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
- 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

- 1R03HG011075-01, Extend and improve the functional annotation tools dbNSFP and WGSA, $50,000 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
- 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*
- **Guest Editor**: *BMC Genomics*, *BMC Bioinformatics*, *BMC Systems Biology*, *BMC Medical Genomics*, *Human Heredity* (ICIBM2018)
- **Manuscript Reviewer**: *Nature Genetics, Nature Methods, Nature Communications, Science Translational Medicine, Genome Research, Genome Biology, Nucleic Acids Research, Molecular Biology and Evolution*, *Circulation Research, National Science Review*, *Biological Psychiatry*, *Genetics in Medicine*, *Systematic Biology*, *Genomics, Proteomics & Bioinformatics, PLoS Genetics*, *Genome Medicine*, *Journal of Medical Genetics*, *Human Mutation*, *Bioinformatics, European Journal of Human Genetics, Human Genetics, Genetics*, *Genome Biology and Evolution*, *Heredity*, *BMC Genomics, BMC Medical Genomics, Current Genomics, BMC Bioinformatics, Molecular Biology of the Cell, Genes, Scientific Reports, PLoS One, G3, Molecular Genetics and Genomics, Molecules, Frontiers in Genetics*
- **Founding Officer**: International Association for Intelligent Biology and Medicine (IAIBM)
- **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)
- **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)
- Member, Program Committee, 2019 International Conference on Intelligent Biology and Medicine (ICIBM 2019)
- 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. **Liu X**. (2020) Human prehistoric demography revealed by the polymorphic pattern of CpG transitions. Molecular Biology and Evolution first published online May 5, 2020.
2. 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.
3. 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.
4. 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.
5. 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.
6. 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.
7. 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.
8. 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.
9. 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.
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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.
18. 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.
19. 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.
20. 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.

21. **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
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. **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
28. **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
29. 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.
30. **Liu X**† and Fu YX. (2015) Exploring population size changes using SNP frequency spectra. Nature Genetics. 47(5):555-559. †corresponding author
31. 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
32. 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
33. 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.
34. 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
35. 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.

36. Bis JC, DeStefano A, **Liu X**, Brody JA, Choi SH, Verhaaren BF, Debette S, Ikram MA, Shahar E, Butler KR Jr, Gottesman RF, Muzny D, Kovar CL, Psaty BM, Hofman A, Lumley T, Gupta M, Wolf PA, van Duijn C, Gibbs RA, Mosley TH, Longstreth WT Jr, Boerwinkle E, Seshadri S, Fornage M. (2014) Associations of NINJ2 Sequence Variants with Incident Ischemic Stroke in the Cohorts for Heart and Aging in Genomic Epidemiology (CHARGE) Consortium. PLoS One 9(6):e99798.
37. Bis JC, White CC, Franceschini N, Brody J, Zhang X, Muzny D, Santibanez J, Gibbs R, **Liu X**, Lin H, Boerwinkle E, Psaty BM, North KE, Cupples LA, O'Donnell CJ; CHARGE Subclinical Atherosclerosis Working Group. (2014) Sequencing of 2 Subclinical Atherosclerosis Candidate Regions in 3669 Individuals: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. Circulation: Cardiovascular Genetics 7(3):359-64.
38. Lin H, Wang M, Brody JA, Bis JC, Dupuis J, Lumley T, McKnight B, Rice KM, Sitlani CM, Reid JG, Bressler J, **Liu X**, Davis BC, Johnson AD, O'Donnell CJ, Kovar CL, Dinh H, Wu Y, Newsham I, Chen H, Broka A, DeStefano AL, Gupta M, Lunetta KL, Liu CT, White CC, Xing C, Zhou Y, Benjamin EJ, Schnabel RB, Heckbert SR, Psaty BM, Muzny DM, Cupples LA, Morrison AC, Boerwinkle E.(2014) Strategies to Design and Analyze Targeted Sequencing Data: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. Circulation: Cardiovascular Genetics 7(3):335-43.
39. Concepcion JP, Reh CS, Daniels M, **Liu X**, Paz VP, Ye H, Highland HM, Hanis CL, Greeley SA. (2014) Neonatal diabetes, gallbladder agenesis, duodenal atresia, and intestinal malrotation caused by a novel homozygous mutation in RFX6. Pediatric Diabetes 15(1):67-72.
40. Han S, Yang B-Z, Kranzler HR, **Liu X**, Zhao H, Farrer LA, Boerwinkle E, Potash JB and Gelernter J. (2013) Integrating GWASs and Human Protein Interaction Networks Identifies a Gene Subnetwork Underlying Alcohol Dependence. American Journal of Human Genetics 93(6):1027-1034.
41. **Liu X**, Jian X, Boerwinkle E. (2013) dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. Human Mutation. 34:E2393-E2402.
42. Morrison AC[†], Voorman A[†], Johnson AD[†], **Liu X**[†], Yu J, Li A, Muzny D, Yu F, Rice K, Zhu C, Bis J, Heiss G, O'Donnell CJ, Psaty BM, Cupples LA, Gibbs R, Boerwinkle E; the Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE) Consortium. (2013) Whole-genome sequence-based analysis of high-density lipoprotein cholesterol. Nature Genetics 45:899–901 [†]contributed equally
43. Line SR, **Liu X**, de Souza AP, Yu F. (2013) Translational signatures and mRNA levels are highly correlated in human stably expressed genes. BMC Genomics 14(1):268
44. Xue C, **Liu X**, Gong Y, Zhao Y, Fu YX. (2013) Significantly fewer protein functional changing variants for lipid metabolism in Africans than in Europeans. Journal of Translational Medicine 11:67.
45. Yao J, Zhao Q, Yuan Y, Zhang L, **Liu X**, Yung WK, Weinstein JN. (2012) Identification of common prognostic gene expression signatures with biological meanings from microarray gene expression datasets. PLoS One 7(9):e45894.
46. Tennessen JA, Bigham AW, O'Connor TD, Fu W, Kenny EE, Gravel S, McGee S, Do R, **Liu X**, Jun G, Kang HM, Jordan D, Leal SM, Gabriel S, Rieder MJ, Abecasis G, Altshuler D, Nickerson DA, Boerwinkle E, Sunyaev S, Bustamante CD, Bamshad MJ, Akey JM; Broad GO; Seattle GO; on behalf of the NHLBI Exome Sequencing Project (2012) Evolution and functional impact of rare coding variation from deep sequencing of human exomes. Science 337:64-69.
47. **Liu X** (2012) jPopGen Suite: population genetic analysis of DNA polymorphism from nucleotide sequences with errors. Methods in Ecology and Evolution 3:624-627.
48. Wei P, **Liu X** and Fu YX (2011) Incorporating predicted functions of nonsynonymous variants into gene-based analysis of exome sequencing data: a comparative study. BMC Proceedings 5(Suppl 9):S20.

49. **Liu X**, Jian X and Boerwinkle E (2011) dbNSFP: a lightweight database of human non-synonymous SNPs and their functional predictions. Human Mutation 32:894-899. (recommended by Faculty of 1000)
50. Xue C, Fu YX, Zhao Y, Gong Y, **Liu X**. (2011) Smaller genetic risk in catabolic process explains lower energy expenditure, more athletic capability and higher prevalence of obesity in Africans. PLoS One 6(10):e26027.
51. Peng B and **Liu X** (2010) Simulating sequences of the human genome with rare variants. Human Heredity 70:287-291.
52. Coventry A, Bull-Otterson L, **Liu X**, Clark AG, Maxwell TJ, Crosby J, Hixson JE, Rea TJ, Muzny DM, Lewis LR, Wheeler DA, Sabo A, Lusk C, Weiss KG, Akbar H, Cree A, Hawes AC, Newsham I, Varghese RT, Villasana D, Gross S, Joshi V, Santibanez J, Morgan M, Chang K, Hale W, Templeton AR, Boerwinkle E, Gibbs R and Sing CF (2010) Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nature Communications 1: 131.
53. **Liu X**[†]**,** Fu YX, Maxwell TJ, and Boerwinkle E (2010) Estimating population genetic parameters and comparing model goodness-of-fit using DNA sequences with error. Genome Research 20:101-109. [†]corresponding author
54. **Liu X**, Maxwell TJ, Boerwinkle E, and Fu YX (2009) Inferring population mutation rate and sequencing error rate using the SNP frequency spectrum in a sample of DNA sequences. Molecular Biology and Evolution 26: 1479-1490.
55. **Liu X**, Fu YX. (2008) Summary statistics of neutral mutations in longitudinal DNA samples. Theoretical Population Biology 74: 56-67.
56. **Liu X**, Fu YX. (2008) Algorithms to estimate lower bounds of recombination with or without recurrent mutations. BMC Genomics 9 (Suppl. I):S24.
57. **Liu X**, Fu YX (2007) Test of genetical isochronism for longitudinal samples of DNA sequences. Genetics 176(1):327-342.
58. **Liu X**, Gutacker MM, Musser JM, Fu YX. (2006) Evidence for recombination in *Mycobacterium tuberculosis*. Journal of Bacteriology 188(23):8169-8177.
59. Daw EW, **Liu X**, Wu CC. (2003) Age-of-onset of hypertension vs. a single measurement of systolic blood pressure in a combined linkage and segregation analysis. BMC Genetics 4 (Suppl. 1):S80.
60. Feng BJ, Huang W, Shugart YY, Lee MK, Zhang F, Xia JC, Wang HY, Huang TB, Jian SW, Huang P, Feng QS, Huang LX, Yu XJ, Li D, Chen LZ, Jia WH, Fang Y, Huang HM, Zhu JL, **Liu XM**, Zhao Y, Liu WQ, Deng MQ, Hu WH, Wu SX, Mo HY, Hong MF, King MC, Chen Z, Zeng YX. (2002) Genome-wide scan for familial nasopharyngeal carcinoma reveals evidence of linkage to chromosome 4. Nature Genetics 31(4):395-99.
61. Chu J, Zhang R, Zhao Z, Zou W, Han Y, Qi Q, Zhang H, Wang JC, Tao S, **Liu X**, Luo Z. (2002) Male fertility is compatible with an Arg(840)Cys substitution in the AR in a large chinese family affected with divergent phenotypes of AR insensitivity syndrome. Journal of Clinical Endocrinology and Metabolism 87(1):347-51.
62. He X, Zhu DL, Chu SL, Jin L, Xiong MM, Wang GL, Zhang WZ, Zhou HF, Mao SY, Zhan YM, Zhuang QN, **Liu XM**, Zhao Y, Huang W. (2001) Alpha-adducin gene and essential hypertension in China. Clinical and Experimental Hypertension 23(7):579-589.
63. Wang G[†], Zhao Y[†], **Liu X**[†], Wang L[†], Wu C, Zhang W, Liu W, Zhang P, Cong W, Zhu Y, Zhang L, Chen S, Wan D, Zhao X, Huang W, Gu J. (2001) Allelic loss and gain, but not genomic instability, as the major somatic mutation in primary hepatocellular carcinoma. Genes Chromosomes and Cancer 31(3):221-227. [†]contributed equally
64. Tao S, Chu J, **Liu X**, Zhang R, Zhang Z, Luo Z. (2001) High-resolution gene mapping using admixture linkage disequilibrium [Article in Chinese]. Chinese Science Bulletin. 46(16):1356-1358.

65. He X, Zhu D, Han Z, **Liu X**, Wang G, Chu S, Zhang W, Zhou H, Mao S, Zhuang Q, Zhao Y, Huang W. (2001) Use of microsatellites in zygosity diagnosis of twins [Article in Chinese]. Chinese Journal of Medical Genetics 18(6):421-425.
66. Tao S, **Liu X**, Chu J, Zhang R, Du L, Luo Z. (2000) Rate of decay in admixture linkage disequilibrium and its implication in gene mapping [Article in Chinese]. Chinese Science Bulletin 45(21):2274-2280.
67. Tao S, Zhang R, Chu J, **Liu X**, Du L, Qi Q, Luo Z. (2000) A population genetics model of linkage disequilibrium in admixed populations [Article in Chinese]. Chinese Science Bulletin 45(19):2041-2047.
68. Zhang RM, Du LP, Peng ZH, Chu JH, **Liu XM**, Tao SH and Luo ZW (2000). Progress in the molecular genetic research in multinodular goiter [Article in Chinese]. Chinese Journal of Medical Genetics 17: 359-361.

B. Peer-reviewed Publications as Part of Research Consortia

69. Patel D, Mez J, Vardarajan BN, Staley L, Chung J, Zhang X, Farrell JJ, Rynkiewicz MJ, Cannon-Albright LA, Teerlink CC, Stevens J, Corcoran C, Gonzalez Murcia JD, Lopez OL, Mayeux R, Haines JL, Pericak-Vance MA, Schellenberg G, Kauwe JSK, Lunetta KL, Farrer LA; Alzheimer's Disease Sequencing Project. (2019) Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry. JAMA Network Open. 2(3):e191350.
70. Rogers J, Raveendran M, Harris RA, Mailund T, Leppälä K, Athanasiadis G, Schierup MH, Cheng J, Munch K, Walker JA, Konkel MK, Jordan V, Steely CJ, Beckstrom TO, Bergey C, Burrell A, Schrempf D, Noll A, Kothe M, Kopp GH, Liu Y, Murali S, Billis K, Martin FJ, Muffato M, Cox L, Else J, Disotell T, Muzny DM, Phillips-Conroy J, Aken B, Eichler EE, Marques-Bonet T, Kosiol C, Batzer MA, Hahn MW, Tung J, Zinner D, Roos C, Jolly CJ, Gibbs RA, Worley KC; Baboon Genome Analysis Consortium. (2019) The comparative genomics and complex population history of Papio baboons. Science Advances 5(1):eaau6947.
71. Vardarajan BN, Barral S, Jaworski J, Beecham GW, Blue E, Tosto G, Reyes-Dumeyer D, Medrano M, Lantigua R, Naj A, Thornton T, DeStefano A, Martin E, Wang LS, Brown L, Bush W, van Duijn C, Goate A, Farrer L, Haines JL, Boerwinkle E, Schellenberg G, Wijsman E, Pericak-Vance MA, Mayeux R; Alzheimer's Disease Sequencing Project (2018) Whole genome sequencing of Caribbean Hispanic families with late-onset Alzheimer's disease. Annals of Clinical and Translational Neurology 5(4):406-417.
72. The 1000 Genomes Project Consortium (2015) A global reference for human genetic variation. Nature 526: 68-74.
73. Auer PL, Nalls M, Meschia JF, Worrall BB, Longstreth WT Jr, Seshadri S, Kooperberg C, Burger KM, Carlson CS, Carty CL, Chen WM, Cupples LA, DeStefano AL, Fornage M, Hardy J, Hsu L, Jackson RD, Jarvik GP, Kim DS, Lakshminarayan K, Lange LA, Manichaikul A, Quinlan AR, Singleton AB, Thornton TA, Nickerson DA, Peters U, Rich SS; National Heart, Lung, and Blood Institute Exome Sequencing Project (2015) Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke: The NHLBI Exome Sequence Project. JAMA Neurology. 72(7):781-8.
74. Do R, Stitziel NO, Won HH, Jørgensen AB, Duga S, Angelica Merlini P, Kiezun A, Farrall M, Goel A, Zuk O, Guella I, Asselta R, Lange LA, Peloso GM, Auer PL; NHLBI Exome Sequencing Project, Girelli D, Martinelli N, Farlow DN, DePristo MA, Roberts R, Stewart AF, Saleheen D, Danesh J, Epstein SE, Sivapalaratnam S, Hovingh GK, Kastelein JJ, Samani NJ, Schunkert H, Erdmann J, Shah SH, Kraus WE, Davies R, Nikpay M, Johansen CT, Wang J, Hegele RA, Hechter E, Marz W, Kleber ME, Huang J, Johnson AD, Li M, Burke GL, Gross M, Liu Y, Assimes TL, Heiss G, Lange EM, Folsom AR, Taylor HA, Olivieri O, Hamsten A, Clarke R, Reilly DF, Yin W, Rivas MA, Donnelly P, Rossouw JE, Psaty BM, Herrington DM, Wilson JG,

Rich SS, Bamshad MJ, Tracy RP, Cupples LA, Rader DJ, Reilly MP, Spertus JA, Cresci S, Hartiala J, Tang WH, Hazen SL, Allayee H, Reiner AP, Carlson CS, Kooperberg C, Jackson RD, Boerwinkle E, Lander ES, Schwartz SM, Siscovick DS, McPherson R, Tybjaerg-Hansen A, Abecasis GR, Watkins H, Nickerson DA, Ardissino D, Sunyaev SR, O'Donnell CJ, Altshuler D, Gabriel S, Kathiresan S. (2015) Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature 518(7537):102-6.

75. Tabor HK, Auer PL, Jamal SM, Chong JX, Yu JH, Gordon AS, Graubert TA, O'Donnell CJ, Rich SS, Nickerson DA; NHLBI Exome Sequencing Project, Bamshad MJ. (2014) Pathogenic variants for Mendelian and complex traits in exomes of 6,517 European and African Americans: implications for the return of incidental results. American Journal of Human Genetics. 95(2):183-93.
76. Colonna V, Ayub Q, Chen Y, Pagani L, Luisi P, Pybus M, Garrison E, Xue Y, Tyler-Smith C; 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA. (2014) Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology. 15(6):R88.
77. Delaneau O, Marchini J; 1000 Genomes Project Consortium; 1000 Genomes Project Consortium. (2014) Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communication. 5:3934.
78. Gordon AS, Tabor HK, Johnson AD, Snively BM, Assimes TL, Auer PL, Ioannidis JP, Peters U, Robinson JG, Sucheston LE, Wang D, Sotoodehnia N, Rotter JI, Psaty BM, Jackson RD, Herrington DM, O'Donnell CJ, Reiner AP, Rich SS, Rieder MJ, Bamshad MJ, Nickerson DA; NHLBI GO Exome Sequencing Project. (2014) Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Human Molecular Genetics. 23(8):1957-63.
79. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, Tang ZZ, Bizon C, Lange EM, Smith JD, Turner EH, Jun G, Kang HM, Peloso G, Auer P, Li KP, Flannick J, Zhang J, Fuchsberger C, Gaulton K, Lindgren C, Locke A, Manning A, Sim X, Rivas MA, Holmen OL, Gottesman O, Lu Y, Ruderfer D, Stahl EA, Duan Q, Li Y, Durda P, Jiao S, Isaacs A, Hofman A, Bis JC, Correa A, Griswold ME, Jakobsdottir J, Smith AV, Schreiner PJ, Feitosa MF, Zhang Q, Huffman JE, Crosby J, Wassel CL, Do R, Franceschini N, Martin LW, Robinson JG, Assimes TL, Crosslin DR, Rosenthal EA, Tsai M, Rieder MJ, Farlow DN, Folsom AR, Lumley T, Fox ER, Carlson CS, Peters U, Jackson RD, van Duijn CM, Uitterlinden AG, Levy D, Rotter JI, Taylor HA, Gudnason V Jr, Siscovick DS, Fornage M, Borecki IB, Hayward C, Rudan I, Chen YE, Bottinger EP, Loos RJ, Sætrom P, Hveem K, Boehnke M, Groop L, McCarthy M, Meitinger T, Ballantyne CM, Gabriel SB, O'Donnell CJ, Post WS, North KE, Reiner AP, Boerwinkle E, Psaty BM, Altshuler D, Kathiresan S, Lin DY, Jarvik GP, Cupples LA, Kooperberg C, Wilson JG, Nickerson DA, Abecasis GR, Rich SS, Tracy RP, Willer CJ; NHLBI Grand Opportunity Exome Sequencing Project. (2014) Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. American Journal of Human Genetics. 94(2):233-45.
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86. Fu W, O'Connor TD, Jun G, Kang HM, Abecasis G, Leal SM, Gabriel S, Rieder MJ, Altshuler D, Shendure J, Nickerson DA, Bamshad MJ; NHLBI Exome Sequencing Project, Akey JM. (2013) Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature. 493(7431):216-20.
87. The 1000 Genomes Project Consortium (2012) An integrated map of genetic variation from 1,092 human genomes. Nature 491: 56-65.
88. Emond MJ, Louie T, Emerson J, Zhao W, Mathias RA, Knowles MR, Wright FA, Rieder MJ, Tabor HK, Nickerson DA, Barnes KC; National Heart, Lung, and Blood Institute (NHLBI) GO Exome Sequencing Project; Lung GO, Gibson RL, Bamshad MJ. (2012) Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic Pseudomonas aeruginosa infection in cystic fibrosis. Nature Genetics. 44(8):886-9.
89. Boileau C, Guo DC, Hanna N, Regalado ES, Detaint D, Gong L, Varret M, Prakash SK, Li AH, d'Indy H, Braverman AC, Grandchamp B, Kwartler CS, Gouya L, Santos-Cortez RL, Abifadel M, Leal SM, Muti C, Shendure J, Gross MS, Rieder MJ, Vahanian A, Nickerson DA, Michel JB; National Heart, Lung, and Blood Institute (NHLBI) Go Exome Sequencing Project, Jondeau G, Milewicz DM. (2012) TGFB2 mutations cause familial thoracic aortic aneurysms and dissections associated with mild systemic features of Marfan syndrome. Nature Genetics 44(8):916-21.

C. Peer-reviewed Conference Paper

89. 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.
90. Naseri A, **Liu X**, Zhang S and Zhi.D. (2017) Ultra-fast Identity by Descent Detection in Biobank-Scale Cohorts using Positional Burrows–Wheeler Transform. The 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB 2017), Hong Kong, China (May 3-7, 2017).

91. **Liu X**, Fu YX. (2007) Estimating the lower bounds of recombination with or without recurrent mutations. BIOCOMP'07 - The 2007 International Conference on Bioinformatics & Computational Biology, Las Vegas, Nevada, USA (June 25-28, 2007).

D. Editorial Articles

92. Wu Z, Yan J, Wang K, **Liu X**, Guo Y, Zhi D, Ruan J, Zhao Z. (2019) The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: genomics with bigger data and wider applications. BMC Genomics 20(Suppl 1):80.
93. Zhi D, Zhao Z, Li F, Wu Z, **Liu X** and Wang K. (2019) The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: genomics meets medicine. BMC Medical Genomics 12(Suppl 1):20.
94. **Liu X**, Xie L, Wu Z, Wang K, Zhao Z, Ruan J and Zhi D. (2018) The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. BMC Bioinformatics 19(Suppl 17):492.
95. Wang K, **Liu X**, Guo Y, Wu Z, Zhi D, Ruan J and Zhao Z. (2018) The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: systems biology on diverse data types. BMC Systems Biology 12(Suppl 8):125.
96. Wang J, Wang K, **Liu X**, Sham P, Zhao Z. (2017/2018) Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity 83:105–106.

E. Book Chapters

97. 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.
98. Djotsa Nono AB*, Chen K, **Liu X**. (2016) Computational Prediction of Genetic Drivers in Cancer. In: eLS. John Wiley & Sons, Ltd: Chichester. DOI: 10.1002/9780470015902.a0025331. *first author is my student.
99. Fu YX, **Liu X**. (2010) Statistical methods for detecting the presence of natural selection in bacterial populations. In: Bacterial Population Genetics in Infectious Disease. (Robinson A., Feil E., Falush D. ed.) Hoboken, New Jersey: Wiley-Blackwell pp. 87-101.
100. Luo Z, Zhang R, Tao S, **Liu X**. (2002) Theories and methods of gene mapping for complex pedigrees. In: Genome Science and Human Disease. (Chen Z., Qiang B., Fang F. ed.) Beijing: Science Press pp. 137-165.
101. **Liu X**, Zhang R, Luo Z. (2000) Bioinformatics and its applications in genomics. In: Decoding Life – Human Genome Project and Post-genome Project. (He L. ed.) Beijing: Science Press pp. 333-351.

F. Abstracts and Proceedings

1. **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.
2. **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.
3. **Liu X**. (2018) Human prehistoric demography revealed by polymorphic pattern of CpG transitions. Population, Evolutionary, and Quantitative Genetics Conference (PEQG), Madison, WI.
4. 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.

5. **Liu X**. (2018) Human prehistoric demography revealed by polymorphic pattern of CpG transitions. AsianEvo2018 Meeting, Shenzhen, Guangdong, China.
6. **Liu X**, Gibbs R, Boerwinkle E. (2017) WGSA 07: updated annotation pipeline for human genome sequencing studies. ASHG 2017 Meeting, Orlando, FL.
7. **Liu X**. (2016) Exploring Detailed Demographic Histories Using Stairway Plot 2. ASHG 2016 Meeting, Vancouver, BC, Canada.
8. **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.
9. **Liu X**, White S, Peng B, Johnson AD, Brody JA, Li AH, Carroll A, Huang Z, Rustagi N, Wei P, Yu F, Gibbs R, Klein RJ and Boerwinkle E. (2015) WGSA: an annotation pipeline for human genome sequencing studies. ASHG 2015 Meeting, Baltimore, MD.
10. Dong C, Yang H, **Liu X**, Wang K (2014) iCAGES: integrated CAncer GEnome Score for understanding personal cancer genomes. ASHG 2014 Meeting, San Diego, CA.
11. **Liu X**, Fu YX (2014) Exploring Detailed Demographic Histories of Human Populations Using SNP Frequency Spectrums. ASHG 2014 Meeting, San Diego, CA.
12. Jian X, **Liu X**. (2014) In silco prediction of splice-altering single nucleotide variants in human genome. ASHG 2014 Meeting, San Diego, CA.
13. Li AH, Morison AC, Metcalf G, Cuples LA, Brody JA, Polfus LM, Yu B, Veraraghavan N, **Liu X**, Lumley T, Muzny D, Mosley TH, Gibbs RA, Boerwinkle E. (2014) Analysis of Los-of-Function Variants in 8,612 Deply-Phenotyped Individuals Identifes Novel Loci for Common Chronic Disease. ASHG 2014 Meeting, San Diego, CA.
14. **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.
15. 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.
16. 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.
17. **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.
18. **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.
19. 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.
20. 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.
21. 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.
22. **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.

23. 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.
24. **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.
25. 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.
26. 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.
27. 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.
28. **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.
29. 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.
30. 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.
31. **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 Presentations:

1. Theory and Application of Demographic History Inference. Oct 22, 2019, Advanced Course on Population Genetics and Genomics, Beijing, China
2. Towards personalized radiotherapy of cancer with gene expression profiling and machine learning. Oct 14, 2019, School of Public Health, UTHealth, Houston, TX
3. Functional interpretation of human DNA variants using existing knowledge and machine learning. Feb 07, 2020, Interdisciplinary Data Sciences Consortium, Tampa, FL
4. Functional interpretation of human DNA variants using existing knowledge and machine learning. Feb 21, 2020, Institute for Artificial Intelligence Seminar (AI+X), Tampa, FL
5. Human history written in our genomes. Feb 15, 2019, Darwin Day 2019, Tampa, FL
6. Human prehistoric demography revealed by polymorphic pattern of CpG transitions. July 11, 2018, SMBE2018, Yokohama, Japan.
7. Whole genome functional annotation using WGSA - TOPMed freeze 5 as an example, Jan 31, 2018, 2nd GSP-TOPMed workshop, Nashville, TN
8. Annotation for CHARGE & TOPMed Sequence Data, Jan 24, 2017, CHARGE and TOPMed Analysis Commons Workshop, Houston, TX
9. Whole Exome Functional Annotation using dbNSFP v3 and WGSA, June 8, 2016, Baylor Miraca Genetics Laboratories, Houston, TX

10. The WGS annotator (WGSA) pipeline for whole genome sequencing data, Feb 12, 2016, Iowa Institute of Human Genetics, University of Iowa, Iowa City, IA
11. 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
12. Inferring demographic histories with the RAD-seq and stairway plot, Jan 6, 2016, School of Life Sciences, East China Normal University, Shanghai, China
13. Exploring Demographic Histories Using SNP Frequency Spectrums, Jan 4, 2016, CAS-MPG Partner Institute for Computational Biology (PICB), Shanghai, China
14. Whole genome annotation with WGSA pipeline, Dec 1, 2015, FHS-OMICS Conference Series (FOCuS), Framingham, MA
15. The WGS annotation pipeline for CHARGE sequence data, 11/2014, CHARGE consortium meeting, DC
16. Whole Genome Annotation - the pipeline proposed for CHARGE, Oct 8, 2014, Baylor College of Medicine, Houston, TX
17. Whole Genome Sequence Analyses of 962 European Americans, 6/2013, Iowa State University, Ames, IA
18. Population Genetic Analysis with Sequencing Errors, 4/2010, Baylor College of Medicine, Houston, TX
19. Application of Statistics in Theoretical Biology - Examples from coalescent theory, Dec 24, 2007, Fudan University, Shanghai, China
20. Coalescent Theory - A Bridge from Population Genetics to Molecular Phylogenetics, 10/2007, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China
21. Estimating the lower bounds of recombination with or without recurrent mutations, 5/2007, Fudan University, Shanghai, China
22. 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- Foundations of Global Health (HSC4624)
- 2019 Lab Rotations in Global Health Research (PHC6722)