

# Hongyan Xu, Ph.D.

Department of Biostatistics  
The Georgia Health Sciences University  
AE-1005, Pavilion I  
1120 15th St  
Augusta, GA 30912

Phone: (706) 721-4697  
Fax: (706) 721-6294  
Office: AE-1018, Pavilion I  
Email: [hxu@georgiahealth.edu](mailto:hxu@georgiahealth.edu)  
Homepage: <http://biostat.georgiahealth.edu/~hxu/>

## Education

Ph.D. Human Population Genetics, University of Texas Houston, Graduate School of Biomedical Sciences, Houston, TX, 2003.

*Dissertation:* Detecting the Signature of Natural Selection with Microsatellites

M.S. Genetics, Fudan University, Shanghai, China, 1999.

B.S. Biophysics, Fudan University, Shanghai, China, 1996.

## Employment

Associate Professor, Department of Biostatistics, The Georgia Health Sciences University, Augusta, GA, July 2011–present.

Deputy Director, Biostatistics, Bioinformatics and Computational Biology Core, The Georgia Health Sciences University Cancer Center, Augusta, GA, July 2011–present.

Assistant Professor, Department of Biostatistics, The Georgia Health Sciences University, Augusta, GA, November 2005–June 2011.

Postdoctoral Fellow, Department of Epidemiology, The University of Texas M. D. Anderson Cancer Center, Houston, TX, June 2003–October 2005.

Graduate Research Assistant, Human Genetics Center, The University of Texas at Houston, Houston, TX, August 1999–May 2003.

## Military Service

Military Training, Dalian Military Academy, Dalian, Liaoning, China

## Research

### *Publications*

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, Olivares 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, 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.
- 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.
- Jin B, Tiedemann RL, Xu H, Ernst J, Kellis M, Dalton S, Liu C, Choi JH, Robertson KD. Linking DNA methyltransferases to epigenetic marks and nucleosome structure genome-wide in human tumor cells. *Cancer Cell* submitted.
- Ryu D, George V, Su S, Wang X, Xu H, Podolsky R. Quantifying and normalizing methylation levels in Illumina arrays. *Bioinformatics* submitted.

### Grant Support

STP 00004, Georgia Health Sciences University, 06/01/06–05/31/09

*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

*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

*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

*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

*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

*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

*Developmental Pathways, Environmental Agents, and Epigenetics in Liver Disease*

The focus of the study is to 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 improved patient survival and quality of life.

Role: Co-investigator

## Teaching

### *The Georgia Health Sciences University*

GNMD 8050 Computational Methods in Genetics & Genomics (Biostatistics & Genomic Medicine Ph.D.) Spring 2006, 2008.

GNMD 8051 Translational Genomics and Proteomics (Genomic Medicine Ph.D.) Fall 2008, 2010

STAT 9150 Advanced Statistical Methods in Genetic Analysis (Biostatistics Ph.D.) Spring 2009

STAT 8880 Special Topics: Introduction to Statistical Genetics (Biostatistics Ph.D.) Fall 2009.

STAT 8510 Programming for Data Analysis (Biostatistics Ph.D.) Fall 2010, Fall 2011.

STAT 8880 Special Topics: Introduction to Statistical Genomics (Biostatistics Ph.D.) Summer 2011

STAT 8550 High Throughput Data Analysis (Biostatistics Ph.D.) Summer 2012

*The University of Texas-Houston*

Population Genetics (Ph.D.), Spring 2002, Teaching Assistant for Dr. Yun-Xin Fu.

*Teaching Certificate*

Classrooms of the 21st Century: Evaluation and Feedback,

Classrooms of the 21st Century: Learner-Centered Instruction.

Conference and Seminar Presentations

*Validity of homozygosity test of selective neutrality at microsatellite loci*, 50th Annual Conference of the American Society of Human Genetics, Philadelphia, PA, October 5, 2000.

*Effects of population substructure on the homozygosity test of neutrality under the stepwise mutation model*, 51st Annual Conference of the American Society of Human Genetics, San Diego, CA, October 15, 2001.

*Microsatellite variation: effects of natural selection, population structure, and demographic changes of population size*

29th Annual Meeting of the Texas Genetics Society, South Padre Island, TX, April 18, 2002

52nd Annual Conference of the American Society of Human Genetics, Baltimore, MD, October 18, 2002

*Estimating effective population size and mutation rate with microsatellites*, 7th Annual Genetic Minisymposium of the University of Texas Graduate School of Biomedical Sciences at Houston, Houston, TX, February 7, 2003

*Familial aggregation of lung cancer*, Charline Daupine Laboratory Dedication, University of Texas M. D. Anderson Cancer Center, Houston, TX, April 19, 2004

*Approaches to complex disorders based on population genetics*, Georgia Health Sciences University, Augusta, GA, January 28, 2005.

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

*Genetic Association Study in Admixed Populations*, Medical University of South Carolina, Department of Biostatistics, Bioinformatics and Epidemiology, Charleston, SC, October 27, 2008.

*Haplotype Construction in Admixed Populations*, 59th Annual Meeting of the American Society of Human Genetics, Honolulu, HI, October 22, 2009

*Gene-based approach for association study with next-generation sequence data*, Department of Mathematical Sciences, Worcester Polytechnic Institute, Worcester, MA, October 15, 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

*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

## Professional Activities

Member, NHLBI special emphasis review panel, 2011, 2012.

Data Collection and Harmonization Committee, Registry and Surveillance for Hemoglobinopathies (RuSH), CDC/NIH, 2010–Present.

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.

Associate Editor for *Frontiers in Genetics*, *American Journal of Biostatistics*, *Advances in Anthropology*.

Reviewer for *Biometrics*, *American Journal of Human Genetics*, *Nucleic Acids Research*, *Genome Research*, *PLoS One*, *PLoS Genetics*, *Journal of Probability & Statistics*, *Diabetes*

Institutional service: Member, Institutional Animal Care and Use Committee (IACUC), 2010–2012.

Departmental service: Chair, Departmental Computing Committee, 2010–12.

Chair, Departmental Seminar & Journal Club Committee, 1997–99.

## Advising

Ph.D. Student, Major Advisor: Jie Huang

Ph.D. Student, Committee Member: Danial Linder, Xiaoxiao Wang.

M.S. Students, Major Advisor: Abe Letter, Bayasid Sarkar.

## Honors, Awards, & Fellowships

SAMSI Travel Award for the Workshop on Discrete Models in Systems Biology, Statistical and Applied Mathematical Sciences Institute, 2008.

Genetic Analysis Workshop (GAW) 14 Scholarship, National Institute on Alcohol Abuse and Alcoholism (NIAAA), 2004.

Dauphin Postdoctoral Fellowship in Cancer Prevention, University of Texas M. D. Anderson Cancer Center, 2003.

First Place in Computer Design Tournament (Project: Othello), Rice University, 2001.

Renmin Scholarship, School of Life Sciences, Fudan University, 1992–1996.

## Conferences and Workshops Attended

2012 Spring Meeting of ENAR/IMS, Washington, DC, April 1–4, 2012.

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

2011 Spring Meeting of ENAR/IMS, Miami, FL, March 20–23, 2011.

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

Genetic Analysis Workshop 17, Boston, MA, October 13–16, 2010.

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