10/20/2025

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: Genetic Epidemiology (formerly Applied Genetic Methods in Public Health) (Summer 2019, Summer 2020, Summer 2021)
PHWM2612: Epidemiology I (Summer 2019, Summer 2020, Summer 2021, Summer 2022)
GS21 1152: GSBS Scientific Writing (Faculty Facilitator: Fall 2022, Fall 2025)
PH2784: Introduction to R Analysis for Epidemiologic Research (Spring 2022, Spring 2023, Spring 2024, Spring 2025)
PHD2711: Advanced Epidemiology (formerly Epidemiology IV) (Fall 2023, Fall 2024, Fall 2025)

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, Spring 2025)

E. Current Research Support

R01 AG081398 (Chen/Zhi) 09/30/2024 – 06/30/2029
NIH/NIA $3,770,993
Efficient IBD mapping for Alzheimer's Disease and related brain imaging phenotypes
Role: PI

R01 HL156991 (Rao) 04/27/2021 – 03/31/2026 (NCE)
NIH/NHLBI/Washington University in St. Louis $436,800 (UTHealth Houston sub)
A Multi-Ancestry Study of Gene-Lifestyle Interactions and Multi-Omics in Cardiometabolic Traits
Role: Co-Investigator

U01 AG070112 (Zhi/Fornage/Ji) 07/01/2021 – 06/30/2026
NIH/NIA $5,999,144
Genetics of Deep-Learning-Derived Neuroimaging Endophenotypes for Alzheimer's Disease
Role: Co-Investigator

75N92024D00008 (Smith) 05/15/2024 – 04/30/2026
NIH/NHLBI/The University of Michigan $849,161 (UTHealth Houston sub)
Trans-Omics for Precision Medicine (TOPMed) Informatics Research Center (IRC)
Role: Co-Investigator

R01 HL160793 (Yu/Vasan) 07/01/2022 – 06/30/2026
NIH/NHLBI $2,676,828
Genetic Architecture of Cardiac Structure and Function and Its Impact on Heart Failure
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

CZI 2021-239847 (Chen) 12/01/2021 – 11/30/2024
Chan Zuckerberg Initiative/Baylor College of Medicine $138,966 (UTHealth Houston sub)
Ancestry Network for the Human Cell Atlas in the Eye

Role: Subcontract PI

R01 HL145025 (Chen/Manning) 07/15/2019 – 06/30/2025
NIH/NHLBI $4,013,193
Methods and Software for Large-Scale Gene-Environment Interaction Studies
Role: PI

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 CA233719 (Scheurer) 08/01/2019 – 07/31/2025
NIH/NCI/Baylor College of Medicine $256,464 (UTHealth Houston sub)
Molecular Epidemiology of Langerhans Cell Histiocytosis: Evaluating the Impact of SMAD6 and Genetic Ancestry on Disease Risk
Role: Subcontract PI

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

Total citations (Google Scholar): 13,530
H-index: 38

[*] Co-first author
[#] Corresponding or senior 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**[*], Hendricks AE[*], 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, Kardia SL, Keinanen-Kiukaanniemi 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, Räikkönen 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, Yaghootkar 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, Burtt 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, Hercberg

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**[#], 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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Purcell SM, Raffield LM, Rich SS, Rotter JI, Saxena R, Smith AV, Stone KL, Zhu X, Cade BE, Sofer T, Redline S, Wang H. Genome-wide Gene by Sleepiness Interaction Analysis for Sleep Apnea. *Sleep.* 2025 Jul 28;. doi: 10.1093/sleep/zsaf212. [Epub ahead of print] PubMed PMID: 40736211.

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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.

[17] Reference-panel-free stochastic summary statistics for diverse populations. Institute of Bioinformatics, University of Georgia, Athens, GA. February, 2025.

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. The American Society of Human Genetics 2023 Annual Meeting. Washington, DC. November, 2023.

[8] Efficient mixed model association test for nonlinear effects in large-scale human genetic studies. Topic-Contributed Session, 2025 Joint Statistical Meetings. Nashville, TN. August, 2025.

[9] High-resolution identity-by-descent mapping test identifies genetic associations for deep-learning-derived brain imaging phenotypes. The International Genetic Epidemiology Society 2025 Annual Meeting. Cologne, Germany. September, 2025.

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.

[3] Nannan Wang. Genetic Architecture of Circulating Metabolites in the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. The American Society of Human Genetics 2024 Annual Meeting. Denver, CO. November, 2024.

[4] Mengyu Zhang. Fine mapping identifies potential causal variants at novel loci for blood pressure in large-scale gene-smoking interaction studies. The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Spring 2025 Meeting. Bethesda, MD. May, 2025.

M. Awards and Honors by Trainees Mentored

Xinyu Wang (Ph.D. Biostatistics 2021), Role: Dissertation Research Supervisor
2019: UTHealth Houston School of Public Health Doctoral Dissertation Research Award

MacKinsey A. Bach (Ph.D. Epidemiology 2023), Role: Dissertation Research Supervisor
2019: Training in Precision Environmental Health Sciences (TPEHS) T32 Fellowship

Holly A. Hill (Ph.D. Epidemiology 2023), Role: Academic Advisor
2022: NCI Predoctoral to Postdoctoral Fellow Transition (F99/K00) Award

Hanxiao Sun (Ph.D. Biostatistics 2024), Role: Dissertation Research Supervisor
2023: UTHealth Houston School of Public Health Doctoral Dissertation Research Award

Pagna Sok (Ph.D. Student in Epidemiology), Role: Academic Advisor
2023: UTHealth Houston School of Public Health Ranajit Chakraborty Fellowship in Human Genetics

Mengyu Zhang (Ph.D. Student in Biostatistics), Role: Dissertation Research Supervisor
2023: UTHealth Houston School of Public Health Robert H. Bigelow Endowed Scholarship
2024: UTHealth Houston School of Public Health Dr. M. Stewart West Memorial Scholarship in Biometry
2025: UTHealth Houston School of Public Health Robert J. Hardy and C. Morton Hawkins Endowed Scholarship in Biostatistics

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 – 2025), 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 – 2025), 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 – 2025), 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.
National Institutes of Health (2024). ZRG1 MGG-A (50). PAR-23-199: ClinGen Genomic Curation Expert Panels (U24).
National Institutes of Health (2025). Maximizing Investigators' Research Award A (MRAA) Study Section (*ad hoc*, 4/14).
National Institutes of Health (2025). Maximizing Investigators' Research Award A (MRAA) Study Section (*ad hoc*, 7/15 – 7/16).
The Dutch Research Council (NWO) (2025).

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 – 2024), Board of Directors, Tsinghua Alumni Academia Club of North America.

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

Member (2022 – 2024), 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 – 2024), Tsinghua Alumni Academia Club of North America.

Moderator, Novel Genetic, Genomic, and Epigenetic Resources in the Era of Big Data. The American Society of Human Genetics 2024 Annual Meeting. Denver, CO. November, 2024.

Session Chair, Recent Advances in Population Health at Scale: Artificial Intelligence, Informatics, and Causal Inference. STATGEN 2025: Conference on Statistics in Genomics and Genetics. Minneapolis, MN. May, 2025.

Session Chair, Poster Highlights 1. The International Genetic Epidemiology Society 2025 Annual Meeting. Cologne, Germany. September, 2025.

Moderator, Better Together: Multi-Ancestry Approaches for Gene Discovery. The American Society of Human Genetics 2025 Annual Meeting. Boston, MA. October, 2025.