Curriculum Vitae

XIAOMING LIU

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RESEARCH INTERESTS:
My research focuses on understanding the variants in human genomes. My work concerns theoretical modeling, statistical method development and practical data analysis, and spans areas of population genetics, computational genomics and human genetic diseases.

EDUCATION:
- Ph.D. in Genetics, The University of Texas MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences, Houston, TX, 2006.
- M.S. in Genetics, Fudan University, Shanghai, China, 2000.
- B.S. in Genetics, Fudan University, Shanghai, China, 1997.

PROFESSIONAL EXPERIENCE:
- 2020- Tenured Associate Professor, College of Public Health, University of South Florida, Tampa, FL.
- 2019- Adjunct Associate Professor, The University of Texas School of Public Health, Houston, TX.
- 2018-2020 Tenure-Track Associate Professor, College of Public Health, University of South Florida, Tampa, FL.
- 2013-2018 Tenure-Track Assistant Professor, The University of Texas School of Public Health, Houston, TX.
- 2007-2013 Research-Track Assistant Professor of Human Genetics, The University of Texas School of Public Health, Houston, TX.
- 2002-2006 Research Assistant, The University of Texas, Graduate School of Biomedical Sciences, Houston, TX.
- 1998-2000 Research Assistant, Chinese National Human Genome Centre (CNHG), Shanghai, China.

FUNDING AND AWARDS
- Conference Support Grant (USF Internal Funding), International Conference on Intelligent Biology and Medicine (ICIBM 2023), $5000, 2023
- 15PNIJ-22-GG-04431-RESS, Improve craniometric ancestry estimation with deep learning methods, $306,271 from 01/01/2023 - 12/31/2024, USF / NIJ / PI
- 1R03HG011075-01, Extend and improve the functional annotation tools dbNSFP and WGSA, $100,000 from 04/01/2020 – 03/31/2022, USF / NIH / PI

- Outstanding Contributions Award, the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, 2017
- Distinguished Service Award, the International Association for Intelligent Biology and Medicine, 2024
- 1R01HG009524-01, Accurately inferring demographic histories of human populations using large whole genome sequence data, $1,528,968 from 07/24/2017 - 05/31/2021, UTSPH / NIH / PI
- FOTE award (UTSPH research funding), Use cancer driver gene detection to find novel Mendelian disease causing genes, $25,000 from 9/1/2016-8/31/2017, PI
- FOTE award (UTSPH research funding), A Leap from Gene Mapping to Black-Box Phenotype Prediction for Complex Disease Studies, $25,000 from 9/1/2012-8/31/2013, PI
- 1R01HL142003, Trans-omics Analysis to Unravel Molecular Underpinnings of Heart, Lung and Blood Disease Risk Factors, 06/01/2018 - 04/30/2020, UTHealth SPH / NIH / / Co-Investigator
- 1R01HG010086, Scalable methods for identity by descent, 06/01/2018-03/31/2022, UTHealth SBMI / NIH / / Co-Investigator
- 1UM1HG008898, Genomic Architecture of Common Disease in Diverse Populations, 1/14/2016 - 11/30/2019, BCM / NIH / Co-Investigator
- 5T32GM074902, Training Grant Program in Biostatistics at UTHSC – SPH, 7/1/2016 - 6/30/2019, NIH / Mentor
- 5U54HG003273, The Human Genome Sequencing Center, 11/1/2011 - 10/31/2016, BCM / NIH / Co-Investigator
- 5R03DE024596, Tooth agenesis as a clinical marker for colon cancer, 8/1/2014 - 7/31/2016, NIH / Subcontract-PI
- 5T32GM074902, Training Grant Program in Biostatistics at UTHSC – SPH, 7/1/2012 - 6/30/2016, NIH / Mentor
- 5U01HG005728, Detecting Natural Selection for the 1000 Genomes Dataset, 04/01/2010 - 10/31/2013, NIH / Co-Investigator
- 5P50GM065509, Genomic Approaches to Common Chronic Disease, 07/01/2007 - 06/30/2013, U of Michigan / NIH / Co-Investigator
- 5UC2HL103010, Human Exome Sequencing in Six Well-Phenotyped NHLBI Cohorts, 09/30/2009 - 03/31/2013, U of Virginia / NIH / Co-Investigator
- 5RC2HL102419, Building on GWAS for NHLBI-Disease: the CHARGE Consortium, 09/30/2009 - 09/30/2012, NIH / NHLBI / Co-Investigator

OTHER EXPERIENCE AND PROFESSIONAL MEMBERSHIPS:

- **Editorial Board Member**: *BMC Genetics* (2014-2020), *BMC Genomics* (2021-), *Frontiers in Genetics* (2021-)
- **Guest Editor**: *BMC Genomics*, *BMC Bioinformatics*, *BMC Systems Biology*, *BMC Medical Genomics*, *Human Heredity* (ICIBM2018)
- **Manuscript Reviewer**: *Nature Genetics, Nature Methods, Nature Machine Intelligence, Nature Biomedical Engineering, Nature Communications, Science Advances, Science Translational Medicine, Genome Research, Genome Biology, Nucleic Acids Research, Molecular Biology and Evolution*, *American Journal of Human Genetics, Genome Medicine, Cell Reports Methods*, *Briefings in Bioinformatics, Circulation Research, National Science Review*, *Biological Psychiatry*, *Global Change Biology, Military Medical Research, Genetics in Medicine*, *The Innovation, Systematic Biology*, *Genomics, Proteomics & Bioinformatics, PLoS Genetics*, *BMC Biology*, *Cancers, Computational and Structural Biotechnology Journal, Journal of Medical Genetics*, *Conservation Biology, Human Mutation*, *Bioinformatics, European Journal of Human Genetics, Human Genetics, Genetics*, *Genome Biology and Evolution*, *Methods*, *Heredity*, *BMC*

Genomics, BMC Medical Genomics, Current Genomics, BMC Bioinformatics, American Journal of Primatology, Molecular Biology of the Cell, Genes, Methods, Gene, Scientific Reports, PLoS One, G3, Molecular Genetics and Genomics, Molecules, Frontiers in Genetics

- **Founding Officer**: International Association for Intelligent Biology and Medicine (IAIBM)
- **General Chair**, 2024 International Conference on Intelligent Biology and Medicine (ICIBM 2024)
- **Program Committee Chair**, 2023 International Conference on Intelligent Biology and Medicine (ICIBM 2023)
- **Local Chair**, 2018 International Conference on Intelligent Biology and Medicine (ICIBM 2018)
- **Session Moderator**, American Society of Human Genetics (ASHG) 2013 Meeting, Boston, MA.
- **Session Moderator**, American Society of Human Genetics (ASHG) 2019 Meeting, Houston, TX.
- **Session Chair**, 2020 International Conference on Intelligent Biology and Medicine (ICIBM 2020), 2021 International Conference on Intelligent Biology and Medicine (ICIBM 2021), 2022 International Conference on Intelligent Biology and Medicine (ICIBM 2022)
- **Session Co-Chair**, 2020 International Chinese Statistical Association (ICSA 2020) Applied Statistics Symposium
- **Leader**, CHARGE Consortium whole genome annotation sub-committee
- **Leader**, whole genome annotation for TOPMed Consortium
- **Co-coordinator**, NHGRI Genome Sequencing Program (GSP) annotation working group
- Program Committee Member, 2019 International Conference on Intelligent Biology and Medicine (ICIBM 2019), 2020 International Conference on Intelligent Biology and Medicine (ICIBM 2020), 2021 International Conference on Intelligent Biology and Medicine (ICIBM 2021), 2022 International Conference on Intelligent Biology and Medicine (ICIBM 2022), 2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM'23)
- Member, 1000 Genomes Project Analysis Group
- Member, NHLBI Exome Sequencing Project Population Genetics Group
- Member, CHARGE Consortium Analysis and Bioinformatics Group
- Member, TOPMed Consortium Population Genetics Group
- Member, American Society of Human Genetics
- Member, Society for Molecular Biology and Evolution

PUBLICATIONS:

A. Peer-reviewed Publications

1. Rastogi R, Chung R, Li S, Li C, Lee K, Woo J, Kim D, Keum C, Babbi G, Martelli P, Savojardo C, Casadio R, Chennen K, Weber T, Poch O, Ancien F, Cia G, Pucci F, Raimondi D, Vranken W, Rooman M, Marquet C, Olenyi T, Rost B, Andreoletti G, Kamandula A, Peng Y, Bakolitsa C, Mort M, Cooper D, Bergquist T, Pejaver V, **Liu X**, Radivojac P, Brenner S, Ioannidis N. (2025) Critical assessment of missense variant effect predictors on disease-relevant variant data. Human Genetics. 144:281–293.
2. Wang C^, Dong Y, Li C, Oberstaller J, Zhang M, Gibbons J, Pires CV, Xiao M, Zhu L, Jiang RH, Kim K, Miao J, Otto TD, Cui L, Adams JH, **Liu X**. (2023) MalariaSED: a deep learning framework to decipher the regulatory contributions of noncoding variants in malaria parasites. Genome Biology. 24:231. ^corresponding author
3. Pang J, **Liu X**. (2023) Evaluation of missing data imputation methods for human osteometric measurements. American Journal of Biological Anthropology. 181(4):666-676.

4. Li C^, Hou I, Ma M, Wang G, Bai Y^, **Liu X**^. (2023) Orthogonal analysis of variants in APOE gene using in-silico approaches reveals novel disrupting variants. Frontiers in Bioinformatics. 3:1122559. ^corresponding authors
5. Pang J, Dong Y, Turner C, Li C, **Liu X**. (2022) Analysis of data consistency identifies measurement abnormality in Howells' craniometric test data set. American Journal of Biological Anthropology. 179(4):687-692.
6. Li C, Zhi D, Wang K, **Liu X**. (2022) MetaRNN: differentiating rare pathogenic and rare benign missense SNVs and InDels using deep learning. Genome Medicine. 14:115.
7. Li C, Ma K, Xu N, Fu C, He A, **Liu X**^, Bai Y^. (2022) SNPAAMapper-Python: A highly efficient genome-wide SNP variant analysis pipeline for Next-Generation Sequencing data. Frontiers in Artificial Intelligence. 5:991733. ^corresponding authors
8. Li C^, Wang R, Wu A, Yuan T, Song K, Bai Y^, **Liu X**^. (2022) SARS-COV-2 as potential microRNA sponge in COVID-19 patients. BMC Medical Genomics. 15:94. ^corresponding authors
9. Li C^, Wu A, Song K, Gao J, Huang E, Bai Y^, **Liu X**^. (2021) Identifying Putative Causal Links between MicroRNAs and Severe COVID-19 Using Mendelian Randomization. Cells. 10(12): 3504. ^corresponding authors
10. Naseri A, Tang K, Geng X, Shi J, Zhang J, Shakya P, **Liu X**, Zhang S, Zhi D. (2021) Personalized genealogical history of UK individuals inferred from biobank-scale IBD segments. BMC Biology. 19: 32.
11. Taliun D, Harris DN, Kessler MD, Carlson J, Szpiech ZA, Torres R, Taliun SAG, Corvelo A, Gogarten SM, Kang HM, Pitsillides AN, LeFaive J, Lee S, Tian X, Browning BL, Das S, Emde A, Clarke WE, Loesch DP, Shetty AC, Blackwell TW, Smith AV, Wong Q, **Liu X**, Conomos MP, Bobo DM, Aguet F, Albert C, Alonso A, Ardlie KG, Arking DE, Aslibekyan S, Auer PL, Barnard J, Barr RG, Barwick L, Becker LC, Beer RL, Benjamin EJ, Bielak LF, Blangero J, Boehnke M, Bowden DW, Brody JA, Burchard EG, Cade BE, Casella JF, Chalazan B, Chasman DI, Chen YI, Cho MH, Choi SH, Chung MK, Clish CB, Correa A, Curran JE, Custer B, Darbar D, Daya M, Andrade MD, DeMeo DL, Dutcher SK, Ellinor PT, Emery LS, Eng C, Fatkin D, Fingerlin T, Forer L, Fornage M, Franceschini N, Fuchsberger C, Fullerton SM, Germer S, Gladwin MT, Gottlieb DJ, Guo X, Hall ME, He J, Heard-Costa NL, Heckbert SR, Irvin MR, Johnsen JM, Johnson AD, Kaplan R, Kardia SLR, Kelly T, Kelly S, Kenny EE, Kiel DP, Klemmer R, Konkle BA, Kooperberg C, Köttgen A, Lange LA, Lasky-Su J, Levy D, Lin X, Lin K, Liu C, Loos RJF, Garman L, Gerszten R, Lubitz SA, Lunetta KL, Mak ACY, Manichaikul A, Manning AK, Mathias RA, McManus DD, McGarvey ST, Meigs JB, Meyers DA, Mikulla JL, Minear MA, Mitchell BD, Mohanty S, Montasser ME, Montgomery C, Morrison AC, Murabito JM, Natale A, Natarajan P, Nelson SC, North KE, O'Connell JR, Palmer ND, Pankratz N, Peloso GM, Peyser PA, Pleiness J, Post WS, Psaty BM, Rao DC, Redline S, Reiner AP, Roden D, Rotter JI, Ruczinski I, Sarnowski C, Schoenherr S, Schwartz DA, Seo J, Seshadri S, Sheehan VA, Sheu WH, Shoemaker MB, Smith NL, Smith JA, Sotoodehnia N, Stilp AM, Tang W, Taylor KD, Telen M, Thornton TA, Tracy RP, Van Den Berg DJ, Vasan RS, Viaud-Martinez KA, Vrieze S, Weeks DE, Weir BS, Weiss ST, Weng L, Willer CJ, Zhang Y, Zhao X, Arnett DK, Ashley-Koch AE, Barnes KC, Boerwinkle E, Gabriel S, Gibbs R, Rice KM, Rich SS, Silverman EK, Qasba P, Gan W, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Papanicolaou GJ, Nickerson DA, Browning SR, Zody MC, Zöllner S, Wilson JG, Cupples LA, Laurie CC, Jaquish CE, Hernandez RD, O'Connor TD, Abecasis GR. (2021) Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature. 590: 290-299.
12. Dong Y^, Li C, Kim K, Cui L, **Liu X**^. (2021) Genome annotation of disease-causing microorganisms. Briefings in Bioinformatics. 22(2):845–854. ^corresponding authors
13. Lin BM, Grinde KE, Brody JA, Breeze CE, Raffield LM, Mychaleckyj JC, Thornton TA, Perry JA, Baier LJ, de las Fuentes L, Guo X, Heavner BD, Hanson RL, Hung YJ, Qian H, Hsiung CA, Hwang SJ, Irvin MR, Jain D, Kelly TN, Kobes S, Lange L, Lash JP, Li Y, **Liu X**, Mi X, Musani

SK, Papanicolaou GJ, Parsa A, Reiner AP, Salimi S, Sheu WHH, Shuldiner AR, Taylor KD, Smith AV, Smith JA, Tin A, Vaidya D, Wallace RB, Yamamoto K, Sakaue S, Matsuda K, Kamatani Y, Momozawa Y, Yanek LR, Young BA, Zhao W, Okada Y, Abecasis G, Psaty BM, Arnett DK, Boerwinkle E, Cai J, Chen IYD, Correa A, Cupples LA, He J, Kardia SLR, Kooperberg C, Mathias RA, Mitchell BD, Nickerson D, Turner ST, Ramachandran VS, Rotter JI, Levy D, Kramer H, Kottgen A, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Kidney Working Group, Rich SS, Lin DY, Browning SR, Franceschini N. (2021) Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine. 63:1031573.

14. **Liu X**^, Li C, Mou C, Dong Y, Tu Y. (2020) dbNSFP v4: a comprehensive database of transcript-specific functional predictions and annotations for human nonsynonymous and splice-site SNVs. Genome Medicine. 12:103. ^corresponding author
15. **Liu X**^ and Fu YX. (2020) Stairway Plot 2: demographic history inference with folded SNP frequency spectra. Genome Biology. 21:280. ^corresponding author
16. **Liu X***^, Cragun D*, Pang J, Adapa SR, Fonseca R, Jiang RHY. (2020) False Alarms in Consumer Genomics Add to Public Fear and Potential Health Care Burden. Journal of Personalized Medicine 10(4): 187. ^corresponding author; *contributed equally.
17. Xue C, Rustagi N, **Liu X**, Raveendran M, Harris RA, Venkata MG, Rogers J, Yu F. (2020) Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. PLoS ONE 15(8): e0236285.
18. Li C, Wu B, Han H, Zhao J, Bai Y, **Liu X**. (2020) Identification of MicroRNA-Related Tumorigenesis Variants and Genes in the Cancer Genome Atlas (TCGA) Data. Genes 11(9): 953.
19. **Liu X**. (2020) Human prehistoric demography revealed by the polymorphic pattern of CpG transitions. Molecular Biology and Evolution 37(9):2691-2698.
20. Bai Y, Baker S, Exoo K, Dai X, Ding L, Khattak NA, Li H, Liu H, **Liu X**. (2020) MMiRNA-Viewer2, a bioinformatics tool for visualizing functional annotation for MiRNA and MRNA pairs in a network. BMC Bioinformatics 21(Suppl 4):247.
21. Li Y, Hu Y, Zhao Y, Wang Q, Mbenda HGN, Kittichai V, Lawpoolsri S, Sattabongkot J, Menezes L, **Liu X**, Cui L, Cao Y. (2020) Dynamics of Plasmodium Vivax Populations in Border Areas of the Greater Mekong Sub-Region During Malaria Elimination. Malaria Journal 19:145.
22. Li C, Mou C, Swartz MD, Yu B, Bai Y, Tu Y, **Liu X**. (2020) dbMTS: a comprehensive database of putative human microRNA target site SNVs and their functional predictions. Human Mutation 41(6):1123–1130.
23. Naseri A, **Liu X**, Tang K, Zhang S, Zhi D. (2019) Ultra-fast, Powerful and Accurate Detection of Segments Identical by Descent (IBD) in Biobank-Scale Cohorts. Genome Biology 20:143.
24. Chen H, Huffman JE, Brody JA, Wang C, Lee S, Li Z, Gogarten SM, Sofer T, Bielak LF, Bis JC, Blangero J, Bowler RP, Cade BE, Cho MH, Correa A, Curran JE, de Vries PS, Glahn DC, Guo X, Johnson AD, Kardia S, Kooperberg C, Lewis JP, **Liu X**, Mathias RA, Mitchell BD, O'Connell JR, Peyser PA, Post WS, Reiner AP, Rich SS, Rotter JI, Silverman EK, Smith JA, Vasan RS, Wilson JG, Yanek LR; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium; TOPMed Hematology and Hemostasis Working Group, Redline S, Smith NL, Boerwinkle E, Borecki IB, Cupples LA, Laurie CC, Morrison AC, Rice KM, Lin X. (2019) Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics 104(2):260-274.
25. Floyd JS, Bloch KM, Brody JA, Maroteau C, Siddiqui MK, Gregory R, Carr DF, Molokhia M, **Liu X**, Bis JC, Ahmed A, Liu X, Hallberg P, Yue Q, Magnusson PKE, Brisson D, Wiggins KL, Morrison AC, Khoury E, McKeigue P, Stricker BH, Lapeyre-Mestre M, Heckbert SR, Gallagher A, Chinoy H, Gibbs RA, Bondon-Guitton E, Tracy R, Boerwinkle E, Gaudet D, Conforti A, van Staa T, Sitlani CM, Rice KM, van der Zee AHM, Wadelius M, Morris AP, Pirmohamed M, Palmer

CAN Psaty BM, Alfirevic A on beharf of the PREDICTION-ADR Consortium and EUDRAGENE. (2019) Pharmacogenomics of statin-related myopathy: meta-analysis of rare variants from whole-exome sequencing. PLoS ONE 14(6): e0218115.

26. Pei G, Sun H, Dai Y, **Liu X**, Zhao Z, Jia P. (2019) Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics 20(Suppl 1):79.
27. Djotsa A*, Chen K and **Liu X**. (2019) Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. BMC Medical Genomics 12(Suppl 1):22. *first author is my student.
28. Feofanova E, Yu B, Metcalf G, **Liu X**, Muzny D, Below J, Wagenknecht L, Gibbs R, Morrison A, Boerwinkle E. (2018) Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics 209(2):607-616.
29. Williams M, Biguetti C, Romero-Bustillos M, Maheshwari K, Dinckan N, Cavalla F, **Liu X**, Silva R, Akyalcin S, Uyguner ZO, Vieira A, Amendt B, Fakhouri W, and Letra A (2018) Colorectal Cancer-Associated Genes Are Associated with Tooth Agenesis and May Have a Role in Tooth Development. Scientific Reports 8:2979.
30. Cristofari R, **Liu X**, Bonadonna F, Cherel Y, Pistorius P, Le Maho Y, Raybaud V, Stenseth N, Le Bohec C, Trucchi E. (2018) Climate-driven range shifts of the king penguin in a fragmented ecosystem. Nature Climate Change 8:245–251.
31. Li C*, Grove-Gaona ML, Yu B, Jones BC, Morrison A, Boerwinkle E^, **Liu X**^. (2018) Genetic variants in microRNA genes and targets associated with cardiovascular disease risk factors in the African-American population. Human Genetics 137(1):85–94. ^Corresponding authors. *first author is my student.
32. Hwang JL, Park S-Y, Ye H, Sanyoura M, Pastore AN, Carmody D, del Gaudio D, Wilson JF, Hanis CL, **Liu X**, Atzmon G, Glaser B, Philipson LH, Greeley SAW, T2D-Genes Consortium. (2018) FOXP3 mutations causing early-onset insulin-requiring diabetes but without other features of immune dysregulation, polyendocrinopathy, enteropathy, X-linked syndrome. Pediatric Diabetes 19(3):388-392.
33. Yuan Q, Zhao M, Liu Q, Tandon B, Maili L, **Liu X**, Zhang A, Baugh EH, Tran T, Silva RM, Hecht JT, Swindell EC, Wagner DS, Letra A. (2017) Role of WNT10A in failure of tooth development in humans and zebrafish. Molecular Genetics and Genomic Medicine 5(6):730-741.
34. Andersen AM, Pietrzak RH, Kranzler HR, Ma L, Zhou H, **Liu X**, Kramer J, Kuperman S, Edenberg HJ, Nurnberger JI Jr, Rice JP, Tischfield JA, Goate A, Foroud TM, Meyers JL, Porjesz B, Dick DM, Hesselbrock V, Boerwinkle E, Southwick SM, Krystal JH, Weissman MM, Levinson DF, Potash JB, Gelernter J, Han S (2017) Polygenic Scores for Major Depressive Disorder and Risk of Alcohol Dependence. JAMA Psychiatry 74(11):1153-1160.
35. Brody JA, Morrison AC, Bis JC, O'Connell JR, Brown MR, Huffman JE, Ames DC, Carroll A, Conomos MP, Gabriel S, Gibbs RA, Gogarten SM, Gupta N, Jaquish CE, Johnson AD, Lewis JP, **Liu X**, Manning AK, Papanicolaou GJ, Pitsillides AN, Rice KM, Salerno W, Sitlani CM, Smith NL, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, TOPMed Hematology and Hemostasis Working Group, CHARGE Analysis and Bioinformatics Working Group, Heckbert SR, Laurie CC, Mitchell BD, Vasan RS, Rich SS, Rotter JI, Wilson JG, Boerwinkle E, Psaty BM, Cupples LA. (2017) Analysis Commons, A Team Approach to Discovery in a Big-Data Environment for Genetic Epidemiology. Nature Genetics 49(11):1560-1563.
36. de Vries PS, Yu B, Feofanova EV, Metcalf GA, Brown MR, Zeighami AL, **Liu X**, Muzny DM, Gibbs RA, Boerwinkle E, Morrison AC. (2017) Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. Human Molecular Genetics. 26(17):3442-3450.
37. Feng Y, Ge X, Meng L, Scull J, Li J, Tian X, Zhang T, Jin W, Cheng H, Wang X, Tokita M, Liu P, Mei H, Wang Y, Li F, Schmitt ES, Zhang WV, Muzny D, Wen S, Chen Z, Yang Y, Beaudet AL, **Liu X**, Eng CM, Xia F, Wong L-J, Zhang J. (2017) The Next-Generation of Spinal Muscular

Atrophy Carrier Screening: Comprehensive Pan-ethnic SMN1 Copy Number and Sequence Variant Analysis by Massively Parallel Sequencing. Genetics in Medicine 19(8):936-944.
38. Morrison AC, Huang Z, Yu B, Metcalf G, **Liu X**, Ballantyne C, Coresh J, Yu F, Muzny D, Feofanova E, Rustagi N, Gibbs R, Boerwinkle E. (2017) Practical Approaches for Whole Genome Sequence Analysis of Complex Traits. American Journal of Human Genetics 100:205–215.
39. **Liu X^**, Li C and Boerwinkle E. (2017) The performance of deleteriousness prediction scores for rare non-protein-changing single nucleotide variants in human genomes. Journal of Medical Genetics 54:134-144. ^corresponding author
40. Dong C, Guo Y, He Z, Yang H, **Liu X**, Wang K. (2016) iCAGES: integrated CAncer GEnome Score for comprehensively prioritizing driver genes in personal cancer genomes. Genome Medicine 8:135.
41. Xue C, Raveendran M, Harris RA, Fawcett GL, **Liu X**, White S, Dahdouli M, Rio Deiros D, Below JE, Salerno W, Cox L, Fan D, Ferguson B, Horvath J, Johnson Z, Kanthaswamy S, Kubisch HM, Liu D, Platt M, Smith DG, Sun B, Vallender EJ, Wang F, Wiseman R, Chen R, Muzny DM, Gibbs RA, Yu F and Rogers J. (2016) The population genomics of rhesus macaques (*Macaca mulatta*) based on whole genome sequences. Genome Research 26(12):1651-1662.
42. Yu B, de Vries P, Metcalf G, Wang Z, Feofanova E, **Liu X**, Muzny D, Wagenknecht L, Gibbs R, Morrison A, Boerwinkle E. (2016) Whole genome sequence analysis of serum amino acid levels. Genome Biology 17:237.
43. Yazdani A, Yazdani A, **Liu X**, Boerwinkle E. (2016) Identification of Rare Variants in Metabolites of the Carnitine Pathway by Whole Genome Sequencing Analysis. Genetic Epidemiology. 40(6):486-91.
44. Huang J, Wang K, Wei P, Liu X, **Liu X**, Tan K, Boerwinkle E, Potash JB and Han S. (2016) FLAGS: A Flexible and Adaptive Association Test for Gene Sets Using Summary Statistics. Genetics. 202(3):919-929.
45. **Liu X^**, Wu C, Li C and Boerwinkle E. (2016) dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Non-synonymous and Splice Site SNVs. Human Mutation. 37(3):235-241. ^corresponding author
46. **Liu X^**, White S, Peng B, Johnson AD, Brody JA, Li AH, Huang Z, Carroll A, Wei P, Gibbs R, Klein RJ and Boerwinkle E. (2016) WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics. 53:111-112. ^corresponding author
47. Li AH, Morrison AC, Kovar C, Cupples LA, Brody JA, Polfus LM, Yu B, Metcalf G, Muzny D, Veeraraghavan N, **Liu X**, Lumley T, Mosley TH, Gibbs RA, Boerwinkle E. (2015) Analysis of loss-of-function variants and 20 risk factor phenotypes in 8,554 individuals identifies loci influencing chronic disease. Nature Genetics. 47(6):640-642.
48. **Liu X^** and Fu YX. (2015) Exploring population size changes using SNP frequency spectra. Nature Genetics. 47(5):555-559. ^corresponding author
49. Yu F*, Lu J*, **Liu X***, Gazave E, Chang D, Raj S, Hunter-Zinck H, Blekhman R, Arbiza L, Van Hout C, Morrison A, Johnson AD, Bis J, Cupples LA, Psaty BM, Muzny D, Yu J, Gibbs RA, Keinan A, Clark AG, Boerwinkle E. (2015) Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. PLoS One. 10(3):e0121644. *contributed equally
50. Dong C, Wei P, Jian X, Gibbs R, Boerwinkle E, Wang K^ and **Liu X^**. (2015) Comparison and integration of deleteriousness prediction methods for nonsynonymous SNVs in whole exome sequencing studies. Human Molecular Genetics 24(8):2125-2137. ^corresponding authors
51. Jian X*, Boerwinkle E and **Liu X**. (2014) *In silico* prediction of splice-altering single nucleotide variants in the human genome. Nucleic Acids Research 42(22):13534-13544. *first author is my student.

52. Li Q, **Liu X**^, Gibbs RA, Boerwinkle E, Polychronakos C, Qu HQ† (2014) Gene-specific function prediction for non-synonymous mutations in monogenic diabetes genes. PLoS One 9(8):e104452. ^corresponding authors
53. Jian X*, Boerwinkle E and **Liu X**. (2014) *In silico* tools for splicing defect prediction: a survey from the viewpoint of end users. Genetics in Medicine 16(7):497–503. *first author is my student.
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B. Peer-reviewed Publications as Part of Research Consortia

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C. Peer-reviewed Conference Paper

109. Dong Y, Gao A, Hou I, Ma K, Huang R, Bai Y, **Liu X**. (2021) A Deep Learning Model for Ancestry Estimation with Craniometric Measurements. 2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Virtual Conference (Dec. 9-12, 2021)
110. Li C*, Swartz MD, Yu B, Bai Y, **Liu X**. (2019) dbMTS: a comprehensive database of putative human microRNA target site SNVs and their functional predictions. International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, Ohio, USA (June 9-11, 2019). *first author is my student.
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D. Editorial Articles

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E. Book Chapters

122. Jian X* and **Liu X**. (2016) In Silico Prediction of Deleteriousness for Nonsynonymous and Splice-Altering Single Nucleotide Variants in the Human Genome. In: In Vitro Mutagenesis. (Reeves A ed.) New York: Springer Nature pp. 191-198. *first author is my student.

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F. Abstracts and Proceedings

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2. Li C, **Liu X**. (5/11/2021) MetaRNN: Differentiating Rare Pathogenic and Rare Benign Missense SNVs and InDels Using Deep Learning. The Biology of Genomes (BOG) 2021, Cold Spring Harbor, NY.
3. **Liu X**. (10/16/2019) Whole genome sequence data reveal global demographic dynamics respond to the last ice age. American Society of Human Genetics (ASHG) 2019 Annual Meeting, Houston, TX.
4. **Liu X**. (7/23/2019) Stairway plot 2: A fast and convenient tool for inferring demographic history using folded or unfolded SNP frequency spectra. Society for Molecular Biology and Evolution (SMBE) 2019 Annual Meeting, Manchester, UK.
5. **Liu X**. (2018) Human prehistoric demography revealed by polymorphic pattern of CpG transitions. Population, Evolutionary, and Quantitative Genetics Conference (PEQG), Madison, WI.
6. Naseri A, Geng X, Tang K, **Liu X**, Zhang S, Zhi D. (2018) Fast and accurate identification of diploid IBD segments in large biobank cohorts. ASHG 2018 Meeting, San Diego, CA.
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10. **Liu X**, Feofanova EV, Yazdani A, Yu B, Wei P, Morrison A, Boerwinkle E. (2016) Functional annotation guided genotype-phenotype association analyses of whole genome sequence data. Biology of Genomes Meeting, Cold Spring Harbor, NY.
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Variants in 8,612 Deply-Phenotyped Individuals Identifes Novel Loci for Common Chronic Disease. ASHG 2014 Meeting, San Diego, CA.

16. **Liu X**, Jian X, Boerwinkle E. (2013) dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. ASHG 2013 Meeting, Boston, MA.
17. Morison AC, Yu F, Lu J, Vorman A, Johnson AD, Reid J, **Liu X**, Muzny D, Folsom AR, O'Donel CJ, Psaty BM, Cuples LA, Clark A, Gibbs R, Eoerwinkle E, The Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE) Consortium. (2013) Functional annotation combined with evolutionary principles facilitate whole genome sequence analyses of complex traits: the Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE) Consortium. ASHG 2013 Meeting, Boston, MA.
18. Van Hout CV, Yu F, **Liu X**, Boerwinkle E, Clark AG. (2013) Paterns of IBD sharing infered from whole genome sequences of 962 European Americans. ASHG 2013 Meeting, Boston, MA.
19. **Liu X**, Blekhman R, Yu F, Voorman A, Yu J, Morrison A, Clark A, Psaty B, Cupples A, Boerwinkle E, Gibbs R. (2012) Population genetics analysis of 962 whole genome sequences - the CHARGE-S consortium. The Biology of Genomes Meeting, Cold Spring Harbor, NY.
20. **Liu X**, Jian X, Boerwinkle E. (2011) dbNSFP 1.1: An integrated database of human non-synonymous substitutions and their functional predictions. ICHG/ASHG 2011 Meeting, Montreal, Canada.
21. Coventry A, Bull-Otterson L, Keinan A., **Liu X**., Clark A., Maxwell T., Hixson J., J. Rea J., Templeton A., Muzny D., Lewis L., Villasana D., Boerwinkle E., Gibbs R., Sing C. "Peeking near the peaks" for large-effect rare variants. ICHG/ASHG 2011 Meeting, Montreal, Canada.
22. Wei P, Jian X, Boerwinkle E, **Liu X**. (2011) Comparison of functional prediction methods for nonsynonymous SNPs in exome sequencing-based study of Mendelian diseases. ICHG/ASHG 2011 Meeting, Montreal, Canada.
23. Coventry A., Bull-Otterson L., **Liu X**., Clark A., Maxwell T., Hixson J., Rea T., Templeton A., Boerwinkle E., Gibbs R., Sing C. (2010) Identifying large-effect rare variants causing synthetic associations by using haplotype association analysis. The 60th Annual Meeting of The American Society of Human Genetics, Washington DC.
24. **Liu X.**, Fu YX., Maxwell T.J., Cohen J.C., Boerwinkle E. (2009) Estimating population genetic parameters and comparing model fitness using DNA sequences with error. The 59th Annual Meeting of The American Society of Human Genetics, Honolulu, Hawaii.
25. Zhu C., Han S., **Liu X**. (2009) Local ancestral inference in admixed populations. The 59th Annual Meeting of The American Society of Human Genetics, Honolulu, Hawaii.
26. **Liu X.**, Maxwell T.J., Bull L., Lohmueller K.E., Rea T.J., Muzny D.M., Wheeler D.A., Hall O., Pankow J.S., Templeton A.R., Clark A.G., Gibbs R.A., Boerwinkle E., Sing C.F. (2008) Opportunities and obstacles of population-based genome resequencing. The 58th Annual Meeting of The American Society of Human Genetics, Philadelphia, Pennsylvania.
27. Clark A. G., Lohmueller K. E., **Liu X**., Rea T. J., Templeton A. R., Pankow J. S., Maxwell T., Boerwinkle E., Muzny D. M., Wheeler D. A., Hall O., Bull L., Gibbs R. A., Sing C. F. (2008) Accommodating uncertainty in SNP calling in population genetic inference from deep resequencing data. The 58th Annual Meeting of The American Society of Human Genetics, Philadelphia, Pennsylvania.
28. Wu X., Deng W., Liu L., Zhao Y., Zhaung Q., Wu C., Liu W., **Liu X.**, Zhang W., Huang W., Chai J. (2000) The localization and cloning of retinitis pigmentosa gene RP26. *The 3rd HUGO Pacific Meeting and the 4th Asia-Pacific Conference on Human Genetics*, Shanghai, China. pp. 77.
29. Xia J., Huang W., Wang H., Feng B., Zhang F., Huang T., Lee M., Shao J., Zhang X., Jian S., Huang P., Feng Q., Huang L., Yu X., Huang H., Zhu J., **Liu X.**, Zhao Y., Min H., Hong M., Deng M., Ma J., King M., Chen Z., Zeng Y. (2000) Nasopharyngeal carcinoma: Genetic susceptibility vs. Epstein-Barr virus infection. *The 3rd HUGO Pacific Meeting and the 4th Asia-Pacific Conference on Human Genetics*, Shanghai, China. pp. 34.

30. **Liu X.**, Luo Z., Wang G., Zhao Y., Wu C., Zhang W., Huang W., Chen Z. (1999) Augment the incomplete LOH data using expectation-maximization algorithm. *Am J Hum Genet* (Suppl.) 65(4):A135.
31. Xiao J., Zhao Y., Xiong M., Huang W., Zhang W., **Liu X.**, Li W., Hu F., Wu H., Lu D., Tan J., Chen Z., Boewrinkle E., Jin L. (1999) Whole-genome linkage disequilibrium mapping of the genes underlying blood pressure variation in an isolated Chinese population. *Am J Hum Genet* (Suppl.) 65(4):A17.
32. Wang G., Zhao Y., **Liu X.**, Wu C., Liu W., Zhang W., Zhao X., Wan D., Huang, W., Gu J. (1999) Comprehensive genotyping of human primary hepatocellular carcinoma. *Human Genome Meeting*, Brisbane, Australia. pp. 84.
33. **Liu X.**, Zhao Y., Wu C., Zhang W., Le W., Rong T., Liu W., Wang G., Luo Z., Jin L., Huang W. (1999) Heterozygosity of 230 microsatellite loci for Shanghainese Han population. *Human Genome Meeting*, Brisbane, Australia. pp. 56.

Invited Talks:

1. MetaRNN: Differentiating Rare Pathogenic and Rare Benign Missense SNVs and InDels Using Deep Learning. March 30, 2024, Florida Chapter of the ASA (American Statistical Association) 2024 Meeting, Tallahassee, FL.
2. dbNSFP and MetaRNN: tools for missense SNVs and non-frameshift INDELs. September 29, 2023, CAGI** (Critical Assessment of Genome Interpretation) Workshop, Boston, MA
3. Deep learning empowers fine-grained population affinity estimation with craniometric data. April 21, 2023, 92nd AABA (American Association of Biological Anthropologists) Annual Meeting, Reno, Nevada
4. MetaRNN: Differentiating Rare Pathogenic and Rare Benign Missense SNVs and InDels Using Deep Learning. Feb 20, 2023, Human Genetics Center Seminar, School of Public Health, The University of Texas Health Science Center at Houston, Houston, TX
5. An Introduction to Demographic History Inference. Sept 21, 2022, Workshop on Eco-Evolutionary Biology Driven by Omics (WEEOmics 2022), Beijing, China
6. MetaRNN: Differentiating Rare Pathogenic and Rare Benign Missense SNVs and InDels Using Deep Learning. Sept 09, 2022, CPH Seminar in Precision Medicine, School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX
7. MetaRNN: Differentiating Rare Pathogenic and Rare Benign Missense SNVs and InDels Using Deep Learning. Aug 9, 2022, International Conference on Intelligent Biology and Medicine (ICIBM 2022), Philadelphia, PA
8. Inference of population demographic history using the stairway plot. Aug 25, 2021, Department of Genetics, University of Georgia, Athens, GA
9. Stairway Plot 2: demographic history inference with folded SNP frequency spectra. Dec 16, 2020, International Chinese Statistical Association (ICSA 2020) Applied Statistics Symposium (On-line), Houston, TX
10. Theory and Application of Demographic History Inference. Sept 24, 2020, Advanced Course on Population Genetics and Genomics II (On-line), Beijing, China
11. Functional interpretation of human DNA variants using existing knowledge and machine learning. Feb 07, 2020, Interdisciplinary Data Sciences Consortium, Tampa, FL
12. Functional interpretation of human DNA variants using existing knowledge and machine learning. Feb 21, 2020, Institute for Artificial Intelligence Seminar (AI+X), Tampa, FL
13. Theory and Application of Demographic History Inference. Oct 22, 2019, Advanced Course on Population Genetics and Genomics, Beijing, China
14. Towards personalized radiotherapy of cancer with gene expression profiling and machine learning. Oct 14, 2019, School of Public Health, UTHealth, Houston, TX
15. Human history written in our genomes. Feb 15, 2019, Darwin Day 2019, Tampa, FL

16. Human prehistoric demography revealed by polymorphic pattern of CpG transitions. July 11, 2018, SMBE2018, Yokohama, Japan.
17. Whole genome functional annotation using WGSA - TOPMed freeze 5 as an example, Jan 31, 2018, 2nd GSP-TOPMed workshop, Nashville, TN
18. Annotation for CHARGE & TOPMed Sequence Data, Jan 24, 2017, CHARGE and TOPMed Analysis Commons Workshop, Houston, TX
19. Whole Exome Functional Annotation using dbNSFP v3 and WGSA, June 8, 2016, Baylor Miraca Genetics Laboratories, Houston, TX
20. The WGS annotator (WGSA) pipeline for whole genome sequencing data, Feb 12, 2016, Iowa Institute of Human Genetics, University of Iowa, Iowa City, IA
21. Functional annotation of whole genome sequence data using the WGS Annotator (WGSA) pipeline, Jan 26, 2016, Cohorts for Heart and Aging Research in Genomic Epidemiology Investigator Meeting, Houston, TX
22. Inferring demographic histories with the RAD-seq and stairway plot, Jan 6, 2016, School of Life Sciences, East China Normal University, Shanghai, China
23. Exploring Demographic Histories Using SNP Frequency Spectrums, Jan 4, 2016, CAS-MPG Partner Institute for Computational Biology (PICB), Shanghai, China
24. Whole genome annotation with WGSA pipeline, Dec 1, 2015, FHS-OMICS Conference Series (FOCuS), Framingham, MA
25. The WGS annotation pipeline for CHARGE sequence data, 11/2014, CHARGE consortium meeting, DC
26. Whole Genome Annotation - the pipeline proposed for CHARGE, Oct 8, 2014, Baylor College of Medicine, Houston, TX
27. Whole Genome Sequence Analyses of 962 European Americans, 6/2013, Iowa State University, Ames, IA
28. Population Genetic Analysis with Sequencing Errors, 4/2010, Baylor College of Medicine, Houston, TX
29. Application of Statistics in Theoretical Biology - Examples from coalescent theory, Dec 24, 2007, Fudan University, Shanghai, China
30. Coalescent Theory - A Bridge from Population Genetics to Molecular Phylogenetics, 10/2007, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China
31. Estimating the lower bounds of recombination with or without recurrent mutations, 5/2007, Fudan University, Shanghai, China
32. Test of Genetical Isochronism for Serial DNA Samples, 12/2006, Fudan University, Shanghai, China

CLASSES TAUGHT:

UTHealth 2007-2018

- 2016-2017 Computational Genomics and NGS Data Analysis (3 credit hours, every Spring and Fall), co-instructor (25%)
- 2013-2018 Practical Computational Genetics and Bioinformatics (3 credit hours, every Spring), principle instructor (100% 2013-2015, 75% 2016-2018)
- 2009-2016 Evolution of DNA & Protein Sequences (3 credit hours, every two years at Fall), co-instructor (25%)
- 2008-2018 Population Genetics (3 credit hours, every Spring), co-instructor (25%)
- 2008-2017 Statistical Genetics (3 credit hours, every Fall), co-instructor (25%)
- 2007-2012 Introduction to Genomics and Bioinformatics (3 credit hours), co-instructor (25%)

Baylor College of Medicine 2017-2018

- 2017-2018 Bioinformatics and Genome Analysis (3 credit hours, every Spring), co-instructor (10%)

USF 2018-

- 2019-2020 Foundations of Global Health (HSC4624)
- 2019 Lab Rotations in Global Health Research (PHC6722)
- 2019- Introduction to Biocomputing (PHC6934, PHC7735)
- 2020 Evolutionary Human Genetics (ANG 6511) - co-teach with Dr. Lorena Madrigal
- 2022- Data Science for Public Health (PHC6934)