004 Wu Zhande Scholarship, Tsinghua University
2003 Freshman Scholarship, First Class, Tsinghua University
2003 Outstanding High School Student, Sichuan Province, China

## Book Chapters

[1] **Chen H**, Dupuis J. Rare Variant Association Analysis: Beyond Collapsing Approaches (Chapter 11, pages 149-167). In "Assessing Rare Variation in Complex Traits: Design and Analysis of Genetic Studies", edited by Zeggini E, Morris A. Springer, New York 2015 (ISBN 978-1-4939-2823-1).

## Journal Publications

[1] Strawbridge RJ, Dupuis J, Prokopenko I, Barker A, Ahlqvist E, Rybin D, Petrie JR, Travers ME, Bouatia-Naji N, Dimas AS, Nica A, Wheeler E, **Chen H** *et al*. Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new

insights into the pathophysiology of type 2 diabetes. *Diabetes* 2011, 60 (10): 2624-2634. PMCID: PMC3178302.

[2] **Chen H**[*], Hendricks AE[*], Cheng Y, Cupples AL, Dupuis J, Liu CT. Comparison of statistical approaches to rare variant analysis for quantitative traits. *BMC Proceedings* 2011, 5 (S9): S113. PMCID: PMC3287837.
[*] Equal contribution

[3] Scott RA, Chu AY, Grarup N, Manning AK, Hivert MF, Shungin D, Tönjes A, Yesupriya A, Barnes D, Bouatia-Naji N, Glazer NL, Jackson AU, Kutalik Z, Lagou V, Marek D, Rasmussen-Torvik LJ, Stringham HM, Tanaka T, Aadahl M, Arking DE, Bergmann S, Boerwinkle E, Bonnycastle LL, Bornstein SR, Brunner E, Bumpstead SJ, Brage S, Carlson OD, **Chen H** *et al*. No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes* 2012, 61 (5): 1291-1296. PMCID: PMC3331745.

[4] Manning AK, Hivert MF, Scott RA, Grimsby JL, Bouatia-Naji N, **Chen H**, Rybin D, Liu CT, Bielak LF, Prokopenko I *et al*. A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics* 2012, 44 (6): 659-669. PMCID: PMC3613127.

[5] Morris AP, Voight BF, Teslovich TM, Ferreira T, Segrè AV, Steinthorsdottir V, Strawbridge RJ, Khan H, Grallert H, Mahajan A, Prokopenko I, Kang HM, Dina C, Esko T, Fraser RM, Kanoni S, Kumar A, Lagou V, Langenberg C, Luan J, Lindgren CM, Müller-Nurasyid M, Pechlivanis S, Rayner NW, Scott LJ, Wiltshire S, Yengo L, Kinnunen L, Rossin EJ, Raychaudhuri S, Johnson AD, Dimas AS, Loos RJ, Vedantam S, **Chen H** *et al*. Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics* 2012, 44 (9): 981-990. PMCID: PMC3442244.

[6] Scott RA, Lagou V, Welch RP, Wheeler E, Montasser ME, Luan J, Mägi R, Strawbridge RJ, Rehnberg E, Gustafsson S, Kanoni S, Rasmussen-Torvik LJ, Yengo L, Lecoeur C, Shungin D, Sanna S, Sidore C, Johnson PC, Jukema JW, Johnson T, Mahajan A, Verweij N, Thorleifsson G, Hottenga JJ, Shah S, Smith AV, Sennblad B, Gieger C, Salo P, Perola M, Timpson NJ, Evans DM, Pourcain BS, Wu Y, Andrews JS, Hui J, Bielak LF, Zhao W, Horikoshi M, Navarro P, Isaacs A, O'Connell JR, Stirrups K, Vitart V, Hayward C, Esko T, Mihailov E, Fraser RM, Fall T, Voight BF, Raychaudhuri S, **Chen H** *et al*. Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics* 2012, 44 (9): 991-1005. PMCID: PMC3433394.

[7] **Chen H**, Manning AK, Dupuis J. A method of moments estimator for random effect multivariate meta-analysis. *Biometrics* 2012, 68 (4): 1278-1284. PMCID: PMC4030295.

[8] **Chen H**, Meigs JB, Dupuis J. Sequence kernel association test for quantitative traits in family samples. *Genetic Epidemiology* 2013, 37 (2): 196-204. PMCID: PMC3642218.

[9] DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium, Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium, South Asian Type 2 Diabetes (SAT2D) Consortium, Mexican American Type 2 Diabetes (MAT2D) Consortium, Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) Consortium, Mahajan A, Go MJ, Zhang W, Below JE, Gaulton KJ, Ferreira T, Horikoshi M, Johnson AD, Ng MC, Prokopenko I, Saleheen D, Wang X, Zeggini E, Abecasis GR, Adair LS, Almgren P, Atalay M, Aung T, Baldassarre D, Balkau B, Bao Y, Barnett AH, Barroso I, Basit A, Been LF, Beilby J, Bell GI, Benediktsson R, Bergman RN, Boehm BO, Boerwinkle E, Bonnycastle LL, Burtt N, Cai Q, Campbell H, Carey J, Cauchi S, Caulfield M, Chan JC, Chang LC, Chang TJ, Chang YC, Charpentier G, Chen CH, **Chen H** *et al*. Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics* 2014, 46 (3): 234-244. PMCID: PMC3969612.

[10] **Chen H**, Lumley T, Brody J, Heard-Costa NL, Fox CS, Cupples LA, Dupuis J. Sequence kernel association test for survival traits. *Genetic Epidemiology* 2014, 38 (3): 191-197. PMCID: PMC4158946.

[11] **Chen H**, Choi SH, Hong J, Lu C, Milton JN, Allard C, Lacey SM, Lin H, Dupuis J. Rare genetic variant analysis on blood pressure in related samples. *BMC Proceedings* 2014, 8 (S1): S35. PMCID: PMC4143757.

[12] Lin H, Wang M, Brody JA, Bis JC, Dupuis J, Lumley T, McKnight B, Rice K, Sitlani CM, Reid JG, Bressler J, Liu X, Davis BC, Johnson AD, O'Donnell CJ, Kovar CL, Dinh H, Wu Y, Newsham I, **Chen H** *et al*. Strategies to design and analyze targeted sequencing data: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. *Circulation: Cardiovascular Genetics* 2014, 7 (3): 335-343. PMCID: PMC4176824.

[13] **Chen H**, Meigs JB, Dupuis J. Incorporating gene-environment interaction in testing for association with rare genetic variants. *Human Heredity* 2014, 78 (2): 81-90. PMCID: PMC4169076.

[14] **Chen H**[*], Malzahn D[*], Balliu B, Li C, Bailey JN. Testing genetic association with rare and common variants in family data. *Genetic Epidemiology* 2014, 38 (S1): S37-S43. PMCID: PMC4324976.

[*] Equal contribution

[15] Gaulton KJ, Ferreira T, Lee Y, Raimondo A, Mägi R, Reschen ME, Mahajan A, Locke A, William Rayner N, Robertson N, Scott RA, Prokopenko I, Scott LJ, Green T, Sparso T, Thuillier D, Yengo L, Grallert H, Wahl S, Frånberg M, Strawbridge RJ, Kestler J, Chheda H, Eisele L, Gustafsson S, Steinthorsdottir V, Thorleifsson G, Qi L, Karssen LC, van Leeuwen EM, Willems SM, Li M, **Chen H** *et al.* Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics* 2015, 47 (12): 1415-1425. PMCID: PMC4666734.

[16] Lin X, Lee S, Wu MC, Wang C, **Chen H**, Li Z, Lin X. Test for rare variants by environment interactions in sequencing association studies. *Biometrics* 2016, 72 (1): 156-164. PMCID: PMC4733434.

[17] **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. Control for population structure and relatedness for binary traits in genetic association studies via logistic mixed models. *The American Journal of Human Genetics* 2016, 98 (4): 653-666. PMCID: PMC4833218.
[*] Equal contribution

[18] Hobbs BD, Parker MM, **Chen H**, Lao T, Hardin M, Qiao D, Hawrylkiewicz I, Sliwinski P, Yim JJ, Kim WJ *et al.* Exome array analysis identifies a common variant in *IL27* associated with chronic obstructive pulmonary disease. *The American Journal of Respiratory and Critical Care Medicine* 2016, 194 (1): 48-57. PMCID: PMC4960630.

[19] Liang J, Cade BE, Wang H, **Chen H**, Gleason KJ, Larkin EK, Saxena R, Lin X, Redline S, Zhu X. Comparison of heritability estimation and linkage analysis for multiple traits using principal component analyses. *Genetic Epidemiology* 2016, 40 (3): 222-232. PMCID: PMC5083066.

[20] Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Fernandez Tajes J, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, **Chen H** *et al.* The genetic architecture of type 2 diabetes. *Nature* 2016, 536 (7614): 41-47. PMCID: PMC5034897.

[21] Horikoshi M, Pasquali L, Wiltshire S, Huyghe JR, Mahajan A, Asimit JL, Ferreira T, Locke AE, Robertson NR, Wang X, Sim X, Fujita H, Hara K, Young R, Zhang W, Choi S, **Chen H** *et al.* Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics* 2016, 25 (10): 2070-2081. PMCID: PMC5062576.

[22] Cade BE, **Chen H**, Stilp AM, Gleason KJ, Sofer T, Ancoli-Israel S, Arens R, Bell GI, Below JE, Bjonnes AC *et al.* Genetic associations with obstructive sleep apnea traits in Hispanic/Latino Americans. *The American Journal of Respiratory and Critical Care Medicine* 2016, 194 (7): 886-897. PMCID: PMC5074655.

[23] Walford GA, Gustafsson S, Rybin D, Stančáková A, **Chen H**, Liu CT, Hong J, Jensen RA, Rice K, Morris AP *et al.* Genome-wide association study of the modified Stumvoll insulin sensitivity index identifies *BCL2* and *FAM19A2* as novel insulin sensitivity loci. *Diabetes* 2016, 65 (10): 3200-3211. PMCID: PMC5033262.

[24] Liu C, Kraja AT, Smith JA, Brody JA, Franceschini N, Bis JC, Rice K, Morrison AC, Lu Y, Weiss S, Guo X, Palmas W, Martin LW, Chen YDI, Surendran P, Drenos F, Cook JP, Auer PL, Chu AY, Tsosie KS, Zhao W, Jakobsdóttir J, Lin LA, Stafford JM, Amin N, Mei H, Yao J, Voorman A, Larson MG, Grove ML, Smith AV, Hwang SJ, **Chen H** *et al.* Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics* 2016, 48 (10): 1162-1170. PMCID: PMC5320952.

[25] Wang H, Cade BE, **Chen H**, Gleason KJ, Saxena R, Feng T, Larkin EK, Ramachandran VS, Lin H, Patel SR *et al.* Variants in Angiopoietin-2 (*ANGPT2*) contribute to variation in Nocturnal Oxyhemoglobin Saturation Level. *Human Molecular Genetics* 2016, 25 (23): 5244-5253. PMCID: PMC6078634.

[26] Joehanes R, Zhang X, Huan T, Yao C, Ying SX, Nguyen QT, Demirkale CY, Feolo ML, Sharopova NR, Sturcke A, Schäffer AA, Heard-Costa N, **Chen H** *et al.* Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. *Genome Biology* 2017, 18: 16. PMCID: PMC5264466.

[27] Scott RA, Scott LJ, Mägi R, Marullo L, Gaulton KJ, Kaakinen M, Pervjakova N, Pers TH, Johnson AD, Eicher JD, Jackson AU, Ferreira T, Lee Y, Ma C, Steinthorsdottir V, Thorleifsson G, Qi L, Van Zuydam NR, Mahajan A, **Chen H** *et al.* An expanded genome-wide association study of type 2 diabetes in Europeans. *Diabetes* 2017, 66 (11): 2888-2902. PMCID: PMC5652602.

[28] Wang Z, Claus Henn B, Wang C, Wei Y, Su L, Sun R, **Chen H**, Wagner PJ, Lu Q, Lin X *et al.* Genome-wide gene by lead exposure interaction analysis identifies *UNC5D* as a candidate gene for neurodevelopment. *Environmental Health* 2017, 16 (1): 81. PMCID: PMC5534076.

[29] Flannick J, Fuchsberger C, Mahajan A, Teslovich TM, Agarwala V, Gaulton KJ, Caulkins L, Koesterer R, Ma C, Moutsianas L, McCarthy DJ, Rivas MA, Perry JRB, Sim X, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines

PS, Lindgren CM, Hartl C, Jackson AU, **Chen H** *et al.* Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data* 2017, 4: 170179. PMCID: PMC5735917.

[30] Jun G, Manning A, Almeida M, Zawistowski M, Wood AR, Teslovich TM, Fuchsberger C, Feng S, Cingolani P, Gaulton KJ, Dyer T, Blackwell TW, **Chen H** *et al.* Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *Proceedings of the National Academy of Sciences of the United States of America* 2018, 115 (2): 379-384. PMCID: PMC5777025.

[31] **Chen H**[*], Cade BE[*], Gleason KJ, Bjonnes AC, Stilp AM, Sofer T, Conomos MP, Ancoli-Israel S, Arens R, Azarbarzin A *et al.* Multi-ethnic meta-analysis identifies *RAI1* as a possible obstructive sleep apnea related quantitative trait locus in men. *The American Journal of Respiratory Cell and Molecular Biology* 2018, 58 (3): 391-401. PMCID: PMC5854957.
[*] Equal contribution

**Invited Talks**

[1] Generalized linear mixed model association test. Statistical Genetics Working Group, Boston University. Boston, MA. December, 2014.

[2] GMMAT: a mixed model approach for correlated data in binary trait association analysis. Bioinformatics Division, Tsinghua University. Beijing, China. April, 2015.

[3] GMMAT: a mixed model approach for correlated data in binary trait association analysis. Cancer Hospital, Chinese Academy of Medical Sciences. Beijing, China. April, 2015.

[4] GMMAT: a mixed model approach for correlated data in binary trait association analysis. School of Public Health, Nanjing Medical University. Nanjing, China. April, 2015.

[5] GMMAT: a mixed model approach for correlated data in binary trait association analysis. Channing Division of Network Medicine, Brigham and Women's Hospital. Boston, MA. December, 2015.

[6] GMMAT: logistic mixed models to control for population stratification and relatedness in genetic association studies with binary traits. 2016 International Chinese Statistical Association Applied Statistical Symposium. Atlanta, GA. June, 2016.

[7] Control for population structure and relatedness for binary traits in genetic association studies via logistic mixed models. The 4th International Biometric Society-China International Biostatistical Conference. Shanghai, China. July, 2016.

[8] Association tests for sparse genetic data in structured and correlated samples. 2017 International Chinese Statistical Association Applied Statistical Symposium. Chicago, IL. June, 2017.

[9] Efficient gene-environment interaction test in related samples. Division of Sleep and Circadian Disorders, Brigham and Women's Hospital. Boston, MA. September, 2017.

[10] Efficient association tests for rare genetic variants in correlated study samples. Biostatistics Seminar Series, Division of Biostatistics, Washington University in St Louis. St Louis, MO. November, 2017.

## Conference Presentations

### Talks

[1] Correction for sampling structure using generalized linear mixed models for discrete and continuous phenotypes in genome-wide association studies. 2014 Joint Statistical Meetings. Boston, MA. August, 2014.

[2] Ordinary linear mixed model approaches may lead to invalid inference in genetic association studies for binary traits. 2015 Joint Statistical Meetings. Seattle, WA. August, 2015.

[3] SMMAT: a powerful and efficient variant Set Mixed Model Association Test for binary and quantitative traits in whole genome sequencing studies with correlated samples. 2018 Joint Statistical Meetings. Vancouver, BC, Canada. July, 2018.

### Posters

[1] Random effect joint meta-analysis of SNP and SNP by environment interaction effect estimates obtained from regression models. 19th Annual International Genetic Epidemiology Society Conference. Boston, MA. October, 2010.

[2] Rare genetic variant analysis on blood pressure in related samples. Genetic Analysis Workshop 18. Stevenson, WA. October, 2012.

[3] Sequence kernel association test for quantitative traits in family samples. 21st Annual International Genetic Epidemiology Society Conference. Stevenson, WA. October, 2012.

[4] Rare variant testing for survival analysis and meta-analysis. The American Society of Human Genetics 62nd Annual Meeting. San Francisco, CA. November, 2012.

[5] Rare variant tests for time-to-event outcomes. 22nd Annual International Genetic Epidemiology Society Conference. Chicago, IL. September, 2013.

[6] Correction for population stratification and relatedness in case-control studies using logistic mixed models. The American Society of Human Genetics 64th Annual Meeting. San Diego, CA. October, 2014.

[7] A general framework of gene-based association tests for correlated case-control samples. ENAR 2015 Spring Meeting. Miami, FL. March, 2015.

[8] GMMAT: logistic mixed models to control for population stratification and relatedness in genetic association studies with binary traits. 24th Annual International Genetic Epidemiology Society Conference. Baltimore, MD. October, 2015.

[9] Generalized linear Mixed Model Association Tests (GMMAT) for rare variants to control for population stratification and relatedness in sequencing studies with continuous and binary phenotypes. The American Society of Human Genetics 65th Annual Meeting. Baltimore, MD. October, 2015.

[10] RVMMAT: Rare-Variant Mixed Model Association Tests for binary traits in structured and related samples. The American Society of Human Genetics 66th Annual Meeting. Vancouver, BC, Canada. October, 2016.

[11] RVMMAT: Rare-Variant Mixed Model Association Tests for binary traits in structured and related samples. 25th Annual International Genetic Epidemiology Society Conference. Toronto, ON, Canada. October, 2016.

[12] RV-GMMAT: Rare-Variant Generalized linear Mixed Model Association Tests for binary traits in structured and related samples. 2016 PQG Conference. Boston, MA. November, 2016.

## Professional Memberships

American Statistical Association
American Society of Human Genetics
International Genetic Epidemiology Society

## Institutional Service

**Member** (2018 – ), Epidemiology Admissions Committee, Department of Epidemiology, Human Genetics and Environmental Sciences, UTHealth School of Public Health
**Member** (2018 – ), IT Faculty Advisory Committee, UTHealth School of Public Health

**Member** (2017 – ), CPH Faculty Search Committee, UTHealth School of Public Health & School of Biomedical Informatics

**Professional Activities**

**Regular Faculty Member** (2018 – ), MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences

**Faculty Affiliate** (2017 – ), Keck Center, Gulf Coast Consortia

**Member** (2017 – ), Communications Committee, International Genetic Epidemiology Society

**Member** (2015 – ), Young Investigators Committee, International Genetic Epidemiology Society

**Organizer and Session Chair**, Making sense of whole genome sequencing data in population science: statistical challenges and solutions, ENAR 2018 Spring Meeting. Atlanta, GA, USA. March, 2018.

**Session Chair**, Next generation sequencing applications and methods, 25th Annual International Genetic Epidemiology Society Conference. Toronto, ON, Canada. October, 2016.

**Organizer** (2013 – 2015), PQG Short Courses, Harvard T.H. Chan School of Public Health

**Reviewer**

Journals

*Annals of Applied Statistics*
*Annals of Human Genetics*
*Bioinformatics*
*Biometrics*
*Biometrika*
*Biostatistics*
*BMC Bioinformatics*
*Circulation: Cardiovascular Genetics*
*Diabetologia*
*Genetic Epidemiology*
*Genetics*
*Genome Research*
*Human Heredity*
*International Journal of Epidemiology*
*PeerJ*
*PLOS Computational Biology*

*PLOS Genetics*
*PLOS ONE*
*Scientific Reports*
*Statistical Methods in Medical Research*
*Statistics in Medicine*
*The American Journal of Human Genetics*

Conferences

American Statistical Association, Section on Statistics in Genomics and Genetics, Distinguished Student Paper Award Competition, 2018 Joint Statistical Meetings.

American Statistical Association, Section on Statistics in Genomics and Genetics, Distinguished Student Paper Award Competition, 2017 Joint Statistical Meetings.

Grants

Science Foundation Ireland.