CURRICULUM VITAE

Name:	Hongyan Xu, Ph.D.
GRU Rank(s):	Associate Professor
GRU Title(s):	None
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EDUCATION

High School:	Guoyang Number 1 High School, 1988-91
College:	Fudan University, Shanghai, China, 1991-96, B.S. in Biophysics
Graduate and Professional:	Fudan University, Shanghai, China, 1996-99, M.S. in Genetics The University of Texas Graduate School of Biomedical Science (GSBS) at Houston, 1999-2003, Ph.D. in Human Population Genetics
Postdoctoral Training:	The University of Texas M. D. Anderson Cancer Center, 2003-05
Board Certification:	N/A

PROFESSIONAL

Academic Appointments

Teaching Assistant, Institute of Genetics, Fudan University, Shanghai, China, 09/1996--01/1997

Research Associate, Institute of Genetics, Fudan University, Shanghai, China, 02/1997--05/1999

Graduate Research Assistant, Human Genetics Center, the University of Texas Health Science Center at Houston, Houston, TX, 09/1999--07/2003

Postdoctoral Fellow, Department of Epidemiology, the University of Texas M. D. Anderson Cancer Center, Houston, TX, 07/2003-10/2005

Assistant Professor, Department of Biostatistics, Georgia Health Sciences University, Augusta, GA, 11/2005-06/2011

Deputy Director, Biostatistics, Bioinformatics and Computational Biology Core, Georgia Health Sciences University Cancer Research Center, Augusta, GA, 07/2011-06/2012

Associate Professor, Department of Biostatistics, Georgia Health Sciences University, Augusta, GA, 07/2011-06/2013

Associate Professor (tenured), Department of Biostatistics & Epidemiology, Medical College of Georgia, Georgia Regents University, Augusta, GA, 07/2013-present

Member, Georgia Regents University Cancer Center, Augusta, GA, 07/2011-present

Administrative Responsibilities/Appointments

Associate Editor:
- Frontiers in Genetics, 2010-present
- Advances in Anthropology, 2009-present
- American Journal of Biostatistics, 2010-present

Referee:
- Biometrics, 2009-present
- American Journal of Human Genetics, 2008-present
- Nucleic Acids Research, 2010-present
- Genome Research, 2009-present
- PLoS ONE, 2010-present
- PLoS Genetics, 2008-present
- Journal of Probabilities & Statistics, 2010-present
- Diabetes, 2011-present
- Human Genetics, 2006-present
- BMC Genomics, 2010-present
- Diabetes, 2011-present

Professional Societies:
- Member, American Statistical Society, 2005-present
- Member, International Biometric Society/Eastern North American Region, 2005-present
- Member, American Society of Human Genetics, 2002-present
- Member, Sigma-Xi, the Scientific Research Society, 2002-present

Administrative Responsibilities/Appointments

Scientific Review Committee, RFA-HL-12-007 *Life After Linkage: The*

Future of Family Studies, National Institute of Health, National Heart Lung and Blood Institute, Bethesda, Maryland, 2011
Scientific Review Committee, RFP NHLBI-CSB-HV-12-12 *Omics in Latinos - Genetic Analysis*, National Institute of Health, National Heart Lung and Blood Institute, Bethesda, Maryland, 2012
Scientific Review Committee, ZRG1 PSE-P (02) *Member Conflict: Chronic Disease, Aging, and Genetics*, National Institute of Health, Special Emphasis Panel, 2013
Data Collection and Harmonization Committee, Registry and Surveillance for Hemoglobinopathies (RuSH), CDC/NIH, 2010–2012
Institutional Animal Care and Use Committee (IACUC), 2010-present
Academic House Advisor at the Medical College of Georgia, Georgia Regents University, 2014-present

Research and Training Grants Awarded (Past Five Years)

STP 00004, Georgia Health Sciences University, 06/01/06–05/31/09 (80% effort, then 30% after R21was awarded)
Effects of Population Structure on Genetic Association Studies
Scientist Training Program: to determine the role of population structure on genetic association studies.
Role: PI

R21 NS057506, NIH/NINDS, 04/01/08–03/31/11 (44% effort)
Association Study of Stroke Risk in an Admixed Population of African Americans This study is to develop
new methodology in large-scale association studies of stroke risk in admixture African American populations.
Role: PI

P01 HL069999, NIH/NHLBI PI: Harshfield, 10/01/07–09/30/12 (15% effort, then 10% since 2010)
Stress-Related Mechanisms of Hypertension Risk in Youth
The overarching goal of the PPG is to evaluate the interrelationships among stress related behavioral, biological and genetic factors pertaining to the pathogenesis of hypertension.
Role: Co-investigator

P20 MD003383, NIH/MCMHD, PI: Kutlar and Gibson, 05/28/09–12/31/13 (20% effort)
NCMHD Southeastern Exploratory Sickle Cell Center of Excellence
Relieving the health disparity of SCD patients is the primary goal of this project.
Role: Co-investigator

R03 CA123565, NIH/NCI, PI: Shi, 07/01/07–03/31/10 (5% effort)
Integrated Genetic and Epigenetic Biomarkers for Molecular Epidemiology
The major goal is to understand the relationship between genetic variation, global methylation patterns and regional hypermethylation of tumor suppressor genes.
Role: Co-investigator

R01 CA114229 , NIH/NCI, PI: Robertson, 09/01/05–06/30/11 (5% effort)
De Novo Methyltransferase Function in Chromatin and Cancer
The major goal is to test the hypothesis that de novo methyltransferase DNMT3B is a major regulator of genomic DNA methylation patterns in normal cells and that disruption of its functions contributes to DNA methylation defects in cancer.
Role: Co-investigator

R01 AA019976, NIH/NIAAA, PI: Robertson, 09/20/11–06/30/16 (5% effort)
Developmental Pathways, Environmental Agents, and Epigenetics in Liver Disease
The focus of the study is undertake a comprehensive analysis of the epigenome in targeted pathways in normal and diseased liver to understand how epigenetic changes lead to HCC and how they may be developed into novel treatments and diagnostic tools to improve patient survival and quality of life.
Role: Co-invetigator

U01 HL117684, NIH/NHLBI, PI: Kutlar, 08/15/13-05/21/18 (20% effort)
Role of Endothilin-1 in Sickle Cell Disease
The goal of the study is to investigate the role of endothelin-1 in the pathogenesis of vasculopathy, inflammation, organ damage, and pain in SCD patients and animal models. A pilot clinical trial will be initiated to study safety and efficacy of an ETA receptor blockade on inflammation, pain, nociception, and the progression of sickle nephropathy and on microvascular blood flow and pulmonary arterial circulation in adults with SCD.
Role: Co-investigator

R01 MH083317, NIH/NIMH, PI: Mei, 03/31/14-03/31/19 (5% effort)
NRG1-ErbB4 regulation of synaptic plasticity and behavior.
The goal of the study is to investigate pathophysiological mechanisms of schizophrenia susceptibility genes neuregulin 1 and ErbB4. Results will provide proof-of-principle evidence that relevant schizophrenia may be treatable by recovering or restoring ErbB4 expression or activity and contribute to development of novel therapeutic strategies of the devastating disorder.

Role: Co-investigator

AWARDS/HONORS

Renmin Scholarship, School of Life Sciences, Fudan University, 12/1992—06/1996

First place in computer design tournament (project: Othello), Rice University, 05/2001

Graduate Research Assistantship, The University of Texas GSBS at Houston, 09/1999--07/2003

Dauphin Postdoctoral Fellowship in Cancer Prevention, the University of Texas M. D. Anderson Cancer Center, 07/2003-07/2005

Genetic Analysis Workshop 14 (GAW14) Scholarship, National Institute on Alcohol Abuse and Alcoholism (NIAAA), 09/2004

SAMSI Travel Award for the Workshop on Discrete Models in Systems Biology, Statistical and Applied Mathematical Sciences Institute, funded by National Science Foundation, 12/2008

Faculty at the The Curriculum in Iron Metabolism & Related Disorders, hosted by the European School of Hematology, 01/2014

Mentor for Dr. Dale Hardy in the PRIDE (Programs to Increase Diversity Among Individuals Engaged in Health-Related Research) Program in Cardiovascular Genetic Epidemiology at the School of Medicine, Washington University in St. Louis

SCIENTIFIC AND PROFESSIONAL SOCIETIES (Include Offices Held)

Member, American Society of Human Genetics

Member, Sigma-Xi, The Scientific Research Society

Member, American Statistical Association (ASA)

Member, Georgia Chapter of ASA

Member, International Genetic Epidemiology Society

Member, International Biometric Society/Eastern North American Region

COMMUNITY ACTIVITIES (Include offices Held)

American Society of Human Genetics DNA day essays Phase II judge, 2015

PRESENTATIONS AT NATIONAL, REGIONAL AND STATE MEETINGS (Last Five Years)

Measures of population structure, 57th Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 25, 2007.

Invited Speaker: *Quantifying population structure and effects on genetic association studies*, International Indian Statistical Association conference, University of Connecticut, Storrs, CT, May 2008

Invited Speaker: *Population structure and genetic association studies*, Unicamp, Campinas, Brazil, September 2008

Invited Speaker: *Genetic Association Study in Admixed Populations*, Medical University of South Carolina, Department of Biostatistics, Bioinformatics and Epidemiology, Charleston, SC, October 2008

Haplotype Construction in Admixed Populations, 59th Annual Meeting of the American Society of Human Genetics, Honolulu, HI, October 2009

Invited Speaker: *Gene-based approach for association study with next-generation sequence data*, Department of Mathematical Sciences, Worcester Polytechnic Institute, Worcester, MA, October, 2010

Genetic association test using next-generation sequencing data, 2011 Spring Meeting of the Eastern North American Region/International Biometric Society, Miami, FL, March 21, 2011

Invited Speaker: *Monte Carlo methods for linkage disequilibrium determination*, International Indian Statistical Association conference, North Carolina State University, Raleigh, NC, April 2011

A robust test for detecting differentially methylated regions, 2012 Spring Meeting of the Eastern North American Region/International Biometric Society, Washington, DC, April 1, 2012

Platform Presentation: *DNA methylation and next generation sequencing*, 2012 International Genetic Epidemiology Society, Stevenson, WA, October 20, 2012

Hierarchal Model for Detecting Differentially Methylated Loci with Next Generation Sequencing, 2013 International Genetic Epidemiology Society, Chicago, IL, September 16, 2013

Platform Presentation: *Accounting for covariates in differential methylation analysis with next-generation sequencing*, 2014 Spring Meeting of the Eastern North American Region/International Biometric Society, Baltimore, MD, March 17, 2014

Invited Speaker: *Differential Methylation with next generation sequencing*, Donghua University, Shanghai, China, March 28, 2014

Invited Speaker: Methods for differential methylation with next generation sequencing, 3rd Workshop on Biostatistics and Bioinformatics, Georgia State Univeristy, Atlanta, GA, May 11, 2014

MEETINGS, VISITING PROFESSIOSHIPS, etc. (Last Five Years)

Genetic Analysis Workshop 15 (GAW15) & Annual meeting of the International Genetic Epidemiology Society, St. Petersburg, FL, November 11-18, 2006

57th Annual meeting of the American Society of Human Genetics, San Diego, CA, October 23-27, 2007

Annual meeting of International Biometric Society Eastern North American Region, Crystal City, Arlington, VA, March 16-19, 2008

International Indian Statistical Association conference, University of Connecticut, Storrs, CT, May 22-25, 2008

Genetic Analysis Workshop 16 (GAW16) & Annual meeting of the International Genetic Epidemiology Society, St. Louis, MO, September 17-20, 2008

Discrete Models in Systems Biology Workshop at SAMSI, Research Triangle Park, NC, December 3-5, 2008

Annual meeting of International Biometric Society Eastern North American Region, San Antonio, TX, March 15-18, 2009

59th Annual meeting of the American Society of Human Genetics & Annual meeting of the International Genetic Epidemiology Society, Honolulu, HI, October 18-24, 2009

Annual meeting of International Biometric Society Eastern North American Region, New Orleans, LA, March 21-24, 2010

Genetic Analysis Workshop 17, Boston, MA, October 13-16, 2010

60th Annual Meeting of the American Society of Human Genetics, Washington, DC, November 2–6, 2010

Annual meeting of International Biometric Society Eastern North American Region, Miami, FL, March 20-23, 2011

2011 Annual Meeting of the International India Statistical Association, North Carolina State University, April 21–24, 2011

Annual meeting of International Biometric Society Eastern North American Region, Washington, DC, April 1-4, 2012

21st Annual International Genetic Epidemiology Society conference, Stevenson, WA, October 18-20, 2012

22nd Annual International Genetic Epidemiology Society conference, Chicago, IL, September 15-17, 2013

Annual meeting of International Biometric Society Eastern North American Region, Washington, DC, March 16-19, 2014

Visiting Professor, Donghua University, Shanghai, China, March 21-April 6, 2014

Senior Visiting Scholar, Fudan University, Shanghai, China, June 4-June18, 2014

64th Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 18-22, 2014

Annual meeting of International Biometric Society Eastern North American Region, Miami, FL, March 15-18, 2015

PROFESSIONAL EXHIBITS AND AUDIOVISUAL PROGRAMS

N/A

PUBLICATIONS IN NON-REFEREED JOURNALS

N/A

ABSTRACTS

Chen H, Akey JM, Xiong MM, **Xu H**, Xiao J, Jin L. Association of variation in the promoter of the Beta-2 adrenergic receptor and essential hypertension in an isolated Chinese population. Am. J. Hum. Gen. 67:S1240, 2000.

Indugula SR, Sun G, Chunhua S, Smelser D, Kaushal R, **Xu H**, Kimmel M, Zhong Y, Chakraborty R, Deka R. Microsatellite loci in the HLA-Class 1 gene region show weak evidence of overdominant selection. Am. J. Hum. Gen. 67:S1280, 2000.

Xu H, Renwick A, Kimmel M, Deka R, Chakraborty R. Validity of homozygosity test of selective neutrality at microsatellite loci. Am. J. Hum. Gen. 67:S1289, 2000.

Xu H, Kimmel M, Renwick A, Chakraborty R. Effects of population substructure on the homozygosity test of neutrality under the stepwise mutation model. Am. J. Hum. Gen. 69:S1393, 2001.

Fu Y-X, **Xu H**, Kimmel M, Renwick A., Chakraborty R. Effects of additive selection and recombination on homozygosity test at microsatellite loci under generalized stepwise mutation model. Am. J. Hum. Gen. 71:S1142, 2002.

Renwick A, **Xu H**, Fu Y-X, Kimmel M, Chakraborty R. Relative heterozygosity contributed by alleles of different frequency class is not invariant at microsatellite loci. Am. J. Hum. Gen. 71:S1150, 2002.

Xu H, Fu Y-X, Renwick A, Kimmel M, Chakraborty R. Microsatellite variation: Effects of natural selection, population structure and demographic changes of population size. Am. J. Hum. Gen. 71:S2392, 2002.

Xu H, Deka R, Kimmel M, Fu Y-X, Chakraborty R. Signature of natural selection revealed at HLA region with microsatellites: Further Data. The 54th Annual Meeting of the American Society of Human Genetics S1183, 2004.

Xu H, George V, Shete S, Effects of population structure on haplotype construction. International Genetic Epidemiology Society meeting, #189, 2006

Xu H, Choi J, Nandram B, A Bayesian Adjustment for an Ascertainment Bias in Human Genetics, International Genetic Epidemiology Society meeting, #A070702, 2009

Xu H, George V, Haplotype construction in admixed populations, 59th Annual meeting of the American Society of Human Genetics #1728, 2009

Xu H, George V, Multiple gene and pathway analysis for rare variants in genome-wide associations, 60th Annual meeting of the American Society of Human Genetics #2102, 2010

Xu H, George V, Simultaneous association testing of genome-wide genes using sequence data, 61st Annual meeting of the American Society of Human Genetics #106, 2011

Xu H, Ryu D, Su S, Wang X, Podolsky RH, George V, Quantifying and normalizing methylation levels in Illumina arrays, 62nd Annual meeting of the American Society of Human Genetics #3418, 2012

S . Meiler, L. Wells, L. Bowman, P. Bora, **H. Xu**, R. Fillingim, B. Clair, G. Sayer, A. Kutlar, Pressure Pain Threshold and Pain Diary Data in Patients with Sickle Cell Disease, Annual meeting of the American Society of Hematology, 2012

PUBLICATIONS IN REFEREED JOURNALS (Author, Title, Journal, Volume, Inclusive pages, Year)

Bao Y, Lu D, **Xu H**, Shi Q, Qiu X, Xue J. Polymorphism of DXS102 locus in Chinese population and its application to gene diagnosis in hemophilia B family. Chin Med J (Engl) 111:527-230, 1998.

Bao Y, Lu D, Shi Q, **Xu H**, Qiu X, Xue J. [Determination of the polymorphism of DXS102 locus and its application in gene diagnosis]. Zhonghua Yi Xue Yi Chuan Xue Za Zhi 15:27-30, 1998.

Zhang W, Hu F, Xiao J, **Xu H**, Lu D-R, Jin L. The Distribution of a 3'A polymorphism of SDF-1 gene in a Chinese random population. Journal of Fudan Univeristy (Natural Science) 37:317--318, 1998.

Luo J, Ji Y, Peng Y, Xiao J, Yao Y, **Xu H**, Yang M, Zhen J, Lu D, Jin L. [Linkage analysis of chromosome 5 and asthma in a Chinese population]. Zhonghua Yi Xue Yi Chuan Xue Za Zhi 16:318-320, 1999.

Yuan W, **Xu H**, Zhao J, Ding W, Jiang H, Gu M, Xue J, Chen J, Fang F, Chen Z, Jin L, Huang W. [Information behavior of microsatellite loci in genome scanning]. Zhonghua Yi Xue Yi Chuan Xue Za Zhi 17:65-71, 2000.

Zhao J, Wang H, Xiong M, Huang W, Zuo J, Chen Z, Qiang B, Sun Q, Li Y, Liu Q, Du W, Chen J, Ding W, Yuan W, Zhao Y, **Xu H**, Jin L, Fang F. The localization of type 2 diabetes susceptibility gene loci in northern Chinese Han

families. Chinese Science Bulletin 45:1792-1795, 2000.

Xiao J, Hu F, **Xu H**, Su B, Jiang Y, Luo J, Zhang W, Tan J, Jin L, Lu D. Provincial distribution of three HIV-1 resistant polymorphisms (CCR5-Δ32, CCR2-64I, and SDF1-3'A) in China. Science in China 43: 16-20, 2000.

Hong W, Cai G, **Xu H**, Chen H, Xiao J, Lu D, Xue J, Qiu X, Jin L. [Single nucleotide polymorphism in beta2-adrenoceptor gene and the distribution in Chinese Han ethnic group]. Zhonghua Yi Xue Yi Chuan Xue Za Zhi 18:1-3, 2001.

Wu H, Wang H, Li H, Oshuaakey J, Xiao F, Ke Y, **Xu H**, Xiao J, Lu D, Parra E, Shriver M, Xiong M, Barton SA, Hewett-Emmett D, Liu W, Jin L. Skin reflectance in the Han Chinese and Tibetan populations. Hum Biol 73: 461-466, 2001.

Xu H, Fu Y-X. Estimating Effective Population Size or Mutation Rate with Microsatellites. Genetics 166:555-563, 2004.

Cortes-Prieto L, Baltazar L, Perea F, Gallegos-Arreola M, Flores S, Sandoval L, Olivares1 N, **Xu H**, Barton S, Chakraborty R, Rivas F. HLA-DQB1, -DQA1, -DRB1 Linkage Disequilibrium Estimate from Segregating Haplotypes in Mestizo Families from Guadalajara, Mexico. Tissue Antigens 63:458-465, 2004.

Xu H, Wu X, Spitz MR, Shete S. Comparison of haplotype inference methods from unrelated population genotype data. Human Heredity 58:63-68, 2004.

Zhao J, Xiong M, Huang W, Wang H, Zuo J, Wu GD, Chen Z, Qiang BQ, Zhang ML, Chen JL, Ding W, Yuan WT, **Xu H**, Jin L, Li YX, Sun Q, Liu QY, Boerwinkle E, Fang FD. An autosomal genomic scan for loci linked to type 2 diabetes in Northern Han Chinese population. Journal of Molecular Medicine 83:209-215, 2005.

Xu H, Spitz MR, Amos CI, Shete S. Complex segregation analysis reveals a multigene model for lung cancer. Human Genetics, 116:121-127, 2005

Xu H, Chakraborty R, Fu Y-X. Mutation rate variation at human dinucleotide microsatellites. Genetics 170:305-312, 2005

Xu H, Shete, S. Effects of population structure on genetic association studies. BMC Genetics 6(Suppl 1):S109, 2005

Xu H, Shete, S. Mixed-effects Logistic Approach for Association Following Linkage Scan for Complex Disorders. Annals of Human Genetics, 71:230-237, 2006.

Shekhawat PS, Srinivas SR, Matern D, Bennett MJ, Boriack R, George V, **Xu H**, Prasad PD, Roon P, Ganapathy V. Spontaneous development of intestinal and colonic atrophy and inflammation in the carnitine-deficient jvs (OCTN2(-/-)) mice. Mol Genet Metab.92:315-324, 2007.

Tan Y-D, Fonage M, George V, **Xu H**, Parent-child pair design for detecting gene-environment interactions in complex diseases. Human Genetics. 121:745-757, 2007

Xu H, George V, A new transmission test for affected sibpair families. BMC Proceedings, 1:S32, 2007.

Gao L, **Xu H**, Comparisons of Mutation Rate Variation at Genome-wide Microsatellites: Evolutionary Insights from Two Cultivated Rice and Their Wild Relatives, BMC Evolutionary Biology, 8:11, 2008

Tan YD, Fornage M, **Xu H**, Ranking analysis of F-statistics for microarray data. BMC Bioinformatics. 9:142, 2008

Ellison GL, Weinrich SP, Lou M, **Xu H**, Powell IJ, Baquet CR., A randomized trial comparing web-based decision aids on prostate cancer knowledge for African-American men. Journal of National Medical Association, 100: 1139-1145, 2008

Xu H, Sarkar B, George V, A new measure of population structure using multiple single nucleotide polymorphisms and its relationship with F_{ST}, BMC Research Notes, 2:21, 2009

Xu H, Mathew G, George V, Family-based genome-wide association study for Simulated Data of Framingham Heart Study. BMC Proceedings, 3:S124, 2009

Mathew G, **Xu H**, George V, Simultaneous Analysis of all SNPs in Genome-Wide Association Study of Rheumatoid Arthritis BMC Proceedings, 3:S11, 2009

Xu H, George V, Assessment of population structure and its effects on genome-wide association studies. Communications in Statistics – Theory and Methods, 38:2843-2855, 2009

Mukhopadhyay S, George V, **Xu H**, Variable selection method for quantitative trait analysis based on parallel genetic algorithm. Annals of Human Genetics, 74:88-96, 2010

Nandram B, Choi JW, **Xu H**, Maximum likelihood estimation for ascertainment bias in sampling siblings. Journal of Data Science, 2011, 9:23-41

Xu H, George V. A Monte Carlo test of linkage disequilibrium for single nucleotide polymorphisms. BMC Research Notes 4: 124, DOI:10.1186/1756-0500-4-124, 2011.

Xu H, George V. A gene-based approach for testing association of rare alleles. BMC Proceedings 5 Suppl 9:S7. PMID: 22373566, 2011.

Nandram B, **Xu H**. Bayesian Corrections of a Selection Bias in Genetics. Journal of Biometrics & Biostatistics 2: 112, DOI:10.4172/2155-6180.1000112, 2011.

Jin B, Ernst J, Tiedemann RL, **Xu H**, Kellis M, Dalton S, Liu C, Choi JH, Robertson KD. Linking DNAmethyltransferases to epigenetic marks and nucleosome structure genome-wide in human tumor cells. Cell Reports 2(5):1411-1424, 2012

Joshi PH, **Xu H**, Lestrange R, Flockhart N, Kirkland B, Vazquez G, Qian Z, Sharma A, Marvasty I, Bhatt K, Brown C, Rinehart S, Miller J, Voros S. The M235T single nucleotide polymorphism in the angiotensinogen gene is associated with coronary artery calcium in patients with a family history of coronary artery disease. Atherosclerosis PMID:23137822, 2012

Das I, Mukhopadhyay S, **Xu H**. Individualized Dosing for Multiple Ordered Groups of Patients. Journal of Statistical Theory and Practice 7(1):95-106, 2013

Xu H, Podolsky R, Ryu D, Wang X, Su S, Shi H, George V. A Method to Detect Differentially Methylated Loci With Next Generation Sequencing. Genetic Epidemiology 37(4):377-382, 2013

Ryu D, **Xu H**, George V, Su S, Wang X, Podolsky R. Quantifying and Normalizing Methylation Levels in Illumina Arrays. Journal of Biometrics & Biostatistics 4:164. doi: 10.4172/2155-6180.1000164, 2013

Tan YD, **Xu H**: A General Method for Accurate Estimation of False Discovery Rates in Identification of Differentially Expressed Genes. Bioinformatics [Epub ahead of print], PMID: 24632499, 2014

Mathew G, George V, **Xu H**: Comparison of Several Sequence-based Association Methods in Pedigrees. BMC Proceedings, 8(Suppl 1):S48. doi: 10.1186/1753-6561-8-S1-S48. eCollection 2014

Hussain S, Nichols F, Bowman L, **Xu H**, Neunert C, Implementation of Transcranial Doppler (TCD) Ultrasonography Screening and Primary Stroke Prevention in Urban and Rural Sickle Cell Disease (SCD) populations, Pediatric Blood & Cancer, doi: 10.1002/pbc.25306

Jaja C, Bowman L, Wells L, Patel N, **Xu H**, Lyon M, Kutlar A, Preemptive genotyping of CYP2C8 and CYP2C9 allelic variants involved in NSAIDs metabolism for sickle cell disease pain management, Clinical and Translational Science, doi: 10.1111/cts.12260

Lu X, Ding ZC, Cao Y, Liu C, Habtetsion T, Yu M, Lemos H, Salman H, **Xu H**, Mellor AL, Zhou G, Alkylating agent melphalan augments the efficacy of adoptive immunotherapy using tumor-specific CD4+ T cells, J Immunol. 2015 94(4):2011-21. doi: 10.4049/jimmunol.1401894

BOOKS AND CHAPTERS

Hongyan Xu, “Differential Methylation Analysis with Next-Generation Sequencing” in Next Generation Sequencing in Cancer Research, Volume 2, Springer.