**CURRICULUM VITAE**

**Xiong MM, Ph.D.**

**Office Address** : Division of Biostatistics

The University of Texas Health Science Center at Houston

School of Public Health

1200 Herman Pressler, Houston, TX 77030

Tel : (713) 500-9894

Fax : (713) 500-0900

E-mail : [Momiao.Xiong@uth.tmc.edu](mailto:Momiao.Xiong@uth.tmc.edu)

**EDUCATION:**

1993-1995 **Postdoctoral Fellows** in Computational Biology

University of Southern California

1990-1993 **Ph.D**. in Statistics

University of Georgia

Dissertation: Mathematical Theory of Neural Learning and its Applications to

Statistics and Molecular Biology

1988-1990 **M.S.** in Statistics

University of Georgia

1963-1968 **B.S**. in Computational Mathematics

Fudan University, Shanghai, China

1957-1963 Jiangxi Anyi Middle School, China

**PRESENT POSITION:**

Professor (tenured), Division of Biostatistics, School of Public Health, Program in Human and Molecular Genetics, Graduate School of Biomedical Science, The University of Texas Health Science Center at Houston

Adjunct Member of Graduate Faculty at Texas A&M University

**PROFESSIONAL EXPERIENCE**

09/11-Present Professor (Tenured)

Division of Biostatistics, School of Public Health, The University of Texas

Health Science Center at Houston

09/08-08/11 Associate Professor (Tenured)

Division of Biostatistics, School of Public Health, The University of Texas

Health Science Center at Houston

09/07-08/08 Associate Professor

Division of Biostatistics, School of Public Health, The University of Texas Health Science Center at Houston

09/00-08/07 Assistant Professor (tenure track)

Human Genetics Center, School of Public Health, The University of Texas

Health Science Center at Houston

06/97‑08/00 Assistant Professor (Non-tenure track)

Human Genetics Center, The University of Texas Health Science Center,

School of Public Health, Houston

01/97-05/97 Visiting Assistant Professor

Division of Epidemiology, University of Minnesota

09/95-12/96 Visiting Assistant Research Scientist

Department of Biostatistics, University of Michigan, Ann Arbor

07/93-08/95 Postdoctoral Fellow

Department of Mathematics, University of Southern California

01/88-06/93 Teaching Assistant

Department of Statistics, University of Georgia

# 08/86-12/87 Visiting Scholar

# Department of Information Systems & Operations Management,

# The University of Texas at Dallas

04/84-07/86 Head of Automation Division

Jiangxi Provincial Power Bureau, Nanchang, China

08/76-03/84 Software Engineer, Head of Computer Section

Jiangxi Provincial Power Bureau, Nanchang, China

07/75-07/76 Lecturer

Department of Mathematics, Jiangxi Electric Engineering School

01/72-06/75 Acting Head of Education Section

Panzhihua Steel Company, China

12/68-12/71 Assistant Engineer

Panzhihua Steel Company, China

**PROFESSIONAL ACTIVITIES**

2005- The International Society for Computational Biology

1994- American Society of Human Genetics

2004- [Eastern North American Region/International Biometric Society](http://www.enar.org/)

1992-1997 American Statistical Association

2005- American Statistical Association

1993-1997 American Society of Neural Networks

**HONORS AND AWARDS**

2014 The first place of poster award in the UT GSBS human and molecular genetics symposium

The Second place of poster award in the UT GSBS human and molecular genetics symposium.

The third place of poster award in the UT GSBS human and molecular genetics symposium.

2013 Supervised postdoctoral fellow Futao Zhang was awarded outstanding postdoctoral fellow in 2013 ASHG meeting

2012Winners of the EJHG/ESHG/NPG Award 2012

2011 Excellence in Research Incentive Award

2010 Excellence in Research Incentive Award

2009 Excellence in Research Incentive Award

2008 Excellence in Research Incentive Award

2007 Highly Cited Researcher (Biological science)

2007 Excellence in Research Incentive Award

2006 Highly Cited Researcher (Biological science)

2006 Excellence in Research Incentive Award

2005 Excellence in Research Incentive Award

2004 White Magnolia Award for Promoting Academic Exchange (Bai Yulan Award), Shanghai Municipal Government

2003-2004 Excellence in Research Incentive Award

1999-2000 Excellence in Research Incentive Award

2001- Who’s Who in America

1994 Best paper award, Neural Networks with Hidden Markov Process, Artificial Neural Networks in Engineering Conference, 1994, St. Louis, Missouri

1991 Phi Kappa Phi, University of Georgia

1990 Best Senior Student, University of Georgia

1989 Best Junior Student, University of Georgia

**PUBLICATIONS**

**Since 2009**

**Citations 6948 3994**

**H\* index: 41 27**

**i10-index : 90 65**

**Research Gate Score: 41.14**

1. **PREPRINTS** 
   * + 1. Ma L and Xiong MM. (2013). An Efficient Sufficient Dimension Reduction Method for Identifying Genetic Variants of Clinical Significance. [arXiv:1301.3528](http://arxiv.org/abs/1301.3528).
       2. Jiang J, Lin N, Guo S, Chen J, Xiong MM. (2014). Methods for Joint Imaging and RNA-seq Data Analysis. [arXiv:1409.3899](http://arxiv.org/abs/1409.3899).
       3. Lin N, Jiang J, Guo S, Xiong MM. (2014). Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis[. arXiv:1408.0204.](http://arxiv.org/abs/1408.0204)
       4. Lee DY, Hanis C, Bell GI, Aguilar DA, Redline S, Below J and Xiong MM. (2014). Genetic Studies of Physiological Traits with Their Application to Sleep Apnea. arXiv:[1410.7363](http://arxiv.org/abs/1410.7363).
       5. Zewdie G and Xiong MM. (2014). Fully Automated Myocardial Infarction Classification using Ordinary Differential Equations. aiXiv: [1410.6984.](http://arxiv.org/abs/1410.6984)
       6. Li L and Xiong MM. (2014). A novel statistical method based on dynamic models for classification. aiXiv: [1410.7029.](http://arxiv.org/abs/1410.7029)
       7. Ma L, Lin N, Amos CI and Xiong MM. (2014). A General Statistic Framework for Genome-based Disease Risk Prediction. aiXiv:[1410.7371](http://arxiv.org/abs/1410.7371)  .
       8. Li L and Xiong MM. (2014). Dynamic Model for RNA-seq Data Analysis.

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|  | [arXiv:1412.1746](http://arxiv.org/abs/1412.1746) |

1. **PAPERS IN REFEREED JOURNALS**
   * + 1. Ma J, Xiong M, You M, Lozano G, Amos CI. (2014). Genome-wide association tests of inversions with application to psoriasis. Hum Genet. 133(8):967-74.
       2. Guo S, Wang YL, Li Y, Jin L, Xiong M, Ji QH, Wang J. (2014). Significant SNPs have limited prediction ability for thyroid cancer. Cancer Med. 3(3):731-5.
       3. Zhang F, Boerwinkle E and Xiong MM. (2014). Epistasis Analysis for Quantitative Trait with Next-generation Sequencing Data. Genome Research. 24(6):989-98. PMC4032862
       4. Zhao J, Zhu Y, Boerwinkle E, Xiong MM. (2014). Pathway analysis with next-generation sequencing data. Eur J Hum Genet. 2014 Jul 2. doi: 10.1038/ejhg.2014.121. [Epub ahead of print].
       5. Fan R, Wang Y, James, Mills JL, Lobach I, Wilson AF, Bailey-Wilson JE, and Xiong MM. (2014). Generalized Functional Linear Models for Gene-based Case-Control Association Studies. Genetic Epidemiology, 38(7):622-37. PMC4189986
       6. Xu K, Xiong MM, Guo W, Zhu L and Jin L. (2014). An Estimating Equation Approach to Dimension Reduction in Longitudinal Data. Biometrika (Revised).
       7. Zhao J, Zhu Y and Xiong MM. (2014). Gene-gene Interaction Analysis for Next-generation

Sequencing. Eur J Hum Genet. (Revised).

* + - 1. Hong, S, Chen X, Jin L and **Xiong MM** (2013) Canonical Correlation Analysis for RNA-seq Co-expression Networks. Nucleic Acids Research. 41(8):e95 .
      2. Fan R, Wang Y, Mills JL, Wilson AF, Bailey-Wilson JE, **Xiong MM**. (2013). Functional linear models for association analysis of quantitative traits. Genet Epidemiol. 37(7):726-42. PMC4163942
      3. **Xiong MM** (2013). New Era for Health Care and Genomics. J Phylogen Evolution Biol. 1:e104.
      4. Luo L, Zhu Y and **Xiong MM** (2013) Smoothed functional principal component analysis for testing association of the entire allelic spectrum of genetic variation . Eur J Hum Genet. 21(2):217-24
      5. **Xiong M**, Xie D, Hu P and Hou Z (2013). Studies of Natural Selection in the Era of Next-generation Sequencing. J Phylogen Evolution Biol. 1:e108
      6. Liang F and **Xiong MM**. (2013). Bayesian detection of causal rare variants under posterior

consistency. PLos ONE. 8(7), e69633. PMC3724943.

* + - 1. Fan R, Zhang Y, Albert PS, Liu A, Wang Y, **Xiong MM**. (2012). Longitudinal Association Analysis of Quantitative Traits. Genet Epidemiol. 36: 856–869.
      2. 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA (2012) An integrated map of genetic variation from 1,092 human genomes. Nature 491(7422):56-65. PMCID: PMC3498066 [Available on 2013/5/1]
      3. Shugart YY, Zhu Y, Guo W, **Xiong MM** (2012) Weighted Pedigree-based Statistics for Testing the Association of Rare Variants. BMC Genomics, 13:667.
      4. Ma J, Xiao F, Xiong MM, Andrew AS, Brenner H, Duell EJ, Haugen A, Hoggart C, Hung RJ, Lazarus P, Liu C, Matsuo K, Mayordomo JI, Schwartz AG, Staratschek-Jox A, Wichmann E, Yang P and Amos CI (2012). Natural and Orthogonal Interaction framework for modeling gene-environment interactions with application to lung cancer. Human Heredity .73(4):185-194
      5. Luo L, Zhu Y and **Xiong MM** (2012) Quantitative Trait Locus (QTL) Analysis for Next-Generation Sequencing with the Functional Linear Models. J Medical Genetics. 49(8):513-24.
      6. Sun H, Samarghandi A, Zhang N, Yao Z, **Xiong MM**, Teng BB. (2012) Proprotein Convertase Subtilisin/Kexin Type 9 Interacts With Apolipoprotein B and Prevents Its Intracellular Degradation, Irrespective of the Low-Density Lipoprotein Receptor. Arterioscler Thromb Vasc Biol. 32(7):1585-95.
      7. Wang C, Yan S, Hou Z, Fu W, **Xiong MM**, Han S, Jin L, Li H. (2012) Present Y chromosomes reveal the ancestry of Emperor CAO Cao of 1800 years ago. J Hum Genet. 57(3):216-8.
      8. Luo L, Zhu Y, **Xiong MM** . (2012) A Novel Genome-Information Content-Based Statistic for Genome-Wide Association Analysis Designed for Next-Generation Sequencing Data. J Comput Biol. 19(6):731-744.
      9. Zhu Y and **Xiong MM** (2012) Family-Based Association Studies for Next-Generation Sequencing. Am J Human Genet. 90(6):1028-1045.
      10. Wei S, Wang LE, McHugh MK, Han Y, **Xiong M**, Amos CI, Spitz M, Wei Q. (2012) Genome-wide gene-environment interaction analysis for asbestos exposure in lung cancer susceptibility. Carcinogenesis. 33(8):1531-7
      11. Qu HQ, Li Q, Xu S, McCormick JB, Fisher-Hoch SP, Xiong MM, Qian J, Jin L. (2012) Ancestry informative marker set for Han Chinese population. Genes, Genomes, Genetics. 2(3):339-41.
      12. \*Siu H, Jin L and **Xiong MM** (2012) Manifold Learning for Human Population Structure

Studies. PLoS ONE, 7: e29901.

* + - 1. Luo Li, Zhu Yun, Xiong Momiao. (2012) Smoothed functional principal component analysis for testing association of the entire allelic spectrum of genetic variation. European Journal of Human Genetics. 2012.
      2. \*Siu H, Zhu Y, Jin L and Xiong MM. (2011) Implication of Next-Generation Sequencing on Association Studies. BMC Genomics, 12:322. PMCID: PMC3148210
      3. Fan RZ, Zhong M, Wang, S, Zhang Y, Andrew A, Karagas M, Chen H, Amos CI, Xiong MM, and Moore J (2011) Entropy-Based Information Gain Approaches to Detect and to Characterize Gene-Gene and Gene-Environment Interactions/Correlations of Complex Diseases. Genet. Epidemiology. 35(7):706-21. NIHMSID: NIHMS316527
      4. He Y, Li C, Amos CI, **Xiong MM**, Ling H, Jin L (2011) [Accelerating haplotype-based genome-wide association study using perfect phylogeny and phase-known reference data.](http://www.ncbi.nlm.nih.gov/pubmed/21789217) PLoS One. 2011;6(7):e22097. PMC3137625.
      5. Hong S, Hua D, Jin L and Xiong MM (2011) Gene co-expression network and functional module analysis of ovarian cancer. International Journal of Computational Biology and Drug Design. 4:147-164.
      6. \*Fang S, \*Fang X, **Xiong MM.** (2011) Psoriasis prediction from genome-wide SNP profiles. BMC Dermatol. 11(1):1. PMC3022824.
      7. \*Luo L, Boerwinkle E and Xiong MM (2011) Association studies for next-generation sequencing. Genome Research, 21(7):1099-1108. PMCID: PMC3129252
      8. \*Wu X, \*Dong H, \*Luo L, \*Zhu Y, \*Peng G, Reveille JD**, Xiong MM.** (2010) Anovel statistic for genome-wide interaction analysis. Plos Genetics. 6 (9), e1001131. PMC2987176
      9. \*Dong H, \*Luo L, \*Hong S, \*Siu H, Xiao Y, Jin L, Chen R**, Xiong MM**. (2010) [Integrated analysis of mutations, miRNA and mRNA expression in glioblastoma.](http://www.ncbi.nlm.nih.gov/pubmed/21114830) BMC Syst Biol. 4(1):163. PMC3002314
      10. \*Dong H, \*SiuH, \*LuoL, \*FangX, JinL, **XiongMM.** (2010) Investigation of gene and microRNA expression in glioblastoma. BMC Genomics. 11 (Suppl 3): S16. PMC2999346
      11. \*Peng G, \*LuoL, \*SiuH, \*ZhuY, \*HuP, \*HongS, \*ZhaoJ, ZhouX, ReveilleJD**,** JinL, **Amos,** CI, **XiongMM.** (2010) Gene and pathway-based second wave analysis of genome-wide association studies. Eur J Hum Genet. 18:111-117. PMC2987176
      12. \*Luo L, \*Peng G, \*Zhu Y, \*Dong H, Amos C, **Xiong MM.** (2010) Genome-wide gene and pathway analysis. Eur J Hum Genet. 18:1045-1053.
      13. Gourh Pravitt, Agarwal Sandeep, Assassi Shervin, Divecha Dipal, Tan Filemon K, Reveille John D, Xiong Momiao, Shete Sanjay, Mayes Maureen D, Arnett Frank C. Gene-gene interaction between IL1A promoter polymorphism (-889C/T) and major histocompatibility complex (MHC) class II alleles in systemic sclerosis. CLINICAL AND EXPERIMENTAL RHEUMATOLOGY; 2010: CLINICAL & EXPER RHEUMATOLOGY VIA SANTA MARIA 31, 56126 PISA, ITALY; 2010. p. S65-S.
      14. Zhou X, Lee JE, Arnett FC, **Xiong MM**, Park MY, Yoo YK, Shin ES, Reveille JD, Mayes MD, Kim JH, Song R, Choi JY, Park JA, Lee YJ, Lee EY, Song YW, Lee EB. (2009) [HLA-DPB1 and DPB2 are genetic loci for systemic sclerosis: A genome-wide association study in Koreans with replication in North Americans.](http://www.ncbi.nlm.nih.gov/pubmed/19950302?itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum&ordinalpos=1) Arthritis Rheum. 60(12):3807-3814. PMC2829245
      15. \*Lin R, Wang Y, Wang Y, Fu W, Zhang D, Zheng H, Yu T, Wang Y, Shen M, Lei R, Wu H, Sun A, Zhang R, Wang X, **Xiong MM**, Huang W, Jin L. (2009) [Common variants of four bilirubin metabolism genes and their association with serum bilirubin and coronary artery disease in Chinese Han population.](http://www.ncbi.nlm.nih.gov/pubmed/19238116?itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum&ordinalpos=14) Pharmacogenet Genomics. 19(4):310-8.
      16. \*Wu X, Jin L**, Xiong MM**. (2009) [Mutual information for testing gene-environment interaction.](http://www.ncbi.nlm.nih.gov/pubmed/19238204?ordinalpos=1&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DefaultReportPanel.Pubmed_RVDocSum) PLoS ONE. 4(2):e4578. PMC2642626**.**
      17. [Chu X](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Chu%20X%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Dong C](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Dong%20C%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Lei R](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Lei%20R%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Sun L](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Sun%20L%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Wang Z](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20Z%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Dong Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Dong%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Shen M](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Shen%20M%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Wang Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Wang B](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20B%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Zhang K](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Zhang%20K%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Yang L](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Yang%20L%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Li Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Li%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Yuan W](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Yuan%20W%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Wang Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Song H](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Song%20H%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Jin L](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Jin%20L%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [**Xiong M**](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Xiong%20M%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus)**M**, [Huang W](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Huang%20W%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus). (2009) Poly-morphisms in the interleukin 3 gene show strong association with susceptibility to Graves' disease in Chinese population. [Genes Immun.](javascript:AL_get(this,%20'jour',%20'Genes%20Immun.');) 10:260-266.
      18. \*Lin R, Wang X, Wang Y, Wang Y, Zhang F, Fu W, Yu T, Li,S, **Xiong MM**, Huang W, Jin L. (2009) Association of polymorphisms in four bilirubin metabolism genes with serum bilirubin in three Asian populations. Hum Mutat.30(4):609-615.
      19. \*Fang XZ, \*Luo L, Reveille J, **Xiong MM.** (2009) Discussion: Why do we test multiple traits in genetic association studies. J Korean Statistical Society. 38: 17-23.
      20. Seitsonen SP, Onkamo P, \*Peng G, **Xiong M**, Tommila PV, Ranta PH, Holopainen JM, Moilanen JA, Palosaari T, Kaarniranta K, Meri S, Immonen IR, Järvelä IE. (2008) [Multi-factor effects and evidence of potential interaction between complement factor H Y402H and LOC387715 A69S in age-related macular degeneration.](http://www.ncbi.nlm.nih.gov/pubmed/19048105) PLoS One. 3(12):e3833. PMC2585793**.**
      21. \*Dong H, Xiao Y, Wang W, Jin L, **Xiong MM.** (2008) Symmetry of metabolic network JCSB 1: 1-20.
      22. \*Sun X, Jin L, **Xiong MM.** (2008) Extended Kalman filter for estimation of parameters in nonlinear state-space models of biochemical networks. Plos One. 3(11):e3758. PMC2582954
      23. Xiao Y, MacArthur BD, Wang H, **Xiong MM**, Wang W. (2008) Network quotients: Structural skeletons of complex systems. Physical Review E. 78: 046102.
      24. Xiao Y, **Xiong MM**, Wang W, Wang H. (2008) Emergence of symmetry in complex networks. Phys Rev E Stat Nonlin Soft Matter Phys. 77 (6 Pt 2):066108.
      25. Xiao Y, \*Dong H, Wang W, **Xiong MM**, Shi B-L, Wu W. (2008) Structure based graph distance measures of high degree of precision. Pattern Recognition. 41: 3547-3561.
      26. \*Wu X, Jin L, **Xiong MM.** (2008) Composite measure of linkage disequilibrium for testing interaction between unlinked loci. Eur J Hum Genet. 16:644-651.
      27. Xiao Y, Wu W, Wang H ,**Xiong MM,** Wang W. (2008) Symmetry-based structure entropy of complex networks. [Physica A: Statistical Mechanics Applications](http://www.sciencedirect.com/science/journal/03784371). 387: 2611-2619.
      28. **Xiong MM**, Arnett FC, Xiong H, Zhou XD. (2008) Differential dynamic properties of scleroderma fibroblasts in response to perturbation of environmental stimuli. Application of state-space model in studies of human complex disease. PLos ONE. 3(2): e1693. PMC2246014
      29. \*Zhao J, Boerwinkle E, **Xiong MM.** (2007) An entropy-based genome-wide transmission/ disequilibrium test. Hum Genet 121:357-367.
      30. [Xu S](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Xu%20S%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [Huang W](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Huang%20W%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [Wang H](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20H%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [He Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22He%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [Wang Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [Wang Y](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Wang%20Y%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [Qian J](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Qian%20J%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus), [**Xiong M**](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Xiong%20M%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus)**M**, [Jin L](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Jin%20L%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVAbstractPlus). (2007)Dissecting linkage disequilibrium in African American genomes: Roles of markers and individuals. Mol Biol Evol. 24:2049-58.
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**G. MANUSCRIPTS SUBMITTED FOR PUBLICATIONS**

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132. Zhao J, **Xiong MM.** (2002) Unbiased quantitative population association test. American Journal of Human Genetics 71: 568.
133. Fan R, **Xiong MM**. (2002) Haplotype linkage disequilibrium mapping of quantitative trait loci. American Journal of Human Genetics 71: 572.
134. Akey JM, Wakeley J, Zhang K, **Xiong MM**, Jin L. (2001) The effect of ascertainment bias on estimates of linkage disequilibrium. American Journal of Human Genetics 69:111.
135. Fan R, Xiong MM. (2001) Combined linkage and association interval mapping of quantitative trait loci. American Journal of Human Genetics. 69: 1252.
136. Fang X, Xiong MM. (2001) Meta-learning for combining multiple classifiers. American Journal of Human Genetics. 69:1552.
137. Sun M, Xiong MM. (2001) A tabu search algorithm for gene selection in whole genome functional analysis. American Journal of Human Genetics. 69: 1671.
138. Zhao J, Xiong MM. (2001) The generalized T2 test for biomarker identification using gene expression data. American Journal of Human Genetics. 69: 1572.
139. Zhang HP, Yu CY, Singer BH, Xiong MM. (2001) Tree-based methods for tumor classification with gene expression microarray. American Journal of Human Genetics. 69: 344.
140. Fornage M, Markgraff C, Xiong MM, Boerwinkle E, Doris PA. (2001) Gene expression profiling and stroke susceptibility. Hypertension 38 (4): PE04.
141. Xiong MM, Zhao J, Jin L, Boerwinkle E. (2001) Dynamic models for mapping quantitative trait with time-dependent genetic effect. American Journal of Human Genetics. 69: 176.
142. Fan R, Jin L, Xiong MM. (2000) Haplotype Linkage Disequilibrium Mapping of Quantitative Trait loci with Phenotypic Selection. American Journal of Human Genetics. 67: 319.
143. Zhao J, Amos C. Boerwinkle E, Xiong MM. (2000) Multiple-Marker-Locus and Multiple Trait-Locus Linkage Disequilibrium Mapping of Quantitative Trait Loci with Epistasis. American Journal of Human Genetics. 67:318.
144. Xiong MM, Zhao J, Jin L, Boerwinkle E. (2000) Fine-Scale Mapping of Quantitative Traits Loci by Interval Mapping in Human Population. American Journal of Human Genetics. 67: 24.
145. Li W, Xiong MM. (2000) Computational Methods for Gene Expression Based Tumor Classification. American Journal of Human Genetics. 67: 78.
146. Zhang K, Xiong MM, Jin L, Rogers L, Amato R, Killary A, Lott S. (2000) Classification of Renal Cell Carcinoma with cDNA Microarray. American Journal of Human Genetics. 67: 96.
147. Akey JM, Jin L, Xiong MM. (2000) Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. American Journal of Human Genetics. 67: 227.
148. Xiao J, Akey JM, Xiong MM, Jin L. (2000) Linkage disequilibrium in isolated and outbred Chinese populations. American Journal of Human Genetics. 67: 225.
149. Jiang Z, Shi J, Akey JM, Xiong MM, Wang Y, Shen Y, Xu X, Chen H, Wu H, Xiao J, Lu D, Huang W, Jin, L. (2000) Association of blood pressure and polymorphisms in the promoter region of catalyses in a Chinese population. American Journal of Human Genetics. 67: 228.
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151. Gu C, Rao DC, Xiong MM. (2000) A generalized regression procedure for mapping complex diseases by linkage disequilibrium and population based samples. Genetic. Epidemiology. 19: 252.
152. Xiong MM, Jin L. (2000) Extent of linkage disequilibrium in human populations and their implications in SNP mapping. Genetic. Epidemiology. 19: 277.
153. Xiong MM, Zhao J, Jin L, Boerwinkle E. (2000) Multiple point linkage disequilibrium fine-scale mapping of quantitative trait locus. Genetic. Epidemiology. 19: 277.
154. Xiong MM, Zhao J, Amos C, Boerwinkle E. (2000) Physiological and statistical genetic models of epistasis. Genetic. Epidemiology. 19: 278.
155. Wang H, Xiong MM, Chu S, Jin L, Wang G, Yuan W, Mao S, Zhang W, Zhu D. (1999) Fine scale mapping confirms the linkage of a region on chromosome 2 with essential hypertension in Chinese. American Journal of Human Genetics. 65, A16.
156. Xiao J, Zhao Y, Xiong MM, Huang W, Zhang W, Liu X., Li W, Hu F, Wu H, Lu D, Tan J, Chen Z, Boerwinkle E, Jin, L. (1999) Whole-genome linkage disequilibrium mapping of the genes underlying blood pressure variation in an isolated Chinese population. American Journal of Human Genetics 65, A17.
157. Akey JM, Jin L, Xiong MM. (1999)The haplotype disequilibrium test: A nonparametric haplotype based method for the genetic mapping of complex traits. American Journal of Human Genetics 65, A42.
158. Xiong MM, Jin L. (1999) Admixture linkage disequilibrium mapping of quantitative trait loci. American Journal of Human Genetics 65, A86.
159. Chu S, Xiong MM, Zhu D, Wang G, Zhan Y, Zhang W, Zhou H, Wang H, Li W, Shen D, Jin L. (1999) Linkage analysis of 50 candidate genes involved in essential hypertension in 95 Chinese nuclear families with 460 affected sib-pairs. American Journal of Human Genetics. 65, A99.
160. Zhao J, Xiong MM, Huang W, Wang H, Zuo J, Chen Z, Qiang BQ, Zhang ML, Du WN, Chen JL, Diang W, Yuan WT, Xu H, Jin L, Li YX, Sun Q, Liu QY, Boerwinkle, E, Fang FD. (1999) Type 2 diabetes susceptibility loci maps on chromosomes 1 and 20 in Chinese Han Families. American Journal of Human Genetics 65, A455.
161. Zhu D, Xiong MM, Chu S, Jin L, Wang G, Yuan W, Zhan Y, Zhang W, Dong S, Gao P, Zhao G, Huang W. (1999) Genome-wide scanning for loci linked to essential hypertension in Chinese families. American Journal of Human Genetics 65, A455.
162. Xiong MM, Jin L, Boerwinkle E. (1998) Linkage disequilibrium based regression: A method for mapping quantitative trait loci in humans. American Journal of Human Genetics 63:A238.
163. Xiao J, Zhang WL, Xiong MM, Lu DR, Hu F, Xu HY, Xue JLD, Tan J, Chen Z, Boerwinkle E, Jin L. (1998) Localization of three candidate regions influencing blood pressure variations to chromosome 5 in an isolated Chinese population. American Journal of Human Genetics 63: A1829.
164. Xiong MM, Jin L. (1997). Biallelic markers in genetics studies of human diseases: their power, accuracy and density in population-based linkage analyses. American Journal of Human Genetics 61:A301.
165. Guo SW and Xiong MM. (1995) Modeling the population dynamics of simple sequence repeats. American Journal of Human Genetics 57: A165.

# ACADAMIC PRESENTATIONS

**Invitational Presentations**

1. Gene-gene interaction analysis for next-generation sequencing. ENAR, March 16-19, 2014, Baltimore, Maryland.
2. Topic contributed: Jiang J, Lin N and Xiong MM. (2014). Image RNA-seq data analysis in clouds. 2014 JSM, Boston, MA.
3. Topic contributed: Xiong MM and Yu J. (2014). New Sparse Canonic correlation analysis for construction of co-association networks with NGS data by cloud computing. 2014 JSM, Boston, MA.
4. Classification analysis of big image data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.
5. QTL and Gene-gene Interaction Analysis for Next-generation Sequencing, ENAR, March 10-13, 2013 Spring Meeting - Orlando, Florida.
6. Alternative Direction Minimization Methods for Phenotype Prediction and variable Selection. Biometrics-2013, June 10-12, Chicago.
7. (Keynote Speaker) International Conference and Exhibition on Biometrics and Biostatistics 5-7 March 2012, Omaha.
8. Genetic and Epigenetic Analysis for Next-Generation Sequencing. March 22, 2012, Department of Epidemiology, MD Anderson Cancer Center.
9. Genetic Studies of Complex Diseases in the Sequence Era. October 5, 2012. Department of Statistics, Texas A&M University.
10. Statistical Challenges Arising from Next-generation Sequencing. December, 14, 2011, Department of Bioinformatics and Computational Biology, Anderson Cancer Center.
11. Association studies for next-generation sequencing. May 30, 2011, National Institute of Mental Health.
12. Mathematical challenges in data analysis raised by next-generation sequencing. School of Mathematics Science, Fudan University, China, November 2, 2011.
13. Data analysis for next-generation sequencing. School of Finance and Statistics, East China Normal University, November 4, 2011.
14. Gene and pathway-based association studies. China-UK Statistical Genetics, Population Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
15. Implication of next-generation sequencing on association studies. China-UK Statistical Genetics, Population Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
16. Integrated genetic and epigenetic analysis in cancer studies. The Second International Conference on Statistical Genetics and Systems Biology, Kunming, China, July 22-25, 2009.
17. Dynamic Pathway Analysis, The First International Conference on Statistical Genetics and Systems Biology, Qingdao, China, June 14-16, 2007.
18. State Space Equations for Modeling Gene Networks. The First International Conference on Computational Systems Biology. Shanghai, July 20-23, 2006
19. Genetic interaction networks and regulatory networks for genetic studies of complex diseases. Computational Biology 2005 – Challenges and Visions. Shanghai, October 13-16.
20. Nonlinear approach to dissecting genetic structure of complex diseases, The International Symposium on Genomic Medicine, June 28-30, 2005. Shanghai, China.
21. A Systems Biology Approach to Genetic Studies of Complex Diseases, March 2, 2004, Yale University.
22. An example of application of bioinformatics to systems biology, Eastern Forum of Science and Technology. July 11-12, 2004, Shanghai, China.
23. Network Biology, July 18, 2004, Shanghai Second Medical University, China.
24. Differentially expressed genetic networks, the 7th World Multiconference on Systemics, Cybernetics and Informatics, July 27-30, 2003, Orlando, Florida.
25. Perspective in Systems Biology, December, 24, 2003, Fudan University, Shanghai, China.
26. Large-scale gene expression data analysis and disease diagnosis, August 26-27, 2002. International Biopharmaceutical Technology Conference, Fujian, China.
27. Gene expression-based tumor classification, December 22, 2002, Department of Statistics, Beijing University, China.
28. Bioinformatics and genomic science research, December, 19, 2001, National Genomic Center at Shanghai, China.
29. Generalized T2 test for whole genome linkage disequilibrium profile analysis, May 23-26, 2001, International conference for mapping complex disease genes, Changsha, China.
30. Biomarker Identification by feature selection. May 21, 2001, Institute of System Science and Mathematics, Chinese Academy of Science, Beijing.
31. Advances in Bioinformatics, May 27, 2001, Department of Genetics, Fudan University, China.
32. Cancer functional genomic analysis, May 30, 2001, Zhejiang University, Hangzhou, China
33. Mapping complex trait loci. Feb. 3, 2000, Workshop at NIH.
34. Neural networks for gene expression based tumor classification, Feb. 21, 2000, Division of Biostatistics, Saint Louis Washington University, Saint Louis, Missouri.
35. Extent of linkage disequilibrium in the modern population and its implications in SNP mapping: How many SNPs are needed for disease gene mapping? March 7, 2000, National Genome Research Institute, Washington, DC.
36. Gene selection in gene expression based tumor classification, April 23, 2000, Department of Computer Science, University of South West Louisiana.
37. Linkage disequilibrium mapping for complex disease, May, 2000, National Institute of Dental and Craniofacial Research Genetics Work Group.
38. Microarray and tumor classification, June 29, 2000, Darlian Institute of Chemistry, Darlian, China.
39. Combined linkage and linkage disequilibrium, July 4, 2000, Department of Statistics Beijing University, China.
40. Microarray and tumor diagnosis, July 5, 2000, Beijing General Hospital, Beijing, China.
41. Genomic circuits and cardiac diseases, July 6, 2000, Chinese Academy of Medical Science, Beijing, China.
42. Pathway identification, July 10, 2000, Chinese Institute of Biochemistry, Shanghai, China.
43. Statistical and computational methods for gene expression based tumor classification, Jan. 9, 2000, Department of Mathematics, University of Southern California, Los Angeles.
44. Linkage and linkage disequilibrium analysis for genetic studies of complex diseases, April, 1999, Chinese Academy of Medical Science, Beijing, China.
45. Advances in cancer genomics, April, 1999, Beijing Institute of Cancer, Beijing, China.
46. Advances in plant genetics, April, 1999, Institute of Plant, Chinese Academy of Science, Beijing, China.
47. Functional genomics in plant science, August, 1999, Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China.
48. Linkage disequilibrium based regression methods for mapping quantitative trait loci, August, 1999, Institute of Genetics, Fudan University, China.
49. Statistical analysis of mapping quantitative trait loci, February, 1997, Department of Statistics, Columbia University, New York.
50. Linkage disequilibrium for fine scale mapping, March, 1997, Department of Biology, Georgia Tech, Atlanta, Georgia.
51. Fine-scale mapping: theory and application, September, 1996, McGill University, Canada.
52. Fine-scale mapping of quantitative trait loci, September, 1996, University of Montreal, Canada.
53. Strategy for mapping complex trait loci, July, 1996, Sequana Therapeutics, Inc., La Jolla, California.

**Presentations**

1. Xiong MM. (2014). Integrate genomic, epigenomic, image, physiological traits, metabolites and clinical phenotype analysis and cloud computing. Department of Biostatistics, University of Texas School of Public Health. Oct 24, 2014.
2. Lin N, Jiang J, Guo S, Yu X, Ma L and Xiong MM. (2014). A Novel Scheme for the Classification Analysis of Big Image Data Based on Functional Principle Component Analysis, matrix completion and Sufficient Dimension Reduction. 2014 JSM, Boston, MA.
3. Li L and Xiong MM. (2014). An Ordinary Differential Equation Model for Gene Regulation with RNA-seq Data. 2014 JSM, Boston, MA.
4. Zhang, F, Boerwinkle E and Xiong MM. (2013). Epistasis analysis for quantitative trait with next-generation sequencing data (Plat form). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
5. Zhao J, Zhu Y and Xiong MM. (2013) Gene-gene interaction analysis for next-generation sequencing (Plat form). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
6. Family-based association studies for next generation sequencing. 30 Years of Computational Biology at USC. March 30-April 1, 2012. Los Angeles, California.
7. Quantitative Trait Locus (QTL) Analysis for Next-Generation Sequencing with the Functional Linear Models (Platform). 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
8. The Smoothed Functional Principal Component Analysis for Pathway Analysis with Next-Generation Sequencing Data (Platform). 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
9. Mixed Functional Linear Model for Sequence-based Quantitative Trait Association Studies Unifying Population and Family Study Designs (Platform). 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
10. Population structure analysis for next-generation sequencing. 2011 IEEE World Congress on Engineering and Technology. Shanghai, China. October 28-Novemeber 2, 2011,
11. A novel genome continuum model for sequence-based association studies. 2010 Joint Statistical Meetings, July 31-August 5, 2010, Vancouver, Canada.
12. Association Studies for Next-Generation Sequencing. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
13. Meta-analysis and Network analysis of five gene expression data sets in ovarian cancer. The Third International Joint Conference on Computational Sciences and Optimization (CSO 2010). May 28-31, 2010, Yellow Mountain, China.
14. Genome-wide association studies of copy number variation in Glioblastoma. The 4th International Conference on Bioinformatics and Biomedical Engineering (iCBBE 2010), June 18-20, 2010, Cheng Du, China.
15. [Genome-wide Gene and Pathway Analysis.](javascript:%20openwin('20755')) 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
16. [Genome-wide interaction analysis of coronary artery disease.](javascript:%20openwin('20793')) 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
17. Information Geometry, Gene-Gene, Gene-Environment Interaction, and Pathway Association. 2008 Joint Statistical Meetings, Colorado, August 3-7, 2008.
18. Composite Measure of Linkage Disequilibrium for Testing Interaction between Unlinked Loci, The 15th International Conference of Forum for Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China May 20-23, 2007.
19. Mutual information for detection of gene-gene interaction. The 15th International Conference of Forum for Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
20. Do Genetic Networks Obey Kirchhoff’s and Ohm’s Laws? The IASTED International Conference on Computational Systems Biology. November 13-14, 2006, Dallas.
21. [Genetic Interaction Networks in Association Studies of Complex Diseases](http://www.amstat.org/meetings/jsm/2006/onlineprogram/index.cfm?fuseaction=abstract_details&abstractid=305905). The 2006 Joint Statistical Meeting, August 6-10, Seattle, Washington.
22. State-space approach to modeling dynamics of gene regulation in networks. 2005 International Conference on Bioinformatics. September 22-24, Busan, Korea.
23. Nonlinear Tests for Categorical Data. ENAR, Austin Texas, March 20-23, 2005.
24. Systems Biology Approaches to Genetic Studies of Complex Diseases. Pathway analysis for Target and Compound Evaluation. San Francisco, CA, April 20-22, 2005.
25. Generalized Circuit Analysis of Biological Networks. 2004 International Conference on Complex Systems, Boston, May 16-21, 2004.
26. Statistical model for function valued traits. Genetic Analysis of Complex Diseases & Human Population, September, 19-21, 2003, Chicago, Illinois.
27. Modeling and identification of genetic networks. ASHG 52th Annual Meeting, Baltimore, 2002.
28. Randomly distributed recombination may generate block-like pattern of linkage disequilibrium: An act of genetic drift. ASHG 52th Annual Meeting, Baltimore, 2002.
29. Differentially regulated genetic networks. 2002 NCRR Bioinformatics Conference. September 27-29, 2002. Boston.
30. The effect of ascertainment bias on estimates of linkage disequilibrium. ASHG 51th Annual Meeting, San Diego, 2001.
31. Dynamic models for mapping quantitative trait with time-dependent genetic effect. ASHG 51th Annual Meeting, San Diego, 2001.
32. Structural equation models for pathway identification. Oncogenomics Conference. January 25-27, 2001, Tucson, Arizona.
33. Population genomic models and their applications to genetic studies of complex traits. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Geogia.
34. Linkage and association studies of QTL for nuclear families by mixed models. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Georgia.
35. Multiple trait-locus model for quantitative trait analysis, 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
36. Linkage disequilibrium mapping of quantitative trait loci: multiple trait analysis, 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
37. Molecular genetic profiling of renal cell carcinoma as an alternative to current histopathologic classification systems. 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
38. The haplotype disequilibrium test for genome-wide screen: Its power and study design***.*** an. 2000. Pacific Symposium of Biocomputing 2000. Maui, Hawaii.
39. Fine-Scale Mapping of Quantitative Traits Loci by Interval Mapping in Human Population. At ASHG 50th Annual Meeting, Philadelphia, Oct.3-7, 2000.
40. Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. ASHG 50th Annual Meeting, Philadelphia, Oct. 3-7, 2000.
41. Single Nucleotide Polymorphisms (SNPs) From 38 *Plasmodium falciparum* transporters and their roles in drug resistances. ASTMH 49th Annual Meeting, Houston, TX. Oct. 29-Nov. 2.
42. Gene expression in myositis biopsies. 64th Annual Scientific Meeting of Rheumatology, October 29 - November 2, Philadelphia.
43. Gene expression profile of muscle biopsies from patients with inflammatory myopathies. 64th Annual Scientific Meeting of Rheumatology, October 29-November 2, Philadelphia.
44. Expression of autoantigen genes is selectively and specifically altered in dermal fibroblasts of systemic sclerosis patients. 64th Annual Scientific Meeting of Rheumatology, October 29-November 2, Philadelphia.
45. Gene expression based tumor classification, IBC’s 6th Annual Biochip Technologies Conference, 1999, Nov. 2-5, Berkeley, CA.
46. The haplotype disequilibrium test: A nonparametric haplotype based method for the genetic mapping of complex traits. 49th Annual Meeting of the American Society of Human Genetics, Oct. 19-23, 1999, San Francisco, CA.
47. Mapping QTL by linkage disequilibrium. Joint Statistical Meetings, August 9-13, 1998, Dallas, Texas.
48. Linkage disequilibrium based regression: A method for mapping quantitative trait loci in humans. 48th Annual Meeting of the American Society of Human Genetics, Oct. 27-31, 1998 Denver, Colorado.
49. Biallelic markers in genetics studies of human diseases: their power, accuracy and density in population-based linkage analyses. 47th Annual Meeting of the American Society of Human Genetics,1997.
50. Modeling the population dynamics of simple sequence repeats. 46th Annual Meeting of the American Society of Human Genetics,1995.
51. Neural Networks with Hidden Markov Processes. Artificial Neural Networks in Engineering Conference, Nov. 13-16, 1994, St. Louis.
52. Weighted neural network models for nonlinear regression with fixed and random effects. World Congress on Neural Networks, June 5-9, 1994, San Diego.
53. An O (n3) Neural Network Model for Linear Programming. World Congress on Neural Networks, Portland, July 11-15, 1993.
54. A neural network model based on differential-algebraic equations for nonlinear programming, IEEE International Conference on Neural Networks, San Francisco, March, 28-April 1, 1993.
55. Hybrid Kohonen self-organizing neural network and multi-layer neural network model for pattern recognition and nonlinear, artificial neural networks in Engineering Conference, Nov. 15-18, 1992, St. Louis.
56. Learning potential functions and differential inclusion. Proceedings of IJCNN '92, Baltimore, June 7-11, 1992.

**ACTIVE GRANTS**

Principal Investigator (30%) 5R01HL106034-02 (0008215)

Statistical Methods for Finding Missing Heritability

NHLBI

Total Costs: $ 1,582,967

1/10/2011 - 12/31-2014

Principal Investigator (40%) 1R01GM104411-01

Unified Statistical Methods for Sequence-Based Association Studies.

NIGMS

Total Cost: $1,737,913

04/01/2013-01/31/2017

Investigator (5%) 1R01 MH101054 (CHEN & KENDLER)

Understanding the genetic architecture of schizophrenia in Chinese population

NIMH

Total Costs: $599,933

08/01/2013-07/31/2016

Investigator (15%) #81373100

Develop statistical methods for genome-wide gene-environment interaction analysis with next-generation sequencing data.

NSF, China

Total Cost: 700,000 Yuan

01/2014-12/2017

Investigator (5%) 2 U54 HG003273-09

The Human Genome Sequencing Center

NIH

Total Costs: $1,249,377

11/01/2011-10/31/2015

**PENDING GRANTS**

Principal Investigator (30%)1 R01 CA195601-01

Combined Image and Biomarker Approach to Early Detection of Pancreatic Cancer.

NCI

Total Costs: 2,382,428

04/01/2015-03/31/2020

**SUBMITTED, BUT NOT FUNDED**

Principal Investigator (15%) GRANT11555208

Point of Care Screening and Diagnosis of Liver Cancer in Chinese

Population

NCI

Total Cost: $3,999,995

07/01/2014 - 06/30/2019

Co-Investigator (10%) 1P01GM09964301A1 (Boerwinkle)

12/01/2012 - 11/30/2107

NIH / U of Michigan

$487,037

Genomic Analysis in a Super-Exponentially Expanding Population

Project 2: Strategies for Identifying Regions of DNA Sequence that Influence Phenotypic Variation in Rapidly Expanding Populations

This project will modify, test and apply analytic methods that will be needed to relate the burgeoning whole-genome sequence data to predict and understand human health and disease. These methods are necessary for fully realizing the benefits of the Human Genome Project in medicine and public health.

Co-Investigator (10%) Integrating genomics with GWAS to discover risk factors to schizophrenia

VIRGINIA COMMONWEALTH U

Total costs: $57,105

09/01/2012 - 08/31/2015 1

I will provide expertise and methods necessary to conduct integrated analyses of RNA sequencing and GWA data, sequence-based association studies to test for the association of both common and rare variants within a gene or pathway with schizophrenia which are applied to pedigree and population data. Dr. Xiong will also provide bioinformatic and statistic services related to the proposed studies in this application.

Co-Principal Investigator (25%) Multi-dimensional Data Reduction and Integration in

Psychiatric Disorders.

Total Cost: $785,361

04/01/2012 - 03/31/2015

Co-Investigator The Human Genome Sequencing Center

Total Cost: $2,912,641

12/01/2011 - 11/30/2015

Principal Investigator of Subcontract (10%)

Integration of Functional Studies with GWA for Smoking Behaviors

Total Cost: $434,055

02/01/2012 - 01/31/2017

Principal Investigator of Subcontract (10%)

Aberrant DNA methylation as a Mechanism of Resistance in ALL

Total Cost: $394,858

10/01/2011 - 09/30/2016

**PAST GRANTS**

Co-Investigator (15%) 1U01HG005728-01

Detecting Natural Selection for the 1000 Genomes Dataset

NIH – National Human Genome Research Institute

Total Costs: $777,305

5/28/10 - 4/30-2012

Principal Investigator (30%): 1R01AR057120-01

Network Approach to GWAS of Rheumatoid Arthritis (RA), Ankylosing Spondylitis (AS) and Psoriasis.

NIAMS

Total Costs: $556,353

09/01/2009 -08/31/2011

Principal Investigator (25%) P01 AR052915-01A1

Genetics and Ankylosing Spondylitis (AS) Pathogenesis

Project 4: Analysis of Genetic-Environmental Networks in

Spondyloarthritis

National Institute of Health

Total Costs: $7,417,127

07/01/2006-06/30/2011

Co-Investigator (15%) NIAMS P50 AR054144-01 CORT

National Institute of Health

Center of Research Translation in Systems Sclerosis

National Institute of Health

Total Costs: $7,382,620

09/01/2006 - 08/31/2011

Co-Investigator (5%) 1 R01  HL084099-01A1

National Institute of Health

Genes of the CYP450-Derived Eicosanoid Pathway in Subclinical

Atherosclerosis

Total Costs: $2,872,877

1/1/2007 - 03/30/2011

Co-Investigator (5%) PR064803

Department of Defense

The Integrative Studies of Genetic and Environmental factors in Systemic Sclerosis

Total Costs: $928,125

1/1/2007 - 03/30/2011

Co-Principal Investigator: Development of Statistical Methods and Software for Testing Gene-Environment Interaction and Construction of Genetic Interaction Networks in Complex Diseases.

Ministry of Science & Technology, China

Total Costs: 1,000,000 Yuan

09/01/2007 - 08/31/2011

Co-Investigator (40%): R01 HL74735-01

National Institute of Health

Antihypertensive Pharmocogenomics

Total Costs: $1,162,816

04/01/2004 - 03/30/2008

Co-Principal Investigator: Study of Dynamics and Network Structure of Biological Systems of Complex Diseases

Science & Technology Commission of Shanghai Municipality, China

Total Costs: 8,000,000 Yuan

11/30/04 - 10/30/07

Consultant: 1R03AR050517-01A2

Study of SPARC in scleroderma skin fibroblasts.

National Institute of Health

Total Costs: $223,062

4/1/05 - 3/31/08

Co-Investigator (10%): 5P50-AR44888-03

Mapping Scleroderma Susceptibility Genes in the Choctaw

National Institute of Health

Total Costs: $4,338,583

09/16/2001 - 09/14/2006

Co-Investigator (15%): U01-HL054481

Genetic Determinants of High BP in Three Racial Groups

(Network)

National Institute of Health

Total Costs: $ 437,846

09/05/1995 - 06/30/2005

Co-Investigator (5%): 5 R01 HL069125-03

Gene-Environment Interactions and Stroke Susceptibility.

National Institute of Health

Total Costs $422,749

09/30/2001 - 09/29/2005

Principal Investigator of subcontract to UT-SPH (50%):

NIH R01 GM5651-03

Statistical Models in Population and Quantitative Genetics

National Institute of Health

Total Cost: $423,791

01/01/1997 - 12/31/2001

Principal Investigator of subcontract to UT-SPH (15%):

NIH ES09912

Linkage and Linkage disequilibrium for Quantitative Traits

National Institute of Health

Total Cost: $1,267,766

01/01/1999 - 12/31/2001

Co-Investigator (20%): NIH HG0 1833-02 A1

Construction and Application of a U. S. Admixture Map

National Institute of Health

Co-Investigator (20%)

Total Cost: $482,961

09/24/1999 - 05/31/2002

**ACADEMIC ACTIVITIES**

**COURSES TAUGHT**

2014 Fall Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer).

Individual Studies in Biostatistics, PH 1999-110 (2)

Thesis Research, PH 9998-304 (2)

Dissertation Research, PH9999-413 (4)

Practicum (Practicum), PH 9997-170 (1)

Spring Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (5)

Dissertation Research, PH9999-413 (4)

Summer Individual Studies in Biostatistics, PH 1999-110 (1)

Dissertation Research, PH9999-413 (2)

Practicum (Practicum), PH 9997-170 (1)

2013 Fall Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer).

Thesis Research, PH 9998-304 (1)

Individual Studies in Biostatistics, PH 1999-110 (2)

Dissertation Research, PH9999-413 (5)

Summer Application of advanced multivariate techniques to genomic analysis, PH 1998

L-150 (Course organizer and Instructor)

Individual Studies in Biostatistics, PH 1999-110 (1)

Dissertation Research, PH9999-413 (2)

Spring Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (3)

Dissertation Research, PH9999-413 (1)

2012 Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (3)

PH 9998 - 304 Culminating Experience/Thesis Research (2)

2012 Spring

Introduction to Computational Systems Biology, PH1998L (Course organizer and

Lead Instructor)

Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (1)

Culminat Exp/Thesis RSCH, PH9998-304 (1)

Dissertation Research, PH9999-413 (2)

2012 Summer

2011 Fall Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (2)

Dissertation Research, PH9999-413 (1)

Culminat Exp/Thesis RSCH, PH9998-304 (2)

2011 Summer

Application of advanced multivariate techniques to genomic analysis, [PH 1998 L-](https://utlink2.uth.tmc.edu/utlink/roster.aspx?crse=PH%20%20%201998%20L%20150)

[150](https://utlink2.uth.tmc.edu/utlink/roster.aspx?crse=PH%20%20%201998%20L%20150) (Course organizer and Instructor)

Culminat Exp/Thesis RSCH, PH9998-304 (1)

2011 Spring Population Genetics, PH1984L, GS110042 (Lecturer)

Culminat Exp/Thesis RSCH, PH9998-304 (2)

Dissertation Research, PH9999-413 (2)

2010 Fall Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Research in Biomedical Science, GS000520

Practicum, PH9997288

Dissertation Research, PH9999-413

Dissertation Research, PH9999-413

2010 Summer

Data Mining in Genetic Epidemiology, PH1998L andGS110053 (Co-Coordinator, Lecturer)

Dissertation Research, PH9999

Dissertation Research, PH9999

Dissertation Research, PH9999

Research in Biomedical Science, GS000520

Research in Biomedical Science, GS000520

Culminating Experience/Thesis Research, PH9998

2010 Spring

Introduction to Computational Systems Biology, PH1998L (Course organizer and

Lead Instructor)

Population Genetics, PH1984L, GS110042 (Lecturer)

Research in Biomedical science, GS000520

Research in Biomedical science, GS000520

Individual Study in Biostatistics, PH1999

Culminating Experience/Thesis Research, PH9998

Dissertation Research, PH9999

Dissertation Research, PH9999

2009 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Study in Biostatistics, PH1999

Practicum, PH9997

Culminating Exp/Thesis Research, PH9998

Dissertation Research, PH9999

Dissertation Research, PH9999

2009 Summer

Data Mining in Genetic Epidemiology, PH1998L andGS110053 (Co-Coordinator, Lecturer)

2009 Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Dissertation Research, PH9999

Dissertation Research, PH9999

Practicum, PH9997

Culminant Exp/Thesis Research, PH9998

2008Spring

Introduction to Computational Systems Biology, PH1998L (Course organizer

and Lead Instructor)

Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Study in Epidemiology, PH2999

Dissertation Research, PH9999

Dissertation Research, PH9999

Summer

Data Mining in Genetic Epidemiology, PH1998L andGS110053 (Lecturer)

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Dissertation Research, PH9999

Dissertation Research, PH9999

Dissertation Research, PH9999

Practicum, PH9997

Culminant Exp/Thesis Research, PH9998

2007 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Study in Biostatistics, PH1999

Individual Study in Epidemiology, PH2999

Practicum, PH9997

Thesis Research, GS000910

Summer

Data Mining in Genetic Epidemiology, PH1998L andGS110053 (Co-Coordinator, Lecturer)

Individual Study in Biostatistics, PH1999

Individual Study in Epidemiology, PH2999

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Dissertation Research, PH9999

2006 Spring

Introduction to Computational Systems Biology, PH1998L (Course organizer

and Lead Instructor)

Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Study in Biostatistics, PH1999

Summer

Data Mining in Genetic Epidemiology, PH1998L andGS110053 (Co-

Coordinator, Lecturer)

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032

(Course organizer and Lead Instructor)

Statistical Genetics, PH1986L, GS110072 (Lecturer)

Individual Study in Epidemiology, PH2999

Practicum , PH9997

2005 Fall

Introduction to Genomics and Bioinformatics, , PH1980L, GS110032 (Course

organizer and Lead Instructor)

2005 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Dissertation Research, PH9999

2004 Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Research in Biomedical Science, GS000520

Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

2003 Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Research in Biomedical Science

Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Summer

Microarrays and Functional Genomics (Course organizer and lead Instructor)

2002 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Dissertation Research, PH9999

Summer

Dissertation Research, PH9999

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lead Instructor)

Statistical Genetics (Lecturer)

2001 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Summer

Methods on Genet Epidemiology and Linkage (Lecturer)

Research in Biomedical Science

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course

organizer and Lecturer)

Microarrays and Functional Genomics (Course organizer and lecturer)

Research in Biomedical Science, GS000520

Tutorial Research Experience, GS000514

2000 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Summer

Research in Biomedical Science, GS000520

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Lecturer)

Microarrays and Functional Genomics (Course organizer and lecturer)

1999 Spring

Population Genetics, PH1984L, GS110042 (Lecturer)

Tutorial Research Experience, GS000514

Tutorial Research experience, GS000514

Summer

Tutorial Research Experience

Research in Biomedical Science

Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Lecturer)

Microarrays and Functional Genomics (Course organizer and lecturer)

Tutorial Research Experience, GS000514

1998 Fall

Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Lecturer) Tutorial Research Experience, GS000514

**GRADUATE STUDENTS/POSTDOCTORAL FELLOW SUPERVISED**

# Graduate School of Biomedical Sciences (GSBS) and School of Public Health

**Postdoctoral Fellow**

1. Azam Yazdani 04/2013-05/2014

2. Futao Zhang, Lecturer, Dept of Computer Science, Hohai University 08/2012-12/2013

3. Dan Xie, Associate Professor, Hubei University of Chinese Medicine 04/2011-05/2012

4. Xuesen Wu 12/2009-06/30/2010

Professor, Char of Department of Public Health, Bengbu Medical College at Bengbu

5. Xiangzhong Fang, Professor, Chair of Dept of Biostatistics, Beijing University, China 01/2008-07/2008 01/2000-01/2001

6. Winston Wa Shing Lau 07/2007-10/2007

7. Jinying Zhao 05/2005- 12/2005

Professor, Department of Epidemiology, Tulane University

8. Jun Li 01/2001-01/2003

**Research Fellow**

1. Shicheng Guo 01/2013-Present

2. Keling Xu 08/2014-Present

3. Panpan Wang 09/2013-Present

4. Minyi Chen 04/2012-06/2013

5. Yan Cui 05/2011-12/2012

6. Yun Zhu 12/2009-08/2011

Ph. D., Department of Epidemiology, Tulane University

7. Shengjun Hong 09/2010-08/2012

Postdoctoral Fellow, CAS-MPG Partner Institute for Computational Biology

8. Pengfei Hu 09/2009-08/2011

Research Associate, School of Life Science, Fudan University, China

9. Hoicheong Siu 01/2010-01/2012

Postdoctoral Fellow, Hong Kong University

10. Hua Dong 09/2007-10/2009

11.Xiaodian Sun 10/2008-04/2009

Postdoctoral Fellow, Department of Statistics, Penn State University

12. Qian Hao 11/2006-06/2007

13. Wuju Li 1998-2000

Professor, Center of Bioinformatics, Institute of Basic Medical Science, China

**Graduate Student Advisor and Committees:**

**Primary PhD Student Advisor**

***Name*  *Discipline/Module Degree Role Graduation***

1. Lerong Li Biostatistics Ph. D. Advisor 08/2013-12/2014

Dissertation Title: Dynamic Model and its Applications to Molecular and Physiological

Analysis

2. Dong-Yang Lee Biostatistics Ph. D. Advisor 02/3013-04/2015

Dissertation Title: Functional linear model with functional response and predictor for temporal

quantitative traits in sleep apnea

3. Long Ma Biostatistics Ph. D. Advisor 09/2011-04/2015

Dissertation Title: A General Statistic Framework for Identifying Genetic Variants of Clinical

Significance

4. Mohammad Rahman Biostatistics Ph. D. Advisor 08/2013-04/2015

Dissertation Title: Sparse structural equation models for genotype-phenotype networks

5. Getie Zewdie Biostatistics Ph. D. Advisor 05/2013-05/2014

Dissertation Title: Applied differential equations to classify myocardial infarction disease from electrocardiography (ECG) signals.

FDA

6. Aaya Nassar Biological Science Ph.D. Advisor 09/2004-08/2012

7. Li Luo Biostatistics Ph.D. Advisor 09/2005-08/10

Dissertation Title: Functional Data Analysis Approaches for genotype-phenotype Association Studies from Next-generation Sequencing.

Assistant Professor, The University of New Mexico

8. Shenying Fang Biostatistics Ph.D. Advisor 01/2007-12/08

Dissertation Title: Information Bottleneck Method for Genome Association Studies in Framingham Population and a Collaborative Association Study of Psoriasis

Assistant Professor, MD Anderson Cancer Center

9. Jinying Zhao Biological Science Ph.D. Advisor 09/2000-05/05

Dissertation Title: Nonlinear Test for Genetic Studies of Complex Disease

Professor, Tulane Univrsity

10..Akey, Joshua, GSBS Ph.D. On-line Supervisor 09/1998-12/02

Professor, Department of Genomic Science, University of Washington

11. Xuehan Ren Biostatistics Ph. D. Advisor 08/2013-Present

12. Junhai Jiang Biostatistics Ph. D. Advisor 08/2013-Present

13. Nan Lin Biostatistics Ph. D. Advisor 05/2013-present

14. Lian Lin Biostatistics Ph.D. Advisor 08/2009-Present

15. Pengyi Gu Biostatistics Ph.D. Advisor 09/2013-Present

16. Shi Pu Biostatistics Ph.D. Advisor 08/2007-05/2008

**PhD dissertation committee**

1. Xia Wang Baylor College of Medicine, Ph. D Mentor 07/2012-Present

2. Zachry Tore Soens Baylor College of Medicine, Ph. D Mentor 09/2014-Present

3.Yulun Liu Biostatistics Ph.D. Member 06/2014-Present

4. Chuan Hong Biostatistics Ph.D. Member 01/2014-Present

5. Jin Su Biostatistics Ph.D. Member 11/2010-Present

6. Hui Peng Biostatistics Ph.D. Member 11/2010-Present

7. Xiang Shu Biostatistics Ph.D. Member 12/2014-Present

8. Xuan Zhang Biostatistics Ph.D. Member 06/2010-Present

9. Hong Wei Tang Biostatistics Ph.D. Member 05/2010-Present

10.Caimiao Wei Biostatistics Ph.D. Member 09/2008-Present

11. E Lin Biostatistics Ph.D. Member 10/2010-11/2014

12. Taebeom Kim Biostatistics Ph.D. Member 10/2012-11/2014

13.Wei Qiao Biostatistics Ph.D. Member 05/2010-11/2014

14. Renke Zhou Biostatistics Ph. D. Member 10/2008-12/2014

15.Vineetkumar Kharat Epidemiology Ph.D. Member 03/2013-05/2014

16. Manandhar, Pratik Biostatistics Ph.D. Member 09/2013-05/2014

15. Nianxiang Zhang Biostatistics Ph.D. Member 08/2010-08/2013

16. Suyu Liu Biostatistics Ph.D. Member 09/2009-08/2013

17. Yi-Ju Chiang Biostatistics Ph.D. Member 09/2009-08/2013

18. Min Yi Biostatistics Ph.D. Member 09/2009-08/2012

19. Shangying Liang Biostatistics Ph.D. Member 10/2009-08/2013

20. Yung Fei Wang Biostatistics Ph.D. Member 10/2008-08/2012

21. Lin Huo Biostatistics Ph.D. Member 10/2008-02/2009

22. Jun Liu Biostatistics Ph. D. Member 10/2008-04/2012

23. Yu-Li Ling Biostatistics Ph.D. Member 07/2008-04/2012

24. Furong Huang Biostatistics Ph.D. Member 09/2006-08/2012

25. Jacy Crosby Biostatistics (GSBS) Ph.D. Member 06/2008-09/2010

26. Bo He Biostatistics Ph.D. Member 09/2008-08/2013

27. Ho, Chung-Han Biostatistics Ph.D. Member 10/2008-08/2013

28. Xuemin Gu Biostatistics Ph.D. Member 09/2009-08/2012

29. Jang H Yun Biostatistics Ph.D. Member 06/2008-08/2013

30.Yaji Xu Biostatistics Ph.D. Member 09/2005-05/2010

31. Ping Liu Biostatistics Ph.D. Member 09/2009-08/2012

32. Sijin Wen Biostatistics Ph.D. Member 2005-05/09

33.Qing Zhang Biostatistics Ph.D. Member 2000-05/09

34. Hui Zhao Biostatistics Ph.D. Member 2003-05/2007

36. Yiqun Zhang Biostatistics Ph.D. Member 2004-2011

37. Liu, Xiaoming GSBS Ph.D. Member 09/2002-08/06

Assistant Professor, SPH

38. Mak, Solida GSBS Ph.D. Member 09/2003-06/08

39. Chung, Charles GSBS Ph.D. Member 09/2003-05/07

40. Dayna Tirpak GSBS Ph.D. Member 09/1998-12/02

41.Kun Zhang GSBS Ph.D. Member 09/1999-05/03

Associate Professor, University of California at San Diego

42. Alanna Morrison GSBS Ph.D. Member 09/1997-05/01

Professor, UTSPH

43. Zhongming Zhao GSBS Ph.D. Member 2000

Associate Professor, Vanderbilt University.

44. Andrei Rodin GSBS Ph.D. Member Fall, 1999

45. Grier P. Page GSBS Ph.D. Member Fall, 1998

Associate Professor, University of Alabama

46. Hong Yan Xu GSBS Ph.D. Member 2001-2003

Associate Professor, Georgia Medical College

47. Qiqing Wang GSBS Ph.D. Member 2001-2003

48. Xi Zhou GSBS Ph.D. Member 2001-2003

49. John C. Huber Jr. Biological Science Ph.D. Member 2000-2004

Associate Professor, Texas A&M University

**Primary MS thesis advisor**

1. Jin Yu Biostatistics M.S. Advisor 08/2013-Present

Thesis Title: Construct gene correlation network with NGS by cloud computing

2. Ruling Liu Biostatistics M.S. Advisor 08/2012-Present

3. Jialing Zhu Biostatistics M.S. Research Supervisor 01/2011-07/2014

Thesis Title: GIS mapping and gene-environment interaction.

4. Jin Li Biostatistics M.S. Advisor 11/2010-12/2012

5. Yang Han Biostatistics M.S. Advisor 08/2010-12/2012

Thesis Title: Identification of genes associated with quantitative traits involved in cardiovascular disease and lipoprotein metabolism.

6. Yue Liao Biostatistics MPHBST Advisor 09/2007-05/2009

Thesis Title: Genome-wide Gene-Gene Interaction Analysis for Cardiovascular Disease

Ph. D student in University of Southern California.

7. Yun Zhu Biostatistics M.S. Advisor 08/2010-12/2011

**MS students thesis committee**

1. Bing Yu Epidemiology M.S. Member 09/2009-08/2011

2. Henry Xingzhi Song Biostatistics M.S. Member 11/2010-08/2012

3. Leslie Rogers GSBS M.S. Member 2000

4.Yu-li Lin Biostatistics M.S. Member 10/2007-08/10

5. Fei Jiang Biostatistics M.S. Member 11/2008-05/10

6. Lihong Long Epidemiology M.S. Member 09/2007-08/2009

7. Kaiyan Jing Biostatistics M.S. Member 09/2007-04/09

8. Jiangong Niu Biostatistics M.S. Member 05/2010-04/2012

9. Yun Gong Biostatistics M.S. Member 05/2010-04/2012

10. Melissa Lee Epidemiology M.S. Member 05/2007-04/2009

11. Yong Quan Dong Biostatistics M.S. Member 2005-05/07

12. Xuemin Gu Biostatistics M.S. Member 08/2007-05/09

13. Yong Dong Biostatistics M.S. Member 09/2005-12/07

**MPH Advisor**

1. Amit Jain MPH Advisor

2. Vivekananda Varma Datla MPH Advisor

**MPH students committee**

1. Kala Yogesh Kamdar MSEPIM Member

2. Maximea Erasmea Vigilant MPHOCN Member

3. Shyam Mohan reddy Teegala MPHHLP Member

4. Erin Renee Steinkamp MPHHLP Member

5. Melissa Anne Lee MSEPIM Member

6. Jennifer Diane Torres MPHHLP Member

7. Shyam Mohan reddy Teegala MPHHLP Member

8. Carl Daniel Tapia MPHHSR Member

9. Sayed O Abdul-kadder MPHHPR Member

10. Jennifer M Bennett MPHHSO Member

11. Andrea Katherine Moore MPHHPR Member

12. Lupita Morgan MPHHPR Member

13. Edith N Napoleon MPHINF Member

14. Jane D Nguyen MPHHSO Member

15. Susan Renee Ninan MPHHSO Member

16. Karen Stewart Stephenson MPHHPR Member

17. Deepa Vasudevan MPHHPR Member

18. Ibrahima Gning*,*  MPHHSO Member

19. Robert Ryan HolmesMPHINF Member

20. Trial Punsalan MPHINF Member

21. Gulshan Ara Ralman MPHINF Member

22. Dea Michelle Taylo MPHINF Member

23. Rodrigo Erana MPHINF Member

24. Robert Bruce Warburton MPHINF Member

25. Julieana Nichols MPHCOM Member

26. Mary Ann Livoti MPHINF Member

27. Ann Nicole Knox MPHCOM Member

**SERVICE INFORMATION**

**PEER REVIEW ACTIVITIES**

**Grant Reviewer**

Estonian Research Council (2014)

Center for Scientific Review/NIH (ZRG1 AARR-G 02 M) (2014)

Clinical Neuroscience and Neurodegeneration (CNN) study section/NIH (2014)

The Research Grants Council (RGC) of Hong Kong (2014)

the Israel Science Foundation (ISF) (2013)

CNSF Grant Review (2013)

The Research Grants Council (RGC) of Hong Kong (2013)

Dutch NOW Innovational Research Incentives Scheme Grant Review (2013)

The Research Grants Council (RGC) of Hong Kong (2012)

CNSF Grant Review (2012)

NIH 201201 ZRG1 GGG M50 Review (2011)

NIH/CSR (2011)

NIH review - biostatistics - GWAS/epigenomics - ZRG1 GGG-M(50) (2011)

CNSF Grant Review (2011)

NIH/CSR, the Genomics and Computational Biology ZRG1 GGG-M(91)Special Emphasis Panel

( March 25 - 26, 2010)

NIH/CSR, Special Emphasis Panel/Scientific Review Group 2010/05 ZRG1 GGG-A (52) R

(01/15/2010-01/25/2010)

Medical Research Council (UK) (2010)

Baylor University (2010)

The Research Grants Council (RGC) of Hong Kong (2010)

Member of the CDC Grants for Public Health Research Dissertation, PAR07-231 (Panel C” Special Emphasis panel (2009)

The Research Grants Council (RGC) of Hong Kong (2009)

NIH/NIMH, Special Emphasis Panel/Scientific Review Group2008/08 ZMH1 ERB-S (06) S (2008)

(07/01/2008-07/01/2008)

NIH/NHLBI Grant Review, the RFA Special Emphasis Panel (ZHL1 CSR-W S1) (2008)

(06/20/2008-06/20/2008)

Grant Review for Florida Centers of Excellence (2008)

The Research Grants Council (RGC) of Hong Kong (2008)

NIH/NIAMS Grant Review (2007)

The Center for Complexity Science, Jerusalem, Israel (2007)

The Research Grants Council (RGC) of Hong Kong (2007)

National Office for Science and Technology, China (2007)

The Center for Complexity Science, Jerusalem, Israel (2006)

NSF Population and Evolutionary Processes Cluster (2005)

NSF BIO/Division of Biological Infrastructure (2005)

The Research Grants Council (RGC) of Hong Kong (2005)

U.K. Genomic Medicine Grant Review (2001)

NIH Tropical Medicine and Parasitology Study Section (2000)

National Science Foundation, China (2001)

**External Reviewer for Promotion**

University of Alabama at Birmingham

New Jersey Institute of Technology

Tulane University

University of Louisville

**Manuscript Reviewer**

Journals: American Journal of Human Genetics

Lancet

Nature

PNAS

Genome Research

Briefs in Bioinformatics

Biometrics

Mathematical Biosciences

Genetics

Genetic Epidemiology

Genetica

Molecular Biology and Evolution

Evolution

Journal of Computational Biology

Genome Biology

Biotechniques

Bioinformatics

Journal of Theoretical Biology

Human Heredity

Atherosclerosis

BMC Bioinformatics

BMC Medical Genetics

BMC Genetics

BMC Genomics

BMC Systems Biology

Statistical Applications in Genetics and Molecular Biology

Journal of Bioinformatics and Computational Biology

Plos One

Human Mutation

Acta Biochimica et Biophysica Sinica

Nucleic Acids Research

Current Genomics

International Journal of Rheumatic Diseases

Conferences: International Conference on Bioinformatics, 2005

Pacific Symposium on Biocomputing, 2006

Student Council: International Society for Computational Systems Biology

Guest Editor: Special Issue on the First International Conference on Computational

Systems Biology. IET Systems Biology. 2007

Guest Editor Special Issue on "Statistical Analysis of High-Dimensional Genetic Data

in Complex Traits, BioMed Research International, 2014

Leading Guest Editor: Special Issue on Next-Generation Sequencing. 2009-2010. Journal of

Biomedicine and Biotechnology

Editorial Advisory Board: (2007-2010) **Recent Patents in** **DNA and Gene Sequences**

Academic Editor: PLoS ONE

Academic Editor: ScienceJet

**Associate Editor: Recent Patents in** **DNA and Gene Sequences**

Board of Editors: Oriental Journal of Statistical Methods, Theory and Applications

**Associate Editor: IASTED/ACTA International Journal of Computational Bioscience**

Associate Editor: BioMed Research International

Associate Editor: Statistics and Its Interface

Editorial Board Member: Current Genomics

Editorial Board Member: Journal of Genetic Disorders & Disease Information (JGDDI)

Editorial Board Member: Journal of Biocomputing

Editorial Board Member: Cancer Medicine

Editorial Board Member: Statistical and Application

Editorial Board Member: International Journal of Statistics in Medical Research

Editorial Board Member: BioMed Research International

Editorial Board Member: Journal of Phylogenetics & Evolutionary Biology

Editorial Board Member: RV Journal of Information Technology and Applications

**CONSULTANT EXPERIENCE**

07/2008**-** Department of Mathematics, University of South Alabama

09/00- Division of Rheumatology, Medical School, University of Texas Health Science Center at Houston

09/99-12/07 Institute of Molecular Medicine for the Prevention of Human Diseases,

University of Texas Health Science at Houston

09/00-08/02 Department of Environmental Health, University of Cincinnati

11/00-12/07 Department of Epidemiology and Public Health, School of Medicine, Yale University

10/99-08/03 Department of Pathology, Medical School, University of Florida

09/00-08/02 Member of Scientific Advisory Board, Cangen International Corporation, California

**ACTIVITIES IN PROFESSIONAL/SCIENTIFIC SOCIETIES**

Member of Organizing Committee, International Conference on Transcriptomics, July 27-29, 2015, Orlando, Florida.

Member of Organizing Committee, The 3rd Genetics and Genomics Conference (GC 2014), December 26-28, 2014 in Suzhou, China.

Chair, Session on mixed effect models for longitudinal, functional, and spatial data, Joint Statistical Meeting-2014, August 2-7, 2014, Boston, MA, USA.

Organizing Committee Member for Genomics-2013, November 12-14, 2013 Chicago-North Shore, USA.

Program Committee. International Conference on Genetic Engineering & Genetically Modified Organisms. August 12-14, 2013, University, North Carolina, USA.

Chair, Session on missing data and data with measurement bias. ENAR, March 10-13, 2013 Spring Meeting - Orlando, Florida.

poster judge, ENAR, March 10-13, 2013 Spring Meeting - Orlando, Florida.

Chair, Statistical Genetics Session. International Conference and Exhibition on Biometrics

and Biostatistics. 5-7 March 2012

Program Committee. The 4th International Congress on Image and Signal Processing. 15-17 October 2011, Shanghai, China.

Program Committee. The 6th IASTED International Conference on Advances in Computer Science and Engineering. March 15 – 17, 2010, [Sharm El Sheikh, Egypt](http://www.iasted.org/conferences/location-egypt2010.html).

Program Committee Member , The 2nd International Conference on Image and Signal Processing (CISP'09), October 17-19, 2009, Tianjin, China.

Organizer, Topic Contributed Session: Application of Functional and Dynamic Data Analysis to Biomedical Research, The Joint Statistical Meetings (2009), Washington, DC, August 1-6, 2009.

Program Committee Member, The IASTED International Symposium on Computational Biology and Bioinformatics (~*CBB* 2008~), November 16-18, 2008 Orlando, Florida**,** USA.

Program Committee Member, The 10th International Conference on Molecular Systems Biology (ICMSB 2008), Feb 25-28, 2008, Diliman, Philippines.

Organizer, Session: Advances in Statistical and Population Genetics, and Computational Systems Biology. The 15th International Conference of Forum for Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, P.R. China, May 20-23, 2007.

Chair, Session 1: Biosystem and Structure, The IASTED International Conference on Computational Systems Biology. November 13-14, 2006, Dallas, Tx.

Chair, program Committee, The First International Conference on Computational Systems Biology, July 20-23, 2006, Shanghai, China.

Co-Chair, Local Organizing Committee, the First International Conference on Computational Systems Biology, July 20-23, 2006, Shanghai, China.

**Program Committee Member,** The Fourth **International Conference on Bioinformatics (BIOINFO 2005)**, September 22-24, 2005, Busan, Korea.

Best Paper Award Committee Member, The Fourth **International Conference on Bioinformatics (BIOINFO 2005)**, September 22-24, 2005, Busan, Korea.

Co-chair and organizer, Understand the Principle and Usefulness of Bioinformatics, The International Symposium on Genomic Medicine, June 28-30, 2005, Shanghai, China.

**EDUCATIONAL OR VOLUNTARY ORGANIZATION PARTICIPATION**

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (August 22-29, 2014, Shanghai, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (November 3-7, 2013, Xiamen, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (July 2011, Xiamen, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (July 21-25, 2009, Kun Ming, China).

Co-Organizer and Lecturer, National Workshop onLarge Scale Genotyping and Linkage Analysis (July, 1997, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics (January 3-8, 2005, China).

Lecturer, Workshop on Genome-wide association studies (July, 2006, Fudan University).

Director, the Theoretical Systems Biology Laboratory, School of Life Science, Fudan University, China (2004- ).

Adjunct Professor, Department of Genetics, Fudan University, Shanghai, China (2000- ).

Cai Guan Shen Lecture Professor, School of Life Science, Fudan University, Shanghai, China (2005- ).

Adjunct Professor, Department of Biochemistry, Peking Union Medical College & Chinese Academy of Medical Sciences, Beijing, China (99- ).

Adjunct Professor, Institute of Cancer Research, Chinese Academy of Medical Sciences, Beijing, China (99- )

Judge, 8th Annual Mini-Symposium, Program in Molecular and Human Genetics, Graduate School of Biomedical Science (2004).

Journal Club Organizer in Genetics (2000).

Interviewer for Graduate Student Candidate, Graduate School of Biomedical Sciences (2000- present).

**DEAPRTMENT/SCHOOL COMMITTEES AND ACTIVITIES**

IFC the Administrative Affairs Subcommittee (2014-Present)

IFC Faculty Status, Rights & Responsibilities Committee (2013)

GSBA, Biostatistics and Bioinformatics Admission Committee (2012-Present)

Admission Committee in Division of Biostatistics (2012-Present)

Big Data Analysis Faculty Search Committee (2013-Present)

Faculty Development Leave Committee (2012)

Burks Scholarship Selection Committee (2011-Present)

Faculty Council Representative in the SPH (2009-Present)

Inter Faculty Council (IFC) Representative (2010-Present)

Member of Curriculum Committee (2006- 2009)

Member of Bioinformatics Proposal Committee (2006-2009)

Member of Faculty Annual Report Evaluation Committee (2006)

Member of Biological Science Admissions Committee (2001-2004)

Member of Faculty Annual Report Evaluation Committee (2003)

Member in M. D. Anderson Genomics Program Steering Committee (1998-2001)

Member of Faculty Annual Report Evaluation Committee (1999)