

10/01/2024

**Han Chen, Ph.D.**

Human Genetics Center  
Department of Epidemiology  
School of Public Health

The University of Texas Health Science Center at Houston (UTHealth Houston)  
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**A. Research Interests**

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

**B. Academic Positions**

2021 – : **Associate Professor**

Human Genetics Center  
Department of Epidemiology  
School of Public Health

The University of Texas Health Science Center at Houston, Houston, Texas, USA.

2018 – : **Regular Faculty Member**

MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences (GSBS)

The University of Texas Health Science Center at Houston, Houston, Texas, USA.

2021 – 2023: **Associate Professor**

Center for Precision Health  
McWilliams School of Biomedical Informatics

The University of Texas Health Science Center at Houston, Houston, Texas, USA.

2016 – 2021: **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 – 2021: **Assistant Professor**

Center for Precision Health  
McWilliams School of Biomedical Informatics

The University of Texas Health Science Center at Houston, Houston, Texas, USA.

### **C. Education**

2003 – 2007: **B.S.** in Biological Sciences

Tsinghua University, Beijing, China.

2008 – 2009: **M.A.** in Statistics

Columbia University, New York, New York, USA.

2009 – 2013: **Ph.D.** in Biostatistics

Dissertation: Statistical Methods for Genetic Association Studies: Multi-Cohort and Rare Genetic Variants Approaches

Boston University School of Public Health, Boston, Massachusetts, USA.

2013 – 2016: **Postdoctoral Research Fellow**

Department of Biostatistics

Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA.

### **D. Teaching**

*Boston University, Boston, Massachusetts, USA.*

SPH BS723: Introduction to Statistical Computing (Fall 2012, Spring 2013)

*Massachusetts Department of Public Health, Boston, Massachusetts, USA.*

Short Course: Introduction to R Programming (Spring 2014)

*The University of Texas Health Science Center at Houston, Houston, Texas, USA.*

PH2998L125: Introduction to R Programming for Epidemiologic Research (Fall 2018, Spring 2020, Spring 2021)

PHW2780: Applied Genetic Methods in Public Health (Summer 2019, Summer 2020, Summer 2021)

PHWM2612: Epidemiology I (Summer 2019, Summer 2020, Summer 2021, Summer 2022)

PH2784: Introduction to R Analysis for Epidemiologic Research (Spring 2022, Spring 2023, Spring 2024)

GS21 1152: GSBS Scientific Writing (Faculty Facilitator: Fall 2022)

PHD2711: Epidemiology IV (Fall 2023, Fall 2024)

#### **Guest Lectures**

BMI5380: Principles and Foundations of Public Health Informatics (Fall 2017)

PH2612: Epidemiology I (Fall 2018)

PH2817: Big Data Foundations (Spring 2020, Spring 2021, Spring 2022, Spring 2023, Spring 2024)

### **E. Current Research Support**

R01 AG081398 (Chen/Zhi)	09/30/2024 – 06/30/2029
NIH/NIA	\$3,770,993
<b>Efficient IBD mapping for Alzheimer’s Disease and related brain imaging phenotypes</b>	
Role: PI	
R01 HL145025 (Chen/Manning)	07/15/2019 – 06/30/2025 (NCE)
NIH/NHLBI	\$4,013,193
<b>Methods and Software for Large-Scale Gene-Environment Interaction Studies</b>	
Role: PI	
R01 CA233719 (Scheurer)	08/01/2019 – 07/31/2025 (NCE)
NIH/NCI/Baylor College of Medicine	\$256,716 (UTHealth Houston sub)
<b>Molecular Epidemiology of Langerhans Cell Histiocytosis: Evaluating the Impact of SMAD6 and Genetic Ancestry on Disease Risk</b>	
Role: Subcontract PI	
R01 HL156991 (Rao)	04/27/2021 – 03/31/2025
NIH/NHLBI/Washington University in St. Louis	\$436,800 (UTHealth Houston sub)
<b>A Multi-Ancestry Study of Gene-Lifestyle Interactions and Multi-Omics in Cardiometabolic Traits</b>	
Role: Co-Investigator	
U01 AG070112 (Zhi/Fornage/Ji)	07/01/2021 – 06/30/2026
NIH/NIA	\$5,999,144
<b>Genetics of Deep-Learning-Derived Neuroimaging Endophenotypes for Alzheimer’s Disease</b>	
Role: Co-Investigator	
CZI 2021-239847 (Chen)	12/01/2021 – 11/30/2024
Chan Zuckerberg Initiative/Baylor College of Medicine	\$138,966 (UTHealth Houston sub)
<b>Ancestry Network for the Human Cell Atlas in the Eye</b>	
Role: Subcontract PI	
TBD (Smith)	05/15/2024 – 04/30/2026
NIH/NHLBI/The University of Michigan	\$849,161 (UTHealth Houston sub)
<b>Trans-Omics for Precision Medicine (TOPMed) Informatics Research Center (IRC)</b>	
Role: Co-Investigator	
R01 HL160793 (Yu/Vasan)	07/01/2022 – 06/30/2026
NIH/NHLBI	\$2,676,828
<b>Genetic Architecture of Cardiac Structure and Function and Its Impact on Heart Failure</b>	

Role: Co-Investigator

R01 EY032768 (Zhi/Chen) 09/30/2022 – 06/30/2025  
NIH/NEI \$1,699,196

**Deep-Learning-Derived Endophenotypes from Retina Images**

Role: Co-Investigator

R01 HL168683 (Yu) 04/01/2023 – 03/31/2027  
NIH/NHLBI \$3,222,024

**Molecular Determinants of Atherosclerotic Cardiovascular Disease in Multi-ethnic Populations**

Role: Co-Investigator

**F. Completed Research Support**

K99 HL130593 (Chen) 12/15/2015 – 11/30/2016  
NIH/NHLBI \$103,680

**Statistical and Computational Methods for Large-Scale Sequencing Studies**

Role: PI

R00 HL130593 (Chen) 12/19/2016 – 11/30/2020  
NIH/NHLBI \$745,911

**Statistical and Computational Methods for Large-Scale Sequencing Studies**

Role: PI

U01 HL120393 (Psaty) 04/01/2017 – 03/31/2019  
NIH/NHLBI/University of Washington \$49,941 (UTHealth Houston sub)

**Rare Variants and NHLBI Traits in Deeply Phenotyped Cohorts**

Role: Subcontract PI

R01 HL142003 (Yu) 05/01/2018 – 04/30/2021  
NIH/NHLBI \$933,667

**Trans-Omics Analysis to Unravel Molecular Underpinnings of Heart, Lung and Blood Disease Risk Factors**

Role: Co-Investigator

R01 HL116720 (Pan/Wei) 09/01/2017 – 07/31/2021  
NIH/NHLBI/University of Minnesota \$102,439 (UTHealth Houston sub)

**Association Analysis of Rare Variants with Sequencing Data**

Role: Co-Investigator

U01 AG058589 (DeStefano *et al.*) 09/30/2018 – 08/31/2023  
NIH/NIA/Boston University \$295,046 (UTHealth Houston sub)  
**Therapeutic Target Discovery in ADSP Data via Comprehensive Whole-Genome Analysis  
Incorporating Ethnic Diversity and Systems Approaches**  
Role: Co-Investigator

R01 HD106056 (Garcia) 02/22/2022 – 11/30/2023  
NIH/NICHD/Baylor College of Medicine \$19,489 (UTHealth Houston sub)  
**Search for new genes involved in male infertility through novel approaches**  
Role: Subcontract PI

1OT2OD032581-02-164 (Prakash/Jiang) 09/17/2023 – 09/16/2024  
NIH/Tuskegee University \$200,000  
**Promoting Health Equity through Ethical AI/ML: A Collaborative Initiative for Data  
Governance and Access in Healthcare**  
Role: Co-Investigator

### **G. Awards and Honors**

- 2003 Freshman Scholarship, First Class, Tsinghua University
- 2004 Wu Zhande Scholarship, Tsinghua University
- 2005 Moutai Scholarship, Tsinghua University
- 2006 China Construction Bank Scholarship, Tsinghua University
- 2012 Travel Award, Genetic Analysis Workshop 18
- 2014 PQG Travel Award, Harvard T.H. Chan School of Public Health
- 2015 NIH Pathway to Independence Award (K99/R00), NIH/NHLBI
- 2016 Stellar Abstract Award, 2016 Program in Quantitative Genomics (PQG) Conference
- 2018 Travel Award, The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Fall 2018 Meeting
- 2021 Golden Tiger Award for CHARGE Contributions, CHARGE Consortium

### **H. 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).

### **I. Peer-Reviewed Journal Publications**

\* Co-first author

# Corresponding author

† Trainees mentored

[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**, Voight BF, Taneera J, Kanoni S, Peden JF, Turrini F, Gustafsson S, Zabena C, Almgren P, Barker DJ, Barnes D, Dennison EM, Eriksson JG, Eriksson P, Eury E, Folkersen L, Fox CS, Frayling TM, Goel A, Gu HF, Horikoshi M, Isomaa B, Jackson AU, Jameson KA, Kajantie E, Kerr-Conte J, Kuulasmaa T, Kuusisto J, Loos RJ, Luan J, Makrilakis K, Manning AK, Martínez-Larrad MT, Narisu N, Nastase Mannila M, Ohrvik J, Osmond C, Pascoe L, Payne F, Sayer AA, Sennblad B, Silveira A, Stancáková A, Stirrups K, Swift AJ, Syvänen AC, Tuomi T, van 't Hooft FM, Walker M, Weedon MN, Xie W, Zethelius B, Ongen H, Mälarstig A, Hopewell JC, Saleheen D, Chambers J, Parish S, Danesh J, Kooner J, Ostenson CG, Lind L, Cooper CC, Serrano-Ríos M, Ferrannini E, Forsen TJ, Clarke R, Franzosi MG, Seedorf U, Watkins H, Froguel P, Johnson P, Deloukas P, Collins FS, Laakso M, Dermitzakis ET, Boehnke M, McCarthy MI, Wareham NJ, Groop L, Pattou F, Gloyn AL, Dedoussis GV, Lyssenko V, Meigs JB, Barroso I, Watanabe RM, Ingelsson E, Langenberg C, Hamsten A, Florez JC. 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 Oct;60(10):2624-34. doi: 10.2337/db11-0415. Epub 2011 Aug 26. PubMed PMID: 21873549; PubMed Central PMCID: PMC3178302.

[2] **Chen H**<sup>\*</sup>, Hendricks AE<sup>\*</sup>, Cheng Y, Cupples AL, Dupuis J, Liu CT. Comparison of statistical approaches to rare variant analysis for quantitative traits. *BMC Proc*. 2011 Nov 29;5 Suppl 9:S113. doi: 10.1186/1753-6561-5-S9-S113. PubMed PMID: 22373209; PubMed Central PMCID: PMC3287837.

[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**, Chen YD, Chines PS, Collins FS, Couper DJ, Dennison EM, Dowling NF, Egan JS, Ekelund U, Erdos MR, Forouhi NG, Fox CS, Goodarzi MO, Grässler J, Gustafsson S, Hallmans G, Hansen T, Hingorani A, Holloway JW, Hu FB, Isomaa B, Jameson KA, Johansson I, Jonsson A, Jørgensen T, Kivimaki M, Kovacs P, Kumari M, Kuusisto J, Laakso M, Lecoeur C, Lévy-Marchal C, Li G, Loos RJ, Lyssenko V, Marmot M, Marques-Vidal P, Morken MA, Müller G, North KE, Pankow JS, Payne F, Prokopenko I, Psaty BM, Renström F, Rice K, Rotter JI, Rybin D, Sandholt CH, Sayer AA, Shrader P, Schwarz PE, Siscovick DS, Stancáková A, Stumvoll M, Teslovich TM, Waeber G, Williams GH, Witte DR, Wood AR, Xie W, Boehnke M, Cooper C, Ferrucci L, Froguel P, Groop L, Kao WH, Vollenweider P, Walker M, Watanabe RM, Pedersen O, Meigs JB, Ingelsson E, Barroso I, Florez JC, Franks PW, Dupuis J, Wareham NJ, Langenberg C. No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes*. 2012 May;61(5):1291-6. doi: 10.2337/db11-0973. Epub 2012 Mar 13. PubMed PMID: 22415877; PubMed Central PMCID: PMC3331745.

[4] Manning AK, Hivert MF, Scott RA, Grimsby JL, Bouatia-Naji N, **Chen H**, Rybin D, Liu CT, Bielak LF, Prokopenko I, Amin N, Barnes D, Cadby G, Hottenga JJ, Ingelsson E, Jackson AU, Johnson T, Kanoni S, Ladenvall C, Lagou V, Lahti J, Lecoeur C, Liu Y, Martinez-Larrad MT, Montasser ME, Navarro P, Perry JR, Rasmussen-Torvik LJ, Salo P, Sattar N, Shungin D, Strawbridge RJ, Tanaka T, van Duijn CM, An P, de Andrade M, Andrews JS, Aspelund T, Atalay M, Aulchenko Y, Balkau B, Bandinelli S, Beckmann JS, Beilby JP, Bellis C, Bergman RN, Blangero J, Boban M, Boehnke M, Boerwinkle E, Bonnycastle LL, Boomsma DI, Borecki IB, Böttcher Y, Bouchard C, Brunner E, Budimir D, Campbell H, Carlson O, Chines PS, Clarke R, Collins FS, Corbatón-Anchuelo A, Couper D, de Faire U, Dedoussis GV, Deloukas P, Dimitriou M, Egan JM, Eiriksdottir G, Erdos MR, Eriksson JG, Eury E, Ferrucci L, Ford I, Forouhi NG, Fox CS, Franzosi MG, Franks PW, Frayling TM, Froguel P, Galan P, de Geus E, Gigante B, Glazer NL, Goel A, Groop L, Gudnason V, Hallmans G, Hamsten A, Hansson O, Harris TB, Hayward C, Heath S, Hercberg S, Hicks AA, Hingorani A, Hofman A, Hui J, Hung J, Jarvelin MR, Jhun MA, Johnson PC, Jukema JW, Jula A, Kao WH, Kaprio J, Kardina SL, Keinanen-Kiukkaanniemi S, Kivimaki M, Kolcic I, Kovacs P, Kumari M, Kuusisto J, Kyvik KO, Laakso M, Lakka T, Lannfelt L, Lathrop GM, Launer LJ, Leander K, Li G, Lind L, Lindstrom J, Lobbens S, Loos RJ, Luan J, Lyssenko V, Mägi R, Magnusson PK, Marmot M, Meneton P, Mohlke KL, Mooser V, Morken MA, Miljkovic I, Narisu N, O'Connell J, Ong KK, Oostra BA, Palmer LJ, Palotie A, Pankow JS, Peden JF, Pedersen NL, Pehlic M, Peltonen L, Penninx B, Pericic M, Perola M, Perusse L, Peyser PA, Polasek O, Pramstaller PP, Province MA, Rääkkönen K, Rauramaa R, Rehnberg E, Rice K, Rotter JI, Rudan I, Ruokonen A, Saaristo T, Sabater-Lleal M, Salomaa V, Savage DB, Saxena R, Schwarz P, Seedorf U, Sennblad B, Serrano-Rios M, Shuldiner AR, Sijbrands EJ, Siscovick DS, Smit JH, Small KS, Smith NL, Smith AV, Stančáková A, Stirrups K, Stumvoll M, Sun YV, Swift AJ, Tönjes A, Tuomilehto J, Trompet S, Uitterlinden AG, Uusitupa M, Vikström M, Vitart V, Vohl MC, Voight BF, Vollenweider P, Waeber G, Waterworth DM, Watkins H, Wheeler E, Widen E, Wild SH, Willems SM, Willemsen G, Wilson JF, Witteman JC, Wright AF, Yaghoobkar H, Zelenika D, Zemunik T, Zgaga L, Wareham NJ, McCarthy MI, Barroso I, Watanabe RM, Florez JC, Dupuis J, Meigs JB, Langenberg C. A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nat Genet.* 2012 May 13;44(6):659-69. doi: 10.1038/ng.2274. PubMed PMID: 22581228; PubMed Central 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**, Florez JC, Fox C, Liu CT, Rybin D, Couper DJ, Kao WH, Li M, Cornelis MC, Kraft P, Sun Q, van Dam RM, Stringham HM, Chines PS, Fischer K, Fontanillas P, Holmen OL, Hunt SE, Jackson AU, Kong A, Lawrence R, Meyer J, Perry JR,

Platou CG, Potter S, Rehnberg E, Robertson N, Sivapalaratnam S, Stančáková A, Stirrups K, Thorleifsson G, Tikkanen E, Wood AR, Almgren P, Atalay M, Benediktsson R, Bonnycastle LL, Burt N, Carey J, Charpentier G, Crenshaw AT, Doney AS, Dorkhan M, Edkins S, Emilsson V, Eury E, Forsen T, Gertow K, Gigante B, Grant GB, Groves CJ, Guiducci C, Herder C, Hreidarsson AB, Hui J, James A, Jonsson A, Rathmann W, Klopp N, Kravic J, Krjutškov K, Langford C, Leander K, Lindholm E, Lobbens S, Männistö S, Mirza G, Mühleisen TW, Musk B, Parkin M, Rallidis L, Saramies J, Sennblad B, Shah S, Sigurðsson G, Silveira A, Steinbach G, Thorand B, Trakalo J, Veglia F, Wennauer R, Winckler W, Zabaneh D, Campbell H, van Duijn C, Uitterlinden AG, Hofman A, Sijbrands E, Abecasis GR, Owen KR, Zeggini E, Trip MD, Forouhi NG, Syvänen AC, Eriksson JG, Peltonen L, Nöthen MM, Balkau B, Palmer CN, Lyssenko V, Tuomi T, Isomaa B, Hunter DJ, Qi L, Shuldiner AR, Roden M, Barroso I, Wilsgaard T, Beilby J, Hovingh K, Price JF, Wilson JF, Rauramaa R, Lakka TA, Lind L, Dedoussis G, Njølstad I, Pedersen NL, Khaw KT, Wareham NJ, Keinanen-Kiukaanniemi SM, Saaristo TE, Korpi-Hyövälti E, Saltevo J, Laakso M, Kuusisto J, Metspalu A, Collins FS, Mohlke KL, Bergman RN, Tuomilehto J, Boehm BO, Gieger C, Hveem K, Cauchi S, Froguel P, Baldassarre D, Tremoli E, Humphries SE, Saleheen D, Danesh J, Ingelsson E, Ripatti S, Salomaa V, Erbel R, Jöckel KH, Moebus S, Peters A, Illig T, de Faire U, Hamsten A, Morris AD, Donnelly PJ, Frayling TM, Hattersley AT, Boerwinkle E, Melander O, Kathiresan S, Nilsson PM, Deloukas P, Thorsteinsdottir U, Groop LC, Stefansson K, Hu F, Pankow JS, Dupuis J, Meigs JB, Altshuler D, Boehnke M, McCarthy MI. Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat Genet.* 2012 Sep;44(9):981-90. doi: 10.1038/ng.2383. Epub 2012 Aug 12. PubMed PMID: 22885922; PubMed Central 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**, Lindgren CM, Morris AP, Rayner NW, Robertson N, Rybin D, Liu CT, Beckmann JS, Willems SM, Chines PS, Jackson AU, Kang HM, Stringham HM, Song K, Tanaka T, Peden JF, Goel A, Hicks AA, An P, Müller-Nurasyid M, Franco-Cereceda A, Folkersen L, Marullo L, Jansen H, Oldehinkel AJ, Bruinenberg M, Pankow JS, North KE, Forouhi NG, Loos RJ, Edkins S, Varga TV, Hallmans G, Oksa H, Antonella M, Nagaraja R, Trompet S, Ford I, Bakker SJ, Kong A, Kumari M, Gigante B, Herder C, Munroe PB, Caulfield M, Antti J, Mangino M, Small K, Miljkovic I, Liu Y, Atalay M, Kiess W, James AL, Rivadeneira F, Uitterlinden AG, Palmer CN, Doney AS, Willemsen G, Smit JH, Campbell S, Polasek O, Bonnycastle LL, Herberg S, Dimitriou M, Bolton JL, Fowkes GR, Kovacs P, Lindström J, Zemunik T, Bandinelli S, Wild SH, Basart HV, Rathmann W, Grallert H, Maerz W, Kleber ME, Boehm BO, Peters A, Pramstaller PP, Province MA, Borecki IB, Hastie ND, Rudan I, Campbell H, Watkins H, Farrall M, Stumvoll



M, Ferrucci L, Waterworth DM, Bergman RN, Collins FS, Tuomilehto J, Watanabe RM, de Geus EJ, Penninx BW, Hofman A, Oostra BA, Psaty BM, Vollenweider P, Wilson JF, Wright AF, Hovingh GK, Metspalu A, Uusitupa M, Magnusson PK, Kyvik KO, Kaprio J, Price JF, Dedoussis GV, Deloukas P, Meneton P, Lind L, Boehnke M, Shuldiner AR, van Duijn CM, Morris AD, Toenjes A, Peyser PA, Beilby JP, Körner A, Kuusisto J, Laakso M, Bornstein SR, Schwarz PE, Lakka TA, Rauramaa R, Adair LS, Smith GD, Spector TD, Illig T, de Faire U, Hamsten A, Gudnason V, Kivimaki M, Hingorani A, Keinanen-Kiukaanniemi SM, Saaristo TE, Boomsma DI, Stefansson K, van der Harst P, Dupuis J, Pedersen NL, Sattar N, Harris TB, Cucca F, Ripatti S, Salomaa V, Mohlke KL, Balkau B, Froguel P, Pouta A, Jarvelin MR, Wareham NJ, Bouatia-Naji N, McCarthy MI, Franks PW, Meigs JB, Teslovich TM, Florez JC, Langenberg C, Ingelsson E, Prokopenko I, Barroso I. Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nat Genet.* 2012 Sep;44(9):991-1005. doi: 10.1038/ng.2385. Epub 2012 Aug 12. PubMed PMID: 22885924; PubMed Central PMCID: PMC3433394.

[7] **Chen H<sup>#</sup>**, Manning AK, Dupuis J. A method of moments estimator for random effect multivariate meta-analysis. *Biometrics.* 2012 Dec;68(4):1278-84. doi: 10.1111/j.1541-0420.2012.01761.x. Epub 2012 May 2. PubMed PMID: 22551393; PubMed Central PMCID: PMC4030295.

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## **J. Invited Presentations**

[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.
- [11] Efficient genetic association tests for correlated samples from large-scale whole genome sequencing studies. Bioinformatics Seminar Series, University of California, Los Angeles. Los Angeles, CA. January, 2019.
- [12] Efficient association tests for sparse genetic and genomic data in correlated samples. 62nd International Statistical Institute World Statistics Congress. Kuala Lumpur, Malaysia. August, 2019.

[13] Efficient gene-environment interaction tests for large biobank-scale sequencing studies with correlated samples. 2020 International Chinese Statistical Association Applied Statistical Symposium. Houston, TX (Virtual Meeting). December, 2020.

[14] GEM: scalable and flexible gene-environment interaction analysis in millions of samples. Biostatistics Seminar Series, Division of Biostatistics, Washington University in St Louis. St Louis, MO (via Zoom). March, 2021.

[15] StocSum: Stochastic summary statistics for whole genome sequencing studies. Division of Epidemiology Seminar, Vanderbilt University Medical Center, Nashville, TN (via Zoom). October, 2022.

[16] StocSum: a reference-panel-free summary statistics framework for diverse populations. Computational Genomics Summer Institute, University of California Los Angeles, Los Angeles, CA. July, 2024.

### **K. Conference Platform Presentations**

[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.

[4] Efficient variant set mixed model association test for continuous and binary traits in large-scale whole genome sequencing studies. The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Fall 2018 Meeting. Baltimore, MD. October, 2018.

[5] An efficient identity by descent mapping test for biobank-scale cohorts. 28th Annual International Genetic Epidemiology Society Conference. Houston, TX. October, 2019.

[6] StocSum: stochastic summary statistics for whole genome sequencing studies. 2023 Joint Statistical Meetings. Toronto, ON, Canada. August, 2023.

[7] StocSum: stochastic summary statistics for whole genome sequencing studies. American Society of Human Genetics 2023 Annual Meeting. Washington, DC. November, 2023.

## **L. Conference Platform Presentations by Trainees Mentored**

[1] Xinyu Wang. Efficient Gene-Environment Interaction Tests for Large-scale Sequencing Studies. 27th Annual International Genetic Epidemiology Society Conference. San Diego, CA. October, 2018.

[2] Mengyu Zhang. Robust Mixed Model Association Test for Gene-Environment Interactions. 2023 Joint Statistical Meetings. Toronto, ON, Canada. August, 2023.

## **M. Mentoring**

### **M.1. Graduated Students**

Tianzhong Yang	Ph.D. Biostatistics (2018)	Dissertation Committee Member
Weiwei Shan	M.S. Biostatistics (2018)	Thesis Committee Member
Jun Yu	Ph.D. Biostatistics (2018)	Dissertation Committee Member
Zhe Wang	Ph.D. Epidemiology (2018)	Dissertation Committee Member
Charee C. Robe	M.S. Biostatistics (2019)	Thesis Committee Member
Hai Zhu	Ph.D. Biostatistics (2019)	Dissertation Committee Member
Garrett T. Miller	M.S. Biostatistics (2019)	Thesis Committee Member
Xiangyu Liu	Ph.D. Biostatistics (2019)	Dissertation Committee Member
Priyadarshani P. Dharia	Ph.D. Epidemiology (2019)	Dissertation Committee Member
Pilar Zaibaq	M.P.H. Epidemiology (2020)	Academic Advisor
Andy B. Castañeda	M.P.H. Epidemiology (2020)	Academic Advisor
Kirsten N. Bevan	M.S. Epidemiology (2020)	Academic Advisor
Sofia Siddiq	M.P.H. Epidemiology (2020)	Academic Advisor
Min Qiao	Ph.D. Biostatistics (2020)	Dissertation Committee Member
Wen Li	Ph.D. Biostatistics (2020)	Dissertation Committee Member
Shudi Li	Ph.D. Biostatistics (2020)	Dissertation Committee Member
Qin Wang	M.S. Biostatistics (2020)	Thesis Committee Member
Jada M. Johnson	Ph.D. Biostatistics (2020)	Dissertation Committee Member
Elena V. Feofanova	Ph.D. Epidemiology (2020)	Dissertation Committee Member
Yiding Ma	Ph.D. Biostatistics (2020)	Dissertation External Reviewer
Yunju Yang	Ph.D. Epidemiology (2020)	Dissertation External Reviewer
Mengchen Ding	M.S. Biostatistics (2020)	Thesis Committee Member
Fadi I. Musfee	Ph.D. Epidemiology (2021)	Dissertation Committee Member
Georgia L. Jenkins	M.P.H. Epidemiology (2021)	Academic Advisor
Maryam Jamil	M.S. Biostatistics (2021)	Thesis Committee Member
Tao Xu	Ph.D. Biostatistics (2021)	Dissertation Committee Member
Cong Zhu	Ph.D. Epidemiology (2021)	Dissertation Committee Member
Xinyu Wang <sup>‡</sup>	Ph.D. Biostatistics (2021)	Dissertation Research Supervisor



*‡ Recipient of the 2019 UTHealth Houston School of Public Health Doctoral Dissertation Research Award*

Heping Wang	Ph.D. Biostatistics (2021)	Dissertation Committee Member
Elisha W. Crane	M.P.H. Epidemiology (2021)	Academic Advisor
Chengxue Zhong	Ph.D. Biostatistics (2022)	Dissertation Committee Member
Sylvia Phan	M.P.H. Epidemiology (2022)	Academic Advisor
Hyunseok Kim	Ph.D. Epidemiology (2022)	Dissertation Committee Member
Han Feng	Ph.D. Biostatistics (2022)	Dissertation Committee Member
Sai Sammitha Cheruvu	M.P.H. Epidemiology (2022)	Academic Advisor
Alykhan H. Bijani	M.P.H. Epidemiology (2022)	Academic Advisor
Yustinah Ndambakuwa	M.S. Biostatistics (2022)	Thesis Committee Member
Ashwin P. Patel	Ph.D. Epidemiology (2022)	Dissertation Committee Member
Rashelly Estrella Batista	M.P.H. Epidemiology (2022)	Academic Advisor
Wenying Quan	M.S. Biostatistics (2022)	Thesis Committee Member
Holly A. Hill <sup>‡</sup>	Ph.D. Epidemiology (2023)	Academic Advisor

*‡ Recipient of an NCI Predoctoral to Postdoctoral Fellow Transition (F99/K00) Award in 2022*

Yuefan Huang	Ph.D. Biostatistics (2023)	Dissertation Committee Member
Shwetha V. Kumar	Ph.D. Epidemiology (2023)	Dissertation Committee Member
Yun Qing	Ph.D. Biostatistics (2023)	Dissertation Committee Member
Rachel L. Atterstrom	M.P.H. Epidemiology (2023)	Thesis Committee Member
Elizabeth B. Grunder	M.P.H. Epidemiology (2023)	Academic Advisor
Jingyan Wang	Ph.D. Biostatistics (2023)	Dissertation Committee Member
Shinhye Chung	Ph.D. Epidemiology (2023)	Dissertation Committee Member
MacKinsey A. Bach <sup>‡</sup>	Ph.D. Epidemiology (2023)	Dissertation Research Supervisor

*‡ Recipient of a Training in Precision Environmental Health Sciences (TPEHS) T32 Fellowship in 2019*

Sarah N. Hinds	M.S. Biostatistics (2023)	Thesis Committee Member
Rachel D. Harris	Ph.D. Epidemiology (2024)	Dissertation Committee Member
Hanxiao Sun <sup>‡</sup>	Ph.D. Biostatistics (2024)	Dissertation Research Supervisor

*‡ Recipient of the 2023 UTHealth Houston School of Public Health Doctoral Dissertation Research Award*

Sahithi Kantamaneni	M.P.H. Epidemiology (2024)	Academic Advisor
Kimberly Carrillo Jaimes	M.P.H. Epidemiology (2024)	Academic Advisor

**M.2. Current Students**

Khush A. Patel	M.P.H. Epidemiology	Academic Advisor
Olivia Lee	Ph.D. GSBS Quant. Sci.	Candidacy Exam Comm. Member
Guning Liu	Ph.D. Environmental Sci.	Dissertation Committee Member
Pagna Sok	Ph.D. Epidemiology	Academic Advisor
Shreya Manocha	M.P.H. Epidemiology	Academic Advisor

Melissa Sponagle	M.P.H. Epidemiology	Academic Advisor
Jiansong Chen	Ph.D. Biostatistics	Dissertation Committee Member
Omobola O. Oluwafemi	Ph.D. Epidemiology	Dissertation Committee Member
Russell Wolters	M.P.H. Epidemiology	Academic Advisor
Geethika Yalavarthy	M.P.H. Epidemiology	Academic Advisor
Kun Hee Kim	Ph.D. GSBS Quant. Sci.	Advisory Committee Member
Ruoxing Li	Ph.D. Biostatistics	Dissertation Committee Member
Yishan Wang	Ph.D. Biostatistics	Dissertation Committee Member
Yuan Li	Ph.D. Biostatistics	Dissertation Committee Member
Mengyu Zhang <sup>‡</sup>	Ph.D. Biostatistics	Dissertation Research Supervisor

<sup>‡</sup> *Recipient of the 2023 UTHHealth Houston School of Public Health Robert H. Bigelow Endowed Scholarship, 2024 UTHHealth Houston School of Public Health Dr. M. Stewart West Memorial Scholarship in Biometry*

Yue Gu	Ph.D. Biostatistics	Dissertation Committee Member
Benjamin Cristol	Ph.D. Epidemiology	Academic Advisor
Joshua Strauss	Ph.D. Epidemiology	Academic Advisor
Zayd A. Ahmed	M.P.H. Epidemiology	Academic Advisor
Alyssa Maio	M.P.H. Epidemiology	Academic Advisor
Nurriya Mohammad	M.P.H. Epidemiology	Academic Advisor
Aishwarya Rajendran	M.P.H. Epidemiology	Academic Advisor
Brian J. Reiber	M.P.H. Epidemiology	Academic Advisor
Zachary Whitham	M.P.H. Epidemiology	Academic Advisor
Qi Miao	Ph.D. Biostatistics	Dissertation Committee Member
Songmi Lee	Ph.D. Epidemiology	Dissertation Committee Member
Xinran Huang	Ph.D. Biostatistics	Dissertation Committee Member
Chunhui Gu	Ph.D. Biostatistics	Dissertation Committee Member
Kai Chen	Ph.D. Biostatistics	Dissertation Committee Member
Naishu Kui	Ph.D. Biostatistics	Dissertation Committee Member
Sylvia D. Phan	Ph.D. Epidemiology	Academic Advisor
Christin Silos	Ph.D. Epidemiology	Academic Advisor
Krishanth S. Thoppe	M.P.H. Epidemiology	Academic Advisor
Akshaya S. Kadam	M.P.H. Epidemiology	Academic Advisor
Shu-Hsien Cho	Ph.D. GSBS Quant. Sci.	Candidacy Exam Comm. Member
Baihong (Bohong) Guo	Ph.D. Biostatistics	Dissertation Research Supervisor

### **M.3. Other Trainees**

Liang Hong	Scientific Programmer	2017 – 2018
Leixin Xia	Graduate Research Assistant	2018 – 2020
Alisha Kalangara	Research Assistant	2019 – 2020
Wenlong Ren	Postdoctoral Research Fellow	2019 – 2020

Duy T. Pham	Scientific Programmer	2019 – 2021
Nannan Wang	Faculty Associate	2020 –
Cong Pan	Scientific Programmer	2021 – 2023
Jiahui Jiang	Graduate Research Assistant	2021 – 2022
Shuyi Guo	Graduate Research Assistant	2023 –
Xiaochun Shao	Graduate Research Assistant	2023 – 2024
Samaneh Salehi Nasab	Scientific Programmer	2024 –

## **N. Memberships and Professional Service**

### **N.1. Professional Memberships**

International Genetic Epidemiology Society (2010 – )

American Statistical Association (2011 – )

American Society of Human Genetics (2012 – )

### **N.2. Institutional Service**

**Member** (2017, 2021 – 2023), Center for Precision Health Faculty Search Committee, UTHealth Houston McWilliams School of Biomedical Informatics

**Member** (2017 – 2018), Genomics and Bioinformatics Certificate *ad hoc* Curriculum Committee, UTHealth Houston School of Public Health

**Member** (2018 – 2019), Faculty Compensation Plan *ad hoc* Committee, UTHealth Houston School of Public Health

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

**Member** (2018 – ), Information Technology Faculty Advisory Committee, UTHealth Houston School of Public Health

**External Reviewer** (2022), Epidemiology Preliminary Exam Committee, Department of Epidemiology, Human Genetics and Environmental Sciences, UTHealth Houston School of Public Health

**Member** (2022 – ), Epidemiology Preliminary Exam Committee, Department of Epidemiology, Human Genetics and Environmental Sciences, UTHealth Houston School of Public Health

**Member** (2023 – ), Student Scholarship Committee, MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences (GSBS)

**Member** (2024 – ), Human Genetics Center Faculty Search Committee, UTHealth Houston School of Public Health

### **N.3. Peer-Review**

#### Grants

Science Foundation Ireland (2017).

National Institutes of Health (2020). ZRG1 PSE-B 04. Special Emphasis Panel, Member Conflict: Epidemiology and Statistical Methods.

National Institutes of Health (2022). Genetics of Health and Disease (GHD) Study Section (*ad hoc*, 6/27 – 6/28).

National Institutes of Health (2022). ZHG1 HGR-W (J1). National Human Genome Research Institute Special Emphasis Panel, U24 Genomic Community Resources.

### Journals

*Annals of Applied Statistics*

*Annals of Human Genetics*

*Bioinformatics*

*Biometrics*

*Biometrika*

*Biostatistics*

*BMC Bioinformatics*

*Circulation: Cardiovascular Genetics*

*Circulation: Genomic and Precision Medicine*

*Diabetologia*

*EBioMedicine*

*Genetic Epidemiology*

*Genetics*

*Genome Research*

*Human Heredity*

*International Journal of Epidemiology*

*Journal of the American Statistical Association*

*National Science Review*

*Nature Communications*

*Nature Medicine*

*PeerJ*

*PLOS Computational Biology*

*PLOS Genetics*

*PLOS ONE*

*Quantitative Biology*

*Scientific Reports*

*Statistical Methods in Medical Research*

*Statistics in Biosciences*

*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, Joint Statistical Meetings (2017 – 2023).

#### **N.4. Other Professional Service**

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

**Member** (2015 – 2018), Young Investigators Committee, International Genetic Epidemiology Society

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

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

**Member** (2017 – 2023), Communications 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**, Novel discoveries in large-scale genome-wide association studies. The American Society of Human Genetics 69th Annual Meeting. Houston, TX. October, 2019.

**Member**, Local Organizing Committee, The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Meeting. Houston, TX. January, 2020.

**Session Chair**, Novel Approaches. The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Meeting. Houston, TX. January, 2020.

**Discussant**, Rare variants and sequence analysis (poster session). 29th Annual International Genetic Epidemiology Society Conference. (Virtual Meeting). July, 2020.

**Member** (2021 – ), Board of Directors, Tsinghua Alumni Academia Club of North America.

**Guest Editor**, *PLOS Genetics*. January, 2021.

**Member** (2022 – ), Finance & Audit Committee (FAC), American Society of Human Genetics

**Member** (2022), Program Committee, 2022 IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM 2022). Las Vegas, NV. December, 2022.

**Secretary** (2023 – ), Tsinghua Alumni Academia Club of North America.