

CURRICULUM VITAE
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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), Department of Biostatistics, School of Public Health,
Human Genetics Center, School of Public Health
Program in Genetics and Epigenetics
Program in Quantitative Sciences

Adjunct Member of Graduate Faculty at Texas A&M University

PROFESSIONAL EXPERIENCE

09/11-Present Professor (Tenured)
Department 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
Panzhuhua Steel Company, China

12/68-12/71 Assistant Engineer
Panzhuhua 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
 1992-1997 American Statistical Association
 2005- American Statistical Association
 1993-1997 American Society of Neural Networks

HONORS AND AWARDS

2015 The first place of poster award in the UT GSBS human and molecular genetics symposium.
 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
 2012 Winners 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
 Second Place Poster Award, University of Texas at Houston Annual Research Day, 2008
 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

Research Interests

Big data in genomics, epigenomics and imaging

Deep learning and causal inference
Bioinformatics

Google Scholar

	All	Since 2013
Citations	13100	8040
h-index	46	28
i10-index	108	72

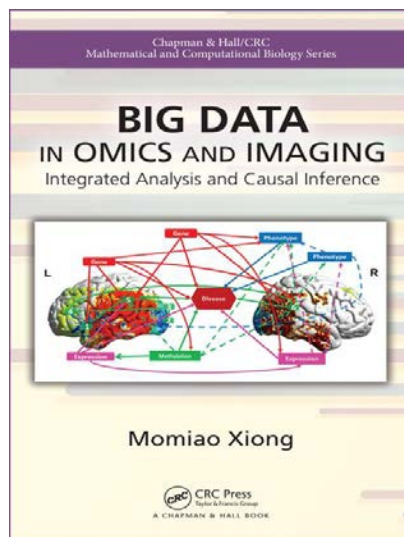
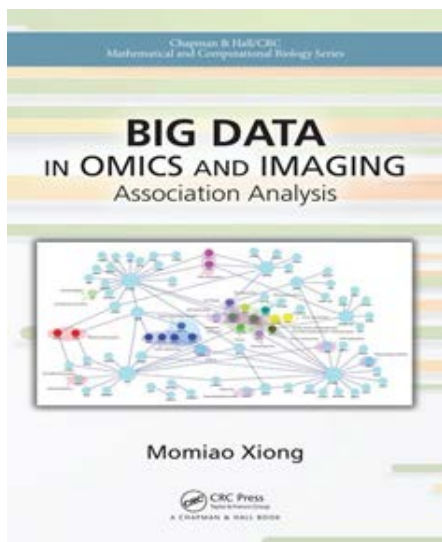
Research Gate Score: 44.41

Website: <https://sph.uth.edu/research/centers/hgc/xiong/>

Books

January 2018

June 2018



A. PREPRINTS

1. Ma L and Xiong MM. (2013). An Efficient Sufficient Dimension Reduction Method for Identifying Genetic Variants of Clinical Significance. [arXiv:1301.3528](https://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](https://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](https://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](https://arxiv.org/abs/1410.7363).
5. Zewdie G and Xiong MM. (2014). Fully Automated Myocardial Infarction Classification using Ordinary Differential Equations. [arXiv:1410.6984](https://arxiv.org/abs/1410.6984).

6. Li L and Xiong MM. (2014). A novel statistical method based on dynamic models for classification. *arXiv:1410.7029*.
7. Ma L, Lin N, Amos CI and Xiong MM. (2014). A General Statistic Framework for Genome-based Disease Risk Prediction. *arXiv:1410.7371*.
8. Li L and Xiong MM. (2014). Dynamic Model for RNA-seq Data Analysis. *arXiv:1412.1746*.
9. Zhang F, Xie D, Laing M and Xiong MM. (2015) Multivariate functional regression models for epistasis analysis. *arXiv:1512.00949*.
10. Wang P, Rahman M, Jin L, Xiong MM. (2015). A New Statistical Framework for Genetic Pleiotropic Analysis of High Dimensional Phenotype Data. *arXiv:1512.00947*.
11. Lin N, Zhu Y, Fan R and Xiong MM. (2016). A Quadratically Regularized Functional Canonical Correlation Analysis for Identifying the Global Structure of Pleiotropy with NGS Data. *arXiv:1609.04902*
12. Jiao R, Lin N, Hu Z, Bennett DA, Jin L, Xiong MM. (2018). Bivariate Causal Discovery and its Applications to Gene Expression and Imaging Data Analysis. *arXiv:1805.04164*.

B. PAPERS IN REFEREED JOURNALS

13. Chiu C, Yuan F, Zhang B, Yuan A, Li X, Fang HB, Lange K, Weeks DE, Wilson AF, Bailey-Wilson JE, Musolf AM, Stambolian D, Lakhal-Chaieb ML, Cook RJ, McMahon FJ, Amos CI, Xiong MM, Fan R. (2018). Linear Mixed Models for Association Analysis of Quantitative Traits with Next-generation Sequencing Data. *Genet Epi. In Press*.
14. Hu P, Jiao R, Jin L, Xiong MM. (2018). Application of Causal Inference to Genomic Analysis: Advances in Methodology. *Front Genet. 9:238*.
15. Jiao R, Lin N, Hu Z, Bennett DA, Jin L, Xiong MM. (2018). Bivariate Causal Discovery and its Applications to Gene Expression and Imaging Data Analysis. *Front Genet*.
16. Wang Y, Li Y, Qiao C, Liu X, Hao M, Shugart YY, Xiong M, Jin L. (2018). Nuclear Norm Clustering: a promising alternative method for clustering tasks. *Sci Rep. 8(1):10873*.
17. Wang Y, Li Y, Liu X, Pu W, Wang X, Wang J, Xiong MM, Shugart YY, Jin L. (2017). Bagging Nearest-Neighbor Prediction independence Test: an efficient method for nonlinear dependence of two continuous variables. *Scientific Report. 7(1):12736*.
18. Lin N, Zhu Y, Fan R and Xiong MM. (2017). A Quadratically Regularized Functional Canonical Correlation Analysis for Identifying the Global Structure of Pleiotropy with NGS Data. *PLOS Computational Biology. 2017 Oct 17;13(10):e1005788*.
19. Chiu CY, Jung J, Chen W, Weeks DE, Ren HB, Boehnke M, Amos CI, Liu AY, Mills JL, Lee MT, Xiong MM, and Fan R. (2017). Meta-analysis of Quantitative Pleiotropic Traits for Next-Generation Sequencing with Multivariate Functional Linear Models. *Eur J Human Genet. Eur J Hum Genet.25(3):350-359*.
20. Chiu CY, Jung J, Wang Y, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Mills JL, Boehnke M, Xiong M, Fan R. (2017). A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for next-generation sequencing. *Genet Epidemiol. 41(1):18-34*.
21. Xu K, Jin L, Xiong M. (2017). Functional regression method for whole genome eQTL epistasis analysis with sequencing data. *BMC Genomics. 18(1):385*.
22. Wang Y, Li Y, Pu W, Wen K, Shugart YY, Xiong M, Jin L. (2016). Random Bits Forest: a Strong Classifier/Regressor for Big Data. *Sci Rep. 2016 Jul 22;6:30086*.

23. Wang P, Rahman M, Jin L, Xiong MM. (2016). A New Statistical Framework for Genetic Pleiotropic Analysis of High Dimensional Phenotype Data. *BMC Genomics*. 17(1):881.
24. Wang Y, Li Y, Xiong MM, Shugart YY and Jin L. (2016). Random bits regression: a strong general predictor for big data. *Big Data Analytics*. (In Press).
25. Guo S, Li Y, Wang Y, Chu H, Chen Y, Liu Q, Guo G, Tu W, Wu W, Zou H, Yang L, Xiao R, Ma Y, Zhang F, Xiong MM, Jin L, Zhou X, Wang J. (2016). Copy Number Variation of HLA-DQA1 and APOBEC3A/3B Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *J Rheumatol*. 43(5):880-6.
26. Zhang F, Xie D, Liang M, Xiong M. (2016). Functional Regression Models for Epistasis Analysis of Multiple Quantitative Traits. *PLoS Genet*. 12(4):e1005965.
27. Zhao J, Zhu Y, Xiong MM. (2016). Genome-wide gene-gene interaction analysis for next-generation sequencing. *Eur J Hum Genet*. 2016 Mar;24(3):421-8
28. Fan R, Chiu C, Jung J, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Chen Z, Mills JL, and Xiong MM. (2016). A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. *Genet Epidemiol*. 2016 Jul 4. doi: 10.1002/gepi.21984. [Epub ahead of print].
29. Xu K, Guo W, Xiong MM, Zhu L, Jin L. (2016). An estimating equation approach to dimension reduction for longitudinal data. *Biometrika*. 103(1):189-203.
30. Fan R, Wang Y, Chiu CY, Chen W, Ren H, Li Y, Boehnke M, Amos CI, Moore JH, Xiong M. (2016). Meta-analysis of Complex Diseases at Gene Level with Generalized Functional Linear Models. *Genetics*. 202(2):457-70. PMID: 26715663. PMCID: PMC4788228.
31. Fan R, Wang Y, Yan Q, Ding Y, Weeks DE, Lu Z, Ren H, Cook RJ, Xiong MM, Swaroop A, Chew EY, and Chen W. (2016). Gene-based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. *Genet Epidemiol*.40(2):133-43. PMCID: PMC4724326.
32. Li L and Xiong MM. (2015). Dynamic Model for RNA-seq Data Analysis. *BioMed Research International*. *Biomed Res Int*. 2015:916352. PMCID: PMC4539434.
33. 1000 Genome Project Consortium. A global reference for human genetic variation. *Nature* (2015) 526(7571): 68-74.
34. Xiong MM. (2015). Causal Genomic and Epigenomic Network Analysis emerges as a New Generation of Genetic Studies of Complex Diseases. *J Phylogen Evolution Biol* 3, e113. PMCID: PMC4675141.
35. Wang Y, Li Y, Cao H, Xiong M, Shugart YY, Jin L. (2015). Efficient test for nonlinear dependence of two continuous variables. *BMC Bioinformatics*. 16(1):260. PMCID: PMC4539721
36. Lin N, Jiang J, Guo S, Xiong M. (2015). Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis. *PLoS One*. 10(7):e0132945. PMCID: PMC4510534
37. Jiang J, Lin N, Guo S, Chen J, Xiong M. (2015). Multiple functional linear model for association analysis of RNA-seq with imaging. *Quantitative Biology* 3, 90-102.
38. Zhao J, Zhu Y, Boerwinkle E, Xiong MM. (2015). Pathway analysis with next-generation sequencing data. *Eur J Hum Genet*. 23(4) 507-515. PMCID: PMC24986826
39. Fan R, Wang Y, Boehnke M, Chen W, Li Y, Ren H, Lobach I, Xiong M. (2015). Gene Level Meta-Analysis of Quantitative Traits by Functional Linear Models. *Genetics*. 200(4):1089-104. PMCID: PMC4574252.

40. Wang Y, Liu A, Mills JL, Boehnke M, Wilson AF, Bailey-Wilson JE, Xiong M, Wu CO, Fan R. (2015). Pleiotropy analysis of quantitative traits at gene level by multivariate functional linear models. *Genet Epidemiol.* 39(4):259-75. PMID: PMC4443751.
41. Park T, Van Steen K, Lou XY, Xiong M. (2015). Statistical Analysis of High-Dimensional Genetic Data in Complex Traits. *Biomed Res Int.* 2015:564273. PMID: PMC4539419.
42. Ma J, Chan W, Tsai C-L, Xiong MM and Tilley BC. (2015). Analysis of transtheoretical model of health behavioral changes in a nutrition intervention study-a continuous time Markov chain model with Bayesian approach. *Statistics in Medicine.* 34(27):3577-3589. PMID: PMC4626363.
43. Guo S, Yan F, Xu J, Bao Y, Zhu J, Wang X, Wu J, Li Y, Pu W, Liu Y, Jiang Z, Ma Y, Chen X, Xiong M, Jin L, Wang J. (2015). Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clin Epigenetics.* 7(1):3 PMID: PMC4318209.
44. Chiu CY, Jung J, Weeks D, Wilson AF, Bailey-Wilson J, Amos CI, Xiong MM. (2015). A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. *GENETIC EPIDEMIOLOGY* 39 (7), 539-539.
45. 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. PMC4281304
46. 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. PMC4101765
47. Zhang F, Boerwinkle E and Xiong MM. (2014). Epistasis Analysis for Quantitative Trait with Next-generation Sequencing Data. *Genome Research.* 24(6):989-98. PMID: PMC4032862.
48. Delaneau O., Marchini J., McVean G., Donnelly P., Lunter G., Marchini J., Myers S., Gupta-Hinch A., Iqbal Z., Mathieson I., Rimmer A., Xifara D., Kerasidou A., Churchhouse C., Altshuler D., Gabriel S., Lander E., Gupta N., Daly M., DePristo M., Banks E., Bhatia G., Carneiro M., Del Angel G., Genovese G., Handsaker R., Hartl C., McCarroll S., Nemes J., Poplin R., Schaffner S., Shakir K., Sabeti P., Grossman S., Tabrizi S., Tariyal R., Li H., Reich D., Durbin R., Hurler M., Balasubramaniam S., Burton J., Danecek P., Keane T., Kolb-Kokocinski A., McCarthy S., Stalker J., Quail M., Ayub Q., Chen Y., Coffey A., Colonna V., Huang N., Jostins L., Scally A., Walter K., Xue Y., Zhang Y., Blackburne B., Lindsay S., Ning Z., Frankish A., Harrow J., Chris T., Abecasis G., Kang H., Anderson P., Blackwell T., Busonero F., Fuchsberger C., Jun G., Maschio A., Porcu E., Sidore C., Tan A., Trost M., Bentley D., Grocock R. (2014). Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications.* 5(), . 10.1038/ncomms4934. PMID: PMC4338501.
49. 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
50. 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. PMID: PMC3632131.
51. 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
52. Xiong MM (2013). New Era for Health Care and Genomics. *J Phylogen Evolution Biol.* 1:e104.

53. 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. PMC3548254
54. **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
55. Liang F and **Xiong MM**. (2013). Bayesian detection of causal rare variants under posterior consistency. *PLoS ONE.* 8(7), e69633. PMC3724943.
56. Fan R, Zhang Y, Albert PS, Liu A, Wang Y, **Xiong MM**. (2012). Longitudinal Association Analysis of Quantitative Traits. *Genet Epidemiol.* 36: 856–869.
57. 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. PMID: PMC3498066 [Available on 2013/5/1]
58. Shugart YY, Zhu Y, Guo W, **Xiong MM** (2012) Weighted Pedigree-based Statistics for Testing the Association of Rare Variants. *BMC Genomics*, 13:667. PMID: PMC3827928.
59. 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. PMID: PMC3534768.
60. 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. PMID: PMC3532851.
61. 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.
62. 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.
63. 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. PMID: PMC3375640.
64. Zhu Y and **Xiong MM** (2012) Family-Based Association Studies for Next-Generation Sequencing. *Am J Human Genet.* 90(6):1028-1045. PMID: PMC3370281
65. 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 . PMID: PMC3499061.
66. 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. PMID: PMC3291503
67. *Siu H, Jin L and **Xiong MM** (2012) Manifold Learning for Human Population Structure Studies. *PLoS ONE*, 7: e29901. PMID: PMC3260176.
68. 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. PMID: PMC3548254.

69. *Siu H, Zhu Y, Jin L and Xiong MM. (2011) Implication of Next-Generation Sequencing on Association Studies. *BMC Genomics*, 12:322. PMID: PMC3148210
70. 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. PMID: PMC3384547.
71. 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. *PLoS One*. 2011;6(7):e22097. PMID: PMC3137625.
72. 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.
73. *Fang S, *Fang X, **Xiong MM**. (2011) Psoriasis prediction from genome-wide SNP profiles. *BMC Dermatol*. 11(1):1. PMID: PMC3022824.
74. Xiong M, Zhang H, Jin L, Ai J, Huang Z, Zhu G. (2011). Association of controlled ovarian hyperstimulation treatment with down-regulation of key regulators involved in embryonic implantation in mice. *J Huazhong Univ Sci Technolog Med Sci*. 31(4):535-42
75. *Luo L, Boerwinkle E and Xiong MM (2011) Association studies for next-generation sequencing. *Genome Research*, 21(7):1099-1108. PMID: PMC3129252
76. *Wu X, *Dong H, *Luo L, *Zhu Y, *Peng G, Reveille JD, **Xiong MM**. (2010) A novel statistic for genome-wide interaction analysis. *Plos Genetics*. 6 (9), e1001131. PMID: PMC2944798.
77. *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. *BMC Syst Biol*. 4(1):163. PMID: PMC3002314
78. *Dong H, *Siu H, *Luo L, *Fang X, Jin L, **Xiong MM**. (2010) Investigation of gene and microRNA expression in glioblastoma. *BMC Genomics*. 11 (Suppl 3): S16. PMID: PMC2999346
79. *Peng G, *Luo L, *Siu H, *Zhu Y, *Hu P, *Hong S, *Zhao J, Zhou X, Reveille JD, Jin L, Amos, CI, **Xiong MM**. (2010) Gene and pathway-based second wave analysis of genome-wide association studies. *Eur J Hum Genet*. 18:111-117. PMID: PMC2987176
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81. 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.
82. Xiong MM, Zhao Z, Arnold J, Yu F. (2010). Next-generation sequencing. *J Biomed Biotechnol*. 2010:370710.
83. 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. *Arthritis Rheum*. 60(12):3807-3814. PMID: PMC2829245
84. *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. *Pharmacogenet Genomics*. 19(4):310-8.
85. *Wu X, Jin L, **Xiong MM**. (2009) Mutual information for testing gene-environment interaction. *PLoS ONE*. 4(2):e4578. PMC2642626.
 86. Chu X, Dong C, Lei R, Sun L, Wang Z, Dong Y, Shen M, Wang Y, Wang B, Zhang K, Yang L, Li Y, Yuan W, Wang Y, Song H, Jin L, **Xiong MM**, Huang W. (2009) Polymorphisms in the interleukin 3 gene show strong association with susceptibility to Graves' disease in Chinese population. *Genes Immun*. 10:260-266.
 87. *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.
 88. *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.
 89. 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) Multifactor effects and evidence of potential interaction between complement factor H Y402H and LOC387715 A69S in age-related macular degeneration. *PLoS One*. 3(12):e3833. PMC2585793.
 90. *Dong H, Xiao Y, Wang W, Jin L, **Xiong MM**. (2008) Symmetry of metabolic network *JCSB* 1: 1-20.
 91. *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
 92. Xiao Y, MacArthur BD, Wang H, **Xiong MM**, Wang W. (2008) Network quotients: Structural skeletons of complex systems. *Physical Review E*. 78: 046102.
 93. 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.
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G. MANUSCRIPTS SUBMITTED FOR PUBLICATIONS

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9. Liu Y, Ge Q, Lin N, Peng W, Jiao R, Wu X, and Xiong MM. (2018). Deep feature selection and causal inference for Alzheimer's disease. Research Symposium on Alzheimer's Disease & Related Dementias. May 2, 2018. Houston Methodist Research Institute.
10. Xiong MM, Lin N, Hu Z, Jiao R, Calhoun VD. (2018). From association to causation: casual inference in imaging-genetic data analysis. ENAR 2018, March 25-28, Atlanta, GA.

11. Lin N, Wang P, Zhu Y, Zhao J, Calhoun VD, Xiong MM. (2018). Big Causal Network Analysis of Imaging and Genomic Data. ENAR 2018, March 25-28, Atlanta, GA.
12. Hu Z, Nan Lin N, Wang P, Zhu Y, Zhao J, Bennett DA, Jin L and Xiong MM. (2017). Integrated causal network analysis of genomic and epigenomic data. ASHG 2017, October 17-21, 2017, Orlando, Florida
13. Peng W, Lin N, Wu X, and Xiong MM. (2017). Gene-gene Interaction Tests for Genetic-Imaging Data Analysis. ASHG 2017, October 17-21, 2017, Orlando, Florida
14. Wang Y, Lin N and Xiong MM. (2017). A Novel Framework for Tumor Classification which Uses Sufficient Dimension Reduction for Feature Selection and Bayesian networks for Integrating CT Image and Epigenomic Data. ASHG 2017, October 17-21, 2017, Orlando, Florida.
15. Jiao R, Hu Z and Xiong MM.(2017). Novel Approach to Construction of Causal Gene Regulatory. ASHG 2017, October 17-21, 2017, Orlando, Florida. ASHG 2017, October 17-21, 2017, Orlando, Florida.
16. Fan R, Chiu C-Y, Sang T, Cook RJ, Ding Y, Chen W, Weeks DE, Lee M, Y. Chew EY, and Xiong MM. (2017). Gene-based pleiotropic analysis of multiple survival traits via functional regressions with applications to eye diseases.
17. Xiong MM, Hu Z, Lin N, Zhu Y, Wang P, Zhao JY, Bennett DA, Jin L. (2016). Deep learning in multi-level causal genomic-epigenomic network analysis and its application to Alzheimer's disease studies. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
18. Fang S, Luo L, Wang P, Lin N, Li D, and Xiong MM. (2016). Network-based sufficient dimension reduction and intelligent classifier for early detection of pancreatic cancer. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
19. Hu P, Lin N, Ma L and Xiong MM. (2016) Smart causal machine learner that combines CT image and RNA-seq markers for cancer diagnosis and precision medicine. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
20. Wang P, Lin N, Zhu Y and Xiong MM. (2016). Most powerful statistics for RNA-seq and image association analysis and its application to kidney cancer study. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
21. Hu Z, Guo S, Zhu Y, Wang P, Bennett DA, Jin L, Xiong MM. (2016). Novel integrated systems approach discovers cell specific genetic-transcriptomic-methylation networks and causal pathways underlying diseases. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
22. Xu K, Jin L, Xiong MM. (2016). Functional Regression Method for Whole Genome eQTL Epistasis Analysis with Sequencing Data. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
23. Hu Z, Wang P, Zhu Y, Zhao J, Jin L, Bennett DA and Xiong M (2016). A Novel Statistical Methods for Inferring Causal Expression – Phenotype Network. 66th annual meeting of The American Society of Human Genetics. October 18-22, 2016, Vancouver, Canada.
24. Xu K, Jin L and Xiong MM. (2016). Functional Regression Method for Whole Genome Epistatic eQTL Analysis with Sequencing Data. 66th annual meeting of The American Society of Human Genetics. October 18-22, 2016, Vancouver, Canada.

25. Xiong MM, Wang P, Lin N, Yun Zhu, Zhao J, Jin L, Bennett DA. (2016). Deep genomic analysis of complex diseases and its potential application to precision medicine. 66th annual meeting of The American Society of Human Genetics. October 18-22, 2016, Vancouver, Canada.
26. Xiong MM, Hu Z, Lin N, Wan P, Zhu Y, Jin L. (2016). Deep causal network analysis for precision medicine. WLSC2016, November 1-3, 2016, Beijing, China.
27. Ma L, Lin N, Amos CI and Xiong MM. (2016). A General statistic framework for genome based disease risk prediction. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
28. Lin N, Wang P, Zhu Y, Zhao J, Calhoun VD, Xiong MM. (2016). Integrative Large-scale Causal Network Analysis of Imaging and Genomic Data and Its Application in Schizophrenia Studies. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
29. Hu Z, Wan P, Zhu Y, Zhao J, Xiong MM. (2016). A novel causal methylation network approach to Alzheimer's disease. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
30. Fan R, Wang Y, Ding Y, Weeks DE, Chen W, Ren H, Cook RJ, Xiong MM, Swaroop A. (2016). Gene-based Association Analysis for Censored Traits via Fixed Effect Functional Regressions. ENAR-2016, March 6-9, Austin, TX.
31. Xiong MM. (2016). Big and deep genomic analysis of complex diseases and its potential application to precision medicine. 2016 Texas FreshAIR Big Data & Data Analytics conference. March 30-31, 2016, San Antonio, TX.
32. Hu Z, Wan P, Zhu Y, Zhao J, Xiong MM. (2016). Big causal methylation network analysis. 2016 Texas FreshAIR Big Data & Data Analytics conference. March 30-31, 2016, San Antonio, TX.
33. Lin N, Wang P, Zhu Y, Zhao J, Calhoun VD, Xiong MM. (2016). Big Causal Network Analysis of Imaging and Genomic Data. 2016 Texas FreshAIR Big Data & Data Analytics conference. March 30-31, 2016, San Antonio, TX.
34. Lee DY, Hanis C, Bell GI, Aguilar DA, Redline S, Below J and Xiong MM. (2015) Epistasis Analysis for temporal Quantitative Trait with both GWAS and Next-Generation Sequencing Data in Sleep Apnea. 2015 JSM, August 8-August 13, 2015, Seattle, WA.
35. Yang M, Wang P, Xiong MM. (2015). Large causal network analysis of transcriptional specialization in the brains of humans. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
36. Fan R, Chiu C, Wang Y, Jung J, Jiang Y, Chen W, Weeks D, Ren H, Amos C, Wilson A, Bailey-Wilson J, Xiong MM. (2015). Functional Regression Models for Gene-based Association Studies of Complex Traits. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
37. Zhang F, Xie D and Xiong MM. (2015). Multivariate functional regression models for epistasis analysis. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
38. Wang P, Chen X, Vladimirov VI, Zhu Y and Xiong MM. (2015). Causal Inference for Integrative Analysis of Genetic and micro RNA variation. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
39. Xiong MM, Wang P and Zhu Y. (2015). Causal gene-gene and gene-environment interaction network analysis- A new generation of genetic interaction studies. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.

40. Rahman M, Wang P, Jin L and Xiong MM. (2015). Sparse Functional Structural Equations for Causal Genotype-Phenotype Network Analysis with Next-Generation Sequencing Data. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
41. Zhu Y, Wang P, Zhao J and Xiong MM. (2015). Causal Genomic Network Analysis emerges as a New Generation of Genetic Studies of Complex Diseases. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
42. Lin N, Wan P, Zu Y, Luo L, Calhoun VD, Xiong MM. (2015). Integrative Causal Network Analysis of Imaging and Genetic Data in Schizophrenia Studies. 65th annual meeting of The American Society of Human Genetics. October 6-10, 2015. Baltimore, MD.
43. Xiong MM, Lin N, Yu J, Ma L, Jiang J, Wang P and Guo S. (2014). Neat-optimal whole genome reconstruction by a small set of genomic variants. 64th annual meeting of The American Society of Human Genetics. October 18-22, 2014, San Diego, California.
44. Lin N, Jiang J, Guo S, and Xiong MM. (2014). Sparse sufficient dimension reduction and matrix subset selection methods for big image data analysis in cancer. 64th annual meeting of The American Society of Human Genetics. October 18-22, 2014, San Diego, California.
45. Jiang J, Lin N, Luo L, Yu J, Calhoun VD, Gupta CN, Xiong MM. (2014). Multiple functional linear models and three dimensional functional principal component analysis for image-genetic data analysis in clouds. 64th annual meeting of The American Society of Human Genetics. October 18-22, 2014, San Diego, California.
46. Lee DY, Hanis C, Bell GI, Aguilar DA, Redline S, Below J and Xiong MM. (2014). Genetic studies of functional quantitative trait with both GWAS and next-generation sequencing data. 64th annual meeting of The American Society of Human Genetics. October 18-22, 2014, San Diego, California.
47. Wang P, Rahman M, Jin L and Xiong MM. (2014). Sparse structural equations for joint phenotype-genotype network analysis. 64th annual meeting of The American Society of Human Genetics. October 18-22, 2014, San Diego, California.
48. Lin N, Jiang J, Guan X, Yu X, Guo S and Xiong MM. (2014). A novel method for ultrasound image analysis. NCI-NIBIB Point of Care Technologies for Cancer Conference. January 8-10, 2014, Natcher Center, NIH campus- Building 45, Bethesda, Maryland.
49. Lin N, Jiang J, Guo S, Yu X, Ma L and Xiong MM. (2014). Classification Analysis of Big Image Data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.
50. Yu J, Lin N, Ma L, Guo S and Xiong MM. (2014). Cloud computing for joint big genetic, epigenetic and image data analysis. Keystone Symposia: Big Data in Biology, March 23—25, 2014. Fairmont San Francisco, San Francisco, California
51. Xiong MM, Zhu Y and Zhao JY. (2014). Gene-gene Interaction Analysis for Next-generation Sequencing. 2014 ENAR Spring Meeting. March 16-19, 2014, Baltimore Marriott Waterfront Hotel, Baltimore, Maryland.
52. Li L and Xiong MM. (2014). A Novel Statistical Method based on Dynamic Models for Classification. 2014 ENAR Spring Meeting. March 16-19, 2014, Baltimore Marriott Waterfront Hotel, Baltimore, Maryland.
53. Ma L, Chen M, Guo S and Xiong MM. (2013) RNA-seq for drug response prediction. for the GTEx Project Community Meeting. June 18, 2013. Boston.
54. 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.

55. Zhang, F, Boerwinkle E and Xiong MM. (2013). Epistasis analysis for quantitative trait with next-generation sequencing data (Platform). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
56. Lee D, Hanis C and Xiong MM. (2013) Functional Linear Model with both Functional Response and Functional Predictors for Genetic Studies of Temporal Quantitative Trait with both GWAS and Next-Generation Sequencing Data. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
57. Li L and Xiong MM. (2013) A Dynamic Model for Classification of Gene Regulation with RNA-seq Data. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
58. Ma L and Xiong MM. (2013) A General Statistic Framework for Identifying Genetic Variants of Clinical Significance. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
59. Lin N, Chen M and Xiong MM. (2013) A Novel General Framework for Imaging Genetics Analysis with Next-generation Sequencing Data. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
60. Zewdie G and Xiong MM. (2013) Genetic Dynamic Model for Temporal Quantitative Trait with both GWAS and Next-Generation Sequencing Data. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
61. Xiong MM, Chen M, Ma L and Guo S. (2013) A novel statistic method for drug response prediction with big RNA-seq data. 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts
62. Li L, Chen M and Xiong MM. (2013). A Novel Statistical Method based on dynamic models for classification. The 2013 SRCOS Summer Research Conference, June 2-5, 2013, Burns, TN.
63. Li L, Chen M and Xiong MM. (2013). A Dynamic Model for QRS Complex Classification. Computing in Cardiology. September 22-25, 2013. Zaragoza, Spain.
64. Ma L, Chen M, Li L and Xiong MM. (2013). Sufficient Dimension Reduction for Heartbeat Classification. Computing in Cardiology. September 22-25, 2013. Zaragoza, Spain.
65. Luo L and Xiong MM. (2012). Gene-gene co-association and pathway-based co-association studies for next-generation sequencing. 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
66. Wang P, Jin L and Xiong MM. (2012). Graphical Models and Intervention Calculus for Causal Inference of Genetic Epidemiology Studies. 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
67. Hu P, Boerwinkle E, Jin L and Xiong MM. (2012). Genome Profile-based Disease Risk Prediction. 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
68. Zhu Y, Zhao JY, Shugart Y and Xiong MM. (2012). A unified statistical framework to correct for unknown population stratification, family structure and cryptic relatedness in the sequence-based association studies. 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.
69. Hong S, Chen X, Jin L and Xiong MM. (2012). Common gene co-expression network analysis in Schizophrenia and bipolar disorder. . 62th annual meeting of The American Society of Human Genetics, Nov 6-10, 2012, San Francisco, California.

70. Xiong MM, Zhu Y and Luo L (2011) Two Novel Statistics for genome-wide association analysis designed for next-generation sequencing data. Gordon Research Conferences: Quantitative Genetics & Genomics. February 20-25, 2011, Galveston, TX.
71. Siu H, Jin L and Xiong MM (2011) Locally Linear Embedding (LLE) for Human Population Structure Studies. Gordon Research Conferences: Human Genetics & Genomics. July 17-22, 2011, Salve Regina University, Newport, RI.
72. Xiong MM and Ming Cao (2011) Manifold learning and causal inference in genome-wide integrated genetic and epigenetic analysis. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
73. Xia D, Zhu Y, Xiong MM, Chen X (2011). Genome-wide interaction analysis of Two independent schizophrenia studies. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
74. Zhu Y, Luo L and Xiong MM (2011). Quantitative trait analysis for next-generation sequencing. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
75. Luo L, Zhu Y, Kang H, Stidley CA, Boerwinkle E and Xiong MM (2011). Smoothed Functional Principal Component Analysis for Next-Generation Association Studies. International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
76. Chen S, Zhu Y and Xiong MM (2011). Smoothed functional principal component analysis identify 67 significantly associated genes in two independent schizophrenia GWA studies. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
77. Dong H, Jin L and Xiong MM (2011). Relative Impact of Genetic and Epigenetic Factors on Gene Expression in Tumor Tissue Samples. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
78. Hong S, Xiong MM and Chen X (2011). Co-expression network analysis of genome-wide RNA-seq in schizophrenia and bipolar samples. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
79. Yao Y, Zhu Y, Guo W and Xiong MM (2011). Developing weighted test statistics for testing association of rare variants using pairs of affected and unaffected individuals. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
80. Fan R, Zhong Z, Wang S, Zhang Y, Andrew A, Karagas M, Moore J, Chen S, Amos C, Xiong MM (2011). Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
81. Siu H, Jin L and Xiong MM (2011). Manifold learning for human genetics studies. 12th International Congress of Human Genetics. October 11-15, 2011, Montreal, Canada.
82. **Xiong MM**, Peng G. (2010) Genome-wide Pair-wise Co-selection Analysis and Co-selection Network Construction. Genomics of Common Diseases, October 6-9, 2010, Baylor College of Medicine, Houston, TX.
83. Luo, L, Zhu Y, **Xiong MM**. (2010) A novel genome-information content-based statistic for genome-wide gene-gene co-association analysis designed for next-generation sequencing data. Genomics of Common Diseases, October 6-9, 2010, Baylor College of Medicine, Houston, TX.
84. **Xiong MM**, Dong H, Hong S, Chen R, Jin L. (2010) Systems biology approach to genome-wide survival analysis of ovarian cancer. Genomics of Common Diseases, October 6-9, 2010, Baylor College of Medicine, Houston, TX.

85. Yu F, Siu H, Zhu Y, Bainbridge M, Gibbs RA, Jin L, **Xiong MM**. (2010) Implications of second generation sequencing technologies on genome-wide association studies. Genomics of Common Diseases, October 6-9, 2010, Baylor College of Medicine, Houston, TX.
86. **Xiong MM**, Luo L, Zhu Y. (2010) A novel genome-information content-based statistic for genome-wide gene-gene co-association analysis designed for next-generation sequencing data. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
87. Hong S, Dong H, Jin L, **Xiong MM**. (2010) Shared Functional Modules Detection in Ovarian Cancer. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
88. Hou Z, Siu H, Jin L and Xiong MM (2010) Allele frequency spectrum-based analysis suggest sequencing bias in pilot 1 data in 1000 Genomes Project. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
89. Siu H, Zhu Y, Bainbridge M, Gibbs R, Yu F, Jin L, **Xiong MM**. (2010) Implication of next-generation sequencing on association studies. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
90. Wu X, Dong H, Luo L, Zhu Y, Peng G, Reveille JD, **Xiong M**. (2010). A Novel Statistic for Genome-wide Interaction Analysis. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
91. Zhao J, Wu X, Zhu Y, **Xiong MM**. (2010) A Novel LD-based statistic for testing interaction between linked loci. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
92. Dong H, Luo L, Siu H, Hong S, Xiao Y, Wei P, Wheeler D, Jin L, Chen R, **Xiong MM**. (2010) Integrated Network Analysis of Genetic and Epigenetic factors in Glioblastoma. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
93. Luo L, Boerwinkle E, **Xiong MM** (2010) Association Studies for Next-Generation Sequencing. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
94. Peng G, Dong H, Siu H, Wang Y, **Xiong MM**. (2010) Genome-wide association studies of copy number variation in glioblastoma. 37th Texas Genetics Society Annual Meeting March 25-27, 2010, Houston.
95. Wang J, Wang X, Xu J, Bao Y, Dong H, Wang Y, Zhao Z, Ma Y, Xu Z, **Xiong MM**, Jin L. (2009) Abnormal expression of candidate genes and miRNAs and their association with lung carcinoma. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
96. Lai S, Zhou X, Luo L, **Xiong MM**. (2009) Genetics of Gene Expressions under Perturbation of Environments. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
97. Zhu Y, Peng G, Dong H, Zhou X, Ward M, Weisman M, Brown M, Reveille J, **Xiong MM**. (2009) Genome-wide Analysis of Gene-Gene Interaction. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
98. **Xiong MM**, Luo L, Peng G, Dong H, Wu X, Siu H, Zhu Y, Xiao Y, Zhou X, Amos C, Jin L, Reveille J. (2009) Comprehensive Genome-wide Association Studies of Psoriasis. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
99. Hu P, Siu H, Hou Z, Yu F, Fu Y, Jin L, **Xiong MM**. (2009) Detecting Natural Selection in

- the Human Genome from Pilot1 Data in the 1000 Genomes Project. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
100. Siu H, Dong H, Peng G, Wang Y, Chen R, **Xiong MM**. (2009) Genome-wide Association Analysis of Copy-Number Variation (CNV) in Glioblastoma. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 101. Dong H, Luo L, Siu H, Xiao Y, Hong S, Peng G, Fang X, Chen R, Wheeler D, Jin L, **Xiong MM**. (2009) Integrated Network Analysis of Genetic and Epigenetic factors in Glioblastoma. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 102. Fang S, Fang X, **Xiong MM**. (2009) Psoriasis prediction from genome-wide SNP profiles. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 103. Zhou X, Luo L, Guo X, Tan F, Arnett F, **Xiong MM**. (2009) Studies of Genetic and Phenotypic Variations under Environmental Stimulation. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 104. Liao Y, Dong H, Peng G, Zhu Y, **Xiong MM**. (2009) Genome-wide interaction analysis of coronary artery disease. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 105. Hou Z, Siu H, Hu P, Yu F, Fu Y, Jin L, **Xiong MM**. (2009) Difference in Estimators of Population Parameter between Data I and Data II in 1000 Genomes Project Pilot 1. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 106. Peng G, Luo L, Zhu Y, Dong H, Amos C, Xiong MM. (2009) Genome-wide Gene and Pathway Analysis. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 107. Luo L, Boerwinkle E, **Xiong MM**. (2009). Functional Principal Component Analysis for Testing Association of Full Spectrum of DNA Variation. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 108. Luo L, **Xiong MM**. (2009) Functional structural equation models for deciphering the path from genomic information to phenotypic variation. JSM 2009. Washington, DC. August 1-6, 2009.
 109. Luo L, Peng G, Boerwinkle E, **Xiong MM**. (2009) Genomics of complex diseases. ENAR 2009 Spring Meeting, San Antonio, Texas, March 15-18, 2009.
 110. Dong H, Fang X, Siu H, Luo L, Peng G, Zhu Y, Chen R, Wheeler D, **Xiong MM**. (2008) Comprehensive analysis of miRNA, mRNA, Methylation and genotype data. 58th annual meeting of The American Society of Human Genetics, Page 175, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 111. Xiao Y, Dong H, Wang W, Jin L, **Xiong MM**. (2008). Symmetry of metabolic network. 58th annual meeting of The American Society of Human Genetics, Page 179, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 112. Xion H, Luo L, Arnett F, Zhou X, **Xiong MM**. (2008) Continuous state-space model for genetic analysis of time-course gene expression data. 58th annual meeting of The American Society of Human Genetics, Page 291, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 113. Zhou X, Xiong H, Luo L, Arnett F, **Xiong MM**. (2008) Three Ways of genome-wide pathway analysis. 58th annual meeting of The American Society of Human Genetics, Page 295, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 114. Fang X, Luo L, Reveille J, **Xiong MM**. (2008) Structural equations as a general framework for modeling phenotype and genotype networks. 58th annual meeting of The American

- Society of Human Genetics, Page 301, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
115. Luo L, Peng G, Siu H, Zhu Y, Hu P, Hong S, Zhao J, Zhou X, Reveille, J, Amos C, Jin L, **Xiong MM**. (2008) Gene and pathway-based analysis: second wave of genome-wide association studies. 58th annual meeting of The American Society of Human Genetics, Page 303, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 116. **Xiong MM**, Luo L, Peng G, Zhu Y, Amos C. (2008) Genome-wide pathway analysis. 58th annual meeting of The American Society of Human Genetics, Page 304, Nov. 11-15, 2008, Philadelphia, Pennsylvania.
 117. **Xiong MM**, Luo L, Peng G. (2008) Information Geometry, Gene-Gene, Gene-Environment Interaction, and Pathway Association. 2008 Joint Statistical Meetings, Colorado, August 3-7, 2008.
 118. Luo L, Reveille J, **Xiong MM**. (2008) Functional genetic models for unraveling path from genomic information to complex phenotypes. 2008 Joint Statistical Meetings, Colorado, August 3-7, 2008.
 119. Luo L, Dong H, Peng G, Zhu Y, Fang X, **Xiong MM**. (2008) Network Approach to complex diseases. Genomics of Complex Disease, Boston, Sept 6-9. 2008.
 120. Wu X, Jin L, **Xiong MM**. (2007) Composite Measure of Linkage Disequilibrium for Testing Interaction between Unlinked Loci. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 121. Siu HC, Jin L, **Xiong MM**. (2007) Automatic biomedical articles clustering via information bottleneck method. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 122. Zhou QH, Wang D, **Xiong MM**. (2007) Application of nonlinear control theory to Dynamic Flux Balance Analysis of Metabolic Networks. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 123. Peng G, Wu X, Jin L, **Xiong MM**. (2007) Mutual information for detection of gene- gene interaction. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 124. Xiao YH, Dong H, Wang W, **Xiong MM**, Shi BL, Wu WT. (2007) Structure based Graph Distance Measures of High Degree of Precision. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 125. Dong H, Xiao YH, Wang W, **Xiong MM**, Shi BL, Wu WT. (2007) . Evolution of biological networks. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 126. Sun XD, Jin L, **Xiong MM**. (2007) State-Space models for genetic networks and extended Kalman Filter with constraints for parameter estimation. The 15th International Conference of Forum or Interdisciplinary Mathematics on Interdisciplinary Mathematical & Statistical Techniques, Shanghai, China, May 20-23, 2007.
 127. **Xiong MM**, Guo X, Xiong H, Arnett FC, Zhou XD. (2007) Differential Dynamic Properties of the TGFB Pathway between Normal Fibroblasts and Scleroderm Fibroblasts in Response to Perturbation by Environmental Stimuli. The 71st annual meeting of the American College of Rheumatology, Boston, Massachusetts, Nov 6-11, 2007.

128. Zhou XD, **Xiong MM**, Weisman MH, Inman RD, Khan MA, Schumacher HR, Martin TM, Rosenbaum JT, Maksymowych WP, Luo L, Diekman L, John RD. (2007) Genetic Studies Of The Interleukin-1A, CTGF, DRB1, DQA1, DQB1, DPB1, HLA-B And HLA A In Multiplex Ankylosing Spondylitis (as) Families. The 71st annual meeting of the American College of Rheumatology, Boston, Massachusetts, Nov 6-11, 2007.
129. **Xiong MM**, Reveille JD. (2007) Dynamic systems approach to complex diseases. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
130. Luo L, **Xiong MM**. (2007) Information Measure-based statistics and relative risk and odds ratio-based statistics for detection of gene-gene and gene-environment Interactions. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
131. Zhou XD, Xiong H, Alert F, **Xiong MM**. (2007) Dynamic Interaction between Gene and Environment. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
132. Sun XD, Jin L, **Xiong MM**. (2007) Two stage state-space models for genetic networks. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
133. Peng G, Jin L, **Xiong MM**. (2007) Multi-information and interaction information for testing total interaction and high-order interaction. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
134. Dong H, Xiao YH, Wang W, Jin L, **Xiong MM**. (2007) Evolution of metabolic networks. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
135. Wu X, Jin L, **Xiong MM**. (2007) Mutual information for testing gene-environment interaction. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
136. Zhou QH, Jin L, **Xiong MM**. (2007) Evolutions of dynamic metabolic networks. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
137. Siu HC, Jin L, **Xiong MM**. (2007) Information Bottleneck Method for Biomedical Paper Clustering. 57th annual meeting of The American Society of Human Genetics, Oct 23-27, 2007, San Diego, California.
138. Zhou XD, **Xiong MM**, Ward MM, Davis JC, Zhang G, Luo JC, Jin L, Weisman MH, Reveille JD. (2006) A genetic network involved in inflammatory reaction may contribute to disease susceptibility to ankylosing spondylitis. *Arthritis Rheuma* 54 (9).
139. Zhou XD, **Xiong MM**, Tan FK, Guo XJ, Arnett FC. (2006) SPARC, an upstream regulator of CTGF in response to TGF- β stimulation. *Arthritis Rheuma* 54 (9) 2006.
140. Peng G, Jin L, **Xiong MM**. (2006) Search for genetic interaction networks in genome wide association studies. *American Journal of Human Genetics*.
141. **Xiong MM**, Luo L. (2006) Multi Information for Testing Association of Gene-Gene Interaction Networks with Disease. *American Journal of Human Genetics*.
142. Dong H, Jin L, **Xiong MM**. (2006) Bayesian networks for modeling SNP markers. *American Journal of Human Genetics*.
143. Wu X, Jin L, **Xiong MM**. Test for interaction between two unlinked loci using Composite linkage disequilibrium. *American Journal of Human Genetics*.

144. Luo L, **Xiong MM**. (2006) Multi Information for Measuring Linkage Disequilibrium among Multiple Loci and its Applications. *American Journal of Human Genetics*.
145. Yang X, Yan P, Sun X, Jin L, **Xiong MM**, Zhou X, Lu D. (2006) Inferring TGF-B pathway using time series data. *American Journal of Human Genetics*.
146. Zhou Q, Jin L, **Xiong MM**. (2006) Energy Balance Analysis of Metabolic Networks. *American Journal of Human Genetics*.
147. Zhou X, **Xiong MM**. (2006) A novel statistic to test for gene-environment interaction. *American Journal of Human Genetics*.
148. Wang X, **Xiong MM**, Jin L. (2006) Haplotype inference error in association studies: two-locus model. *American Journal of Human Genetics*.
149. **Xiong MM**. (2005) Statistical methods for construction of genetic interaction networks. The Sixth International Conference on Systems Biology (ICSB 2005) P. 341. Boston, October 19 - 22, 2005.
150. Zhao JY, Jin L, **Xiong MM**. (2005) Nonlinear tests for genome-wide association studies. *American Journal of Human Genetics* 77: 434.
151. **Xiong MM**, Zhao JY, Amos C, Boerwinkle E. (2005) Nonlinear transmission/ disequilibrium test. *American Journal of Human Genetics* 77: 276.
152. Wang Y, He Y, Wang H, Xu L, Liu L, Liu Y, Sun W, Xiong X, Sun A, Ge J, **Xiong MM**, Jin L, Huang W. (2005) A systemic SNP survey of 123 candidate genes from important pathways for genetic susceptibility of coronary atherosclerosis in Chinese population. *American Journal of Human Genetics* 77: 322.
153. Zhou XD, Arnett F, **Xiong MM**. (2005) A Network Approach to Genetic Studies of Complex diseases. *American Journal of Human Genetics* 77:36.
154. Sun, XD, Jin L, Qian J, **Xiong MM**. (2005) State space methods for studying dynamic behavior of gene regulation. *American Journal of Human Genetics* 77: 208.
155. Shen Y, Jin L, **Xiong MM**. (2005) Modeling of dynamic genetic networks. *American Journal of Human Genetics* 77: 238.
156. Yu Z, Wang W, Jin L, **Xiong MM**. (2005) A Novel statistic for testing association of pathway with disease. *American Journal of Human Genetics* 77: 418.
157. Wang Y, Zhao JY, Zhou XD, Wang W, Jin L, **Xiong MM**. (2005) Identification of genetic interaction networks. *American Journal of Human Genetics* 77: 422.
158. Lin L, Fang X, **Xiong MM**. (2004) Nonlinear structural equations for reconstructing genetic networks. *American Journal of Human Genetics*. 75: 287.
159. Fang X, Jin L, **Xiong MM**. (2004) Subspace identification for genetic networks. *American Journal of Human Genetics*. 75: 289.
160. Li Y, Feng Q, **Xiong MM**, Zuo J, Meng F, Fang F. (2004) Proteomics analysis of L-6TG cell line constitutively expressed pantothenate kinase 4 (PANK4). *American Journal of Hum Genet*. 75: 393.
161. Sun M, **Xiong MM**. (2004) Longitudinal models for interactions between gene and time varying environments in qualitative traits. *American Journal of Human Genetics*. 75: 511.
162. **Xiong MM**, Zhao J, Boerwinkle E. (2004) Dynamic models for quantitative genetics. *American Journal of Human Genetics*. 75: 511.
163. Zhao J, **Xiong MM**. (2004) Global test for genome-wide association studies. *American Journal of Human Genetics*. 75: 511.
164. **Xiong MM**. (2004) Genetic network circuit and its application to genetic studies of complex diseases. 2004 Meeting on Systems Biology: Genomic Approaches to Transcriptional

- Regulation. p106. March 4 – March 7, Cold Spring Harbor Laboratory, New York.
165. Fan R, Knapp M, Zhao C, **Xiong MM**. (2003) High Resolution association studies of complex diseases using parents as controls. *American Journal of Human Genetics* 73: 609.
 166. Zhou X, Zhao J, Arnett FC, **Xiong MM**. (2003) Candidate pathway approach to genetic studies of complex traits. *American Journal of Human Genetics* 73:366.
 167. Sun M, **Xiong MM**. (2003) Multiple objective linear programming for metabolic networks. *American Journal of Human Genetics*. 73:420.
 168. **Xiong MM**, Zhao J. (2003) Genetic and transcriptional analysis of metabolic networks. *American Journal of Human Genetics*. 73: 422.
 169. Zhao J, **Xiong MM**. (2003) Genetic analysis of function-valued traits. *American Journal of Human Genetics* 73:604.
 170. **Xiong MM**. (2002) Modeling and identification of genetic networks. *American Journal of Human Genetics* 71: 390.
 171. Zhang K, Akey JM, Wang N, **Xiong MM**, Chakraborty R, Jin L. (2002) Randomly distributed recombination may generate block-like pattern of linkage disequilibrium: An act of genetic drift. *American Journal of Human Genetics* 71: 220.
 172. Sun M, **Xiong MM**. (2002) A mathematical programming approach for gene selection and tumor classification. *American Journal of Human Genetics* 71: 229.
 173. Sun H, Zhao J, Du W, Wang H, Zuo J, Qiang B, Shen Y, Yao Z, Huang W, Chen, Z, Luo H, **Xiong MM**, Fang F. (2002) SNP analysis of candidate genes associated with type 2 diabetes in Chinese Han population. *American Journal of Human Genetics* 71: 455.
 174. Zhao J, **Xiong MM**. (2002) Unbiased quantitative population association test. *American Journal of Human Genetics* 71: 568.
 175. Fan R, **Xiong MM**. (2002) Haplotype linkage disequilibrium mapping of quantitative trait loci. *American Journal of Human Genetics* 71: 572.
 176. 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.
 177. Fan R, Xiong MM. (2001) Combined linkage and association interval mapping of quantitative trait loci. *American Journal of Human Genetics*. 69: 1252.
 178. Fang X, Xiong MM. (2001) Meta-learning for combining multiple classifiers. *American Journal of Human Genetics*. 69:1552.
 179. Sun M, Xiong MM. (2001) A tabu search algorithm for gene selection in whole genome functional analysis. *American Journal of Human Genetics*. 69: 1671.
 180. Zhao J, Xiong MM. (2001) The generalized T2 test for biomarker identification using gene expression data. *American Journal of Human Genetics*. 69: 1572.
 181. 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.
 182. Fornage M, Markgraff C, Xiong MM, Boerwinkle E, Doris PA. (2001) Gene expression profiling and stroke susceptibility. *Hypertension* 38 (4): PE04.
 183. 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.
 184. 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.
 185. 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.
186. 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.
 187. Li W, Xiong MM. (2000) Computational Methods for Gene Expression Based Tumor Classification. *American Journal of Human Genetics*. 67: 78.
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 189. Akey JM, Jin L, Xiong MM. (2000) Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. *American Journal of Human Genetics*. 67: 227.
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 191. 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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 193. 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.
 194. Xiong MM, Jin L. (2000) Extent of linkage disequilibrium in human populations and their implications in SNP mapping. *Genetic Epidemiology*. 19: 277.
 195. Xiong MM, Zhao J, Jin L, Boerwinkle E. (2000) Multiple point linkage disequilibrium fine-scale mapping of quantitative trait locus. *Genetic Epidemiology*. 19: 277.
 196. Xiong MM, Zhao J, Amos C, Boerwinkle E. (2000) Physiological and statistical genetic models of epistasis. *Genetic Epidemiology*. 19: 278.
 197. 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.
 198. 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.
 199. 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.
 200. Xiong MM, Jin L. (1999) Admixture linkage disequilibrium mapping of quantitative trait loci. *American Journal of Human Genetics* 65, A86.
 201. 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.
 202. 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.
203. 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.
204. 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.
205. 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.
206. 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.
207. 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. Xiong MM, Jiao R, Kiu Y, Ge Q, Chen X and Jinying Zhao. (2018). Association or Causation. 4th International Conference on Big Data and Information Analytics, December 17-19, 2018, Houston, Texas
2. Xiong MM. (2018). Identify disease causing paths. The first international symposium on genomics and translation medicine. June 14-17, 2018, Suzhou, China.
3. Xiong MM, Lin N, Hu Z, Jiao R., Calhoun VD. (2018). From association to causation: casual inference in imaging-genetic data analysis. ENAR 2018, March 25-28, Atlanta, GA
4. Fan R, Jiang Y, Chiu C-Y; Xiong MM, Amos CI, Weeks D, Cook RJ, Lakhal-Chaieb M, Yan Q, Chen W, Gorin MB, Conley YP, Wilson AF, Bailey-Wilson J, Francis M. (2017). Gene-Based Association Testing of Dichotomous Traits with Generalized Functional Linear Mixed Models Using Extended Pedigrees. JSM 2017, July 29-August 3, 2017. Baltimore.
5. Hu Z, Lin N, Jiao R, Wang P, Zhu Y, Zhao J, Bennett DA, Jin L and Xiong MM. (2017). Causal network analysis of big genomi, epigenomic and imaging data. Conference on Big Data and Information Analytics", September 18 - 22, 2017, the Fields Institute in Toronto, Ontario, Canada.
6. Xiong MM, Hu Z, Lin N, Zhu Y, Wang P, Zhao JY, Bennett DA, Jin L. (2016). Deep learning in multi-level causal genomic-epigenomic network analysis and its application to Alzheimer's disease studies. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
7. Fang S, Luo L, Wang P, Lin N, Li D, and Xiong MM. (2016). Network-based sufficient dimension reduction and intelligent classifier for early detection of pancreatic cancer. The

- 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
8. Hu P, Lin N, Ma L and Xiong MM. (2016). Smart causal machine learner that combines CT image and RNA-seq markers for cancer diagnosis and precision medicine. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
 9. Wang P, Lin N, Zhu Y and Xiong MM. (2016). Most powerful statistics for RNA-seq and image association analysis and its application to kidney cancer study. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
 10. Hu Z, Guo S, Zhu Y, Wang P, Bennett DA, Jin L, Xiong MM. (2016). Novel integrated systems approach discovers cell specific genetic-transcriptomic-methylation networks and causal pathways underlying diseases. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
 11. Xu K, Jin L, Xiong MM. (2016). Functional Regression Method for Whole Genome eQTL Epistasis Analysis with Sequencing Data. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.
 12. Integrative image and RNA-seq data analysis. Transcriptomics-2015. Orlando, FL, July 27-29, 2015.
 13. Gene-gene interaction analysis for next-generation sequencing. ENAR, March 16-19, 2014, Baltimore, Maryland.
 14. Topic contributed: Jiang J, Lin N and Xiong MM. (2014). Image RNA-seq data analysis in clouds. 2014 JSM, Boston, MA.
 15. 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.
 16. Classification analysis of big image data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.
 17. QTL and Gene-gene Interaction Analysis for Next-generation Sequencing, ENAR, March 10-13, 2013 Spring Meeting - Orlando, Florida.
 18. Alternative Direction Minimization Methods for Phenotype Prediction and variable Selection. Biometrics-2013, June 10-12, Chicago.
 19. (Keynote Speaker) International Conference and Exhibition on Biometrics and Biostatistics 5-7 March 2012, Omaha.
 20. Genetic and Epigenetic Analysis for Next-Generation Sequencing. March 22, 2012, Department of Epidemiology, MD Anderson Cancer Center.
 21. Genetic Studies of Complex Diseases in the Sequence Era. October 5, 2012. Department of Statistics, Texas A&M University.
 22. Statistical Challenges Arising from Next-generation Sequencing. December, 14, 2011, Department of Bioinformatics and Computational Biology, Anderson Cancer Center.
 23. Association studies for next-generation sequencing. May 30, 2011, National Institute of Mental Health.
 24. Mathematical challenges in data analysis raised by next-generation sequencing. School of Mathematics Science, Fudan University, China, November 2, 2011.
 25. Data analysis for next-generation sequencing. School of Finance and Statistics, East China Normal University, November 4, 2011.

26. Gene and pathway-based association studies. China-UK Statistical Genetics, Population Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
27. Implication of next-generation sequencing on association studies. China-UK Statistical Genetics, Population Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
28. Integrated genetic and epigenetic analysis in cancer studies. The Second International Conference on Statistical Genetics and Systems Biology, Kunming, China, July 22-25, 2009.
29. Dynamic Pathway Analysis, The First International Conference on Statistical Genetics and Systems Biology, Qingdao, China, June 14-16, 2007.
30. State Space Equations for Modeling Gene Networks. The First International Conference on Computational Systems Biology. Shanghai, July 20-23, 2006
31. Genetic interaction networks and regulatory networks for genetic studies of complex diseases. Computational Biology 2005 – Challenges and Visions. Shanghai, October 13-16.
32. Nonlinear approach to dissecting genetic structure of complex diseases, The International Symposium on Genomic Medicine, June 28-30, 2005. Shanghai, China.
33. A Systems Biology Approach to Genetic Studies of Complex Diseases, March 2, 2004, Yale University.
34. An example of application of bioinformatics to systems biology, Eastern Forum of Science and Technology. July 11-12, 2004, Shanghai, China.
35. Network Biology, July 18, 2004, Shanghai Second Medical University, China.
36. Differentially expressed genetic networks, the 7th World Multiconference on Systemics, Cybernetics and Informatics, July 27-30, 2003, Orlando, Florida.
37. Perspective in Systems Biology, December, 24, 2003, Fudan University, Shanghai, China.
38. Large-scale gene expression data analysis and disease diagnosis, August 26-27, 2002. International Biopharmaceutical Technology Conference, Fujian, China.
39. Gene expression-based tumor classification, December 22, 2002, Department of Statistics, Beijing University, China.
40. Bioinformatics and genomic science research, December, 19, 2001, National Genomic Center at Shanghai, China.
41. Generalized T^2 test for whole genome linkage disequilibrium profile analysis, May 23-26, 2001, International conference for mapping complex disease genes, Changsha, China.
42. Biomarker Identification by feature selection. May 21, 2001, Institute of System Science and Mathematics, Chinese Academy of Science, Beijing.
43. Advances in Bioinformatics, May 27, 2001, Department of Genetics, Fudan University, China.
44. Cancer functional genomic analysis, May 30, 2001, Zhejiang University, Hangzhou, China
45. Mapping complex trait loci. Feb. 3, 2000, Workshop at NIH.
46. Neural networks for gene expression based tumor classification, Feb. 21, 2000, Division of Biostatistics, Saint Louis Washington University, Saint Louis, Missouri.
47. 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.
48. Gene selection in gene expression based tumor classification, April 23, 2000, Department of Computer Science, University of South West Louisiana.
49. Linkage disequilibrium mapping for complex disease, May, 2000, National Institute of Dental and Craniofacial Research Genetics Work Group.

50. Microarray and tumor classification, June 29, 2000, Darlian Institute of Chemistry, Darlian, China.
51. Combined linkage and linkage disequilibrium, July 4, 2000, Department of Statistics Beijing University, China.
52. Microarray and tumor diagnosis, July 5, 2000, Beijing General Hospital, Beijing, China.
53. Genomic circuits and cardiac diseases, July 6, 2000, Chinese Academy of Medical Science, Beijing, China.
54. Pathway identification, July 10, 2000, Chinese Institute of Biochemistry, Shanghai, China.
55. Statistical and computational methods for gene expression based tumor classification, Jan. 9, 2000, Department of Mathematics, University of Southern California, Los Angeles.
56. Linkage and linkage disequilibrium analysis for genetic studies of complex diseases, April, 1999, Chinese Academy of Medical Science, Beijing, China.
57. Advances in cancer genomics, April, 1999, Beijing Institute of Cancer, Beijing, China.
58. Advances in plant genetics, April, 1999, Institute of Plant, Chinese Academy of Science, Beijing, China.
59. Functional genomics in plant science, August, 1999, Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China.
60. Linkage disequilibrium based regression methods for mapping quantitative trait loci, August, 1999, Institute of Genetics, Fudan University, China.
61. Statistical analysis of mapping quantitative trait loci, February, 1997, Department of Statistics, Columbia University, New York.
62. Linkage disequilibrium for fine scale mapping, March, 1997, Department of Biology, Georgia Tech, Atlanta, Georgia.
63. Fine-scale mapping: theory and application, September, 1996, McGill University, Canada.
64. Fine-scale mapping of quantitative trait loci, September, 1996, University of Montreal, Canada.
65. Strategy for mapping complex trait loci, July, 1996, Sequana Therapeutics, Inc., La Jolla, California.

Presentations

1. Lin N, Wang P, Zhu Y, Zhao J, Calhoun VD, Xiong MM. (2018). Big Causal Network Analysis of Imaging and Genomic Data. ENAR 2018, March 25-28, Atlanta, GA.
2. Lin N, Hu Z, Jiao R, Luo L, Calhoun DV and Xiong MM. (2017). Casual inference in imaging-genetic data analysis. ASHG 2017, October 17-21, 2017, Orlando, Florida
3. Lin N and Xiong MM. (2017). Sparse Dynamic Bayesian Network and its Application to Longitudinal Genetic-Imaging Data Analysis. Rice Data Science Conference, 9-10, 2017, Houston, Texas.
4. Jiao R, Hu Z, Xiong MM. (2017). Causal Inference Models for Large-Scale Gene Regulatory Network Analysis. Rice Data Science Conference, 9-10, 2017, Houston, Texas.
5. Xiong MM. (2016). Wearable Computing for Fully Automated Myocardial Infarction Classification. 8th International Conference on Bioinformatics and Computational Biology (BICoB). April 4-6, Las Vegas, Nevada, USA.
6. Ma L, Lin N, Amos CI and Xiong MM. (2016). A General statistic framework for genome based disease risk prediction. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
7. Lin N, Wang P, Zhu Y, Zhao J, Calhoun VD, Xiong MM. (2016). Integrative Large-scale

- Causal Network Analysis of Imaging and Genomic Data and Its Application in Schizophrenia Studies. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
8. Hu Z, Wan P, Zhu Y, Zhao J, Xiong MM. (2016). A novel causal methylation network approach to Alzheimer's disease. Translational Genomics. Feb 28-March 2, 2016, Houston, TX.
 9. Lee DY, Hanis C, Bell GI, Aguilar DA, Redline S, Below J and Xiong MM. (2015). Genetic studies of physiological traits with their application to sleep apnea. 2015 JSM, Seattle, August 8-13, 2015.
 10. Lin Nan, Wang P, Zhu Y and Xiong MM. (2015). Structure Equation Models and Integer Programming for Joint Imaging and Genomic Data analysis and its Application to Kidney Renal Clear Cell Carcinoma
 11. 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.
 12. 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.
 13. Li L and Xiong MM. (2014). An Ordinary Differential Equation Model for Gene Regulation with RNA-seq Data. 2014 JSM, Boston, MA.
 14. Zhang, F, Boerwinkle E and Xiong MM. (2013). Epistasis analysis for quantitative trait with next-generation sequencing data (Platform). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
 15. Zhao J, Zhu Y and Xiong MM. (2013) Gene-gene interaction analysis for next-generation sequencing (Platform). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.
 16. Family-based association studies for next generation sequencing. 30 Years of Computational Biology at USC. March 30-April 1, 2012. Los Angeles, California.
 17. 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.
 18. 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.
 19. 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.
 20. Population structure analysis for next-generation sequencing. 2011 IEEE World Congress on Engineering and Technology. Shanghai, China. October 28-November 2, 2011,
 21. A novel genome continuum model for sequence-based association studies. 2010 Joint Statistical Meetings, July 31-August 5, 2010, Vancouver, Canada.
 22. Association Studies for Next-Generation Sequencing. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.
 23. 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.
 24. 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.
25. Genome-wide Gene and Pathway Analysis. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 26. Genome-wide interaction analysis of coronary artery disease. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.
 27. Information Geometry, Gene-Gene, Gene-Environment Interaction, and Pathway Association. 2008 Joint Statistical Meetings, Colorado, August 3-7, 2008.
 28. 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.
 29. 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.
 30. Do Genetic Networks Obey Kirchoff's and Ohm's Laws? The IASTED International Conference on Computational Systems Biology. November 13-14, 2006, Dallas.
 31. Genetic Interaction Networks in Association Studies of Complex Diseases. The 2006 Joint Statistical Meeting, August 6-10, Seattle, Washington.
 32. State-space approach to modeling dynamics of gene regulation in networks. 2005 International Conference on Bioinformatics. September 22-24, Busan, Korea.
 33. Nonlinear Tests for Categorical Data. ENAR, Austin Texas, March 20-23, 2005.
 34. Systems Biology Approaches to Genetic Studies of Complex Diseases. Pathway analysis for Target and Compound Evaluation. San Francisco, CA, April 20-22, 2005.
 35. Generalized Circuit Analysis of Biological Networks. 2004 International Conference on Complex Systems, Boston, May 16-21, 2004.
 36. Statistical model for function valued traits. Genetic Analysis of Complex Diseases & Human Population, September, 19-21, 2003, Chicago, Illinois.
 37. Modeling and identification of genetic networks. ASHG 52th Annual Meeting, Baltimore, 2002.
 38. Randomly distributed recombination may generate block-like pattern of linkage disequilibrium: An act of genetic drift. ASHG 52th Annual Meeting, Baltimore, 2002.
 39. Differentially regulated genetic networks. 2002 NCCR Bioinformatics Conference. September 27-29, 2002. Boston.
 40. The effect of ascertainment bias on estimates of linkage disequilibrium. ASHG 51th Annual Meeting, San Diego, 2001.
 41. Dynamic models for mapping quantitative trait with time-dependent genetic effect. ASHG 51th Annual Meeting, San Diego, 2001.
 42. Structural equation models for pathway identification. Oncogenomics Conference. January 25-27, 2001, Tucson, Arizona.
 43. Population genomic models and their applications to genetic studies of complex traits. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Georgia.
 44. Linkage and association studies of QTL for nuclear families by mixed models. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Georgia.
 45. Multiple trait-locus model for quantitative trait analysis, 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
 46. Linkage disequilibrium mapping of quantitative trait loci: multiple trait analysis, 27th Annual

- Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
47. 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.
 48. The haplotype disequilibrium test for genome-wide screen: Its power and study design. an. 2000. Pacific Symposium of Biocomputing 2000. Maui, Hawaii.
 49. Fine-Scale Mapping of Quantitative Traits Loci by Interval Mapping in Human Population. At ASHG 50th Annual Meeting, Philadelphia, Oct.3-7, 2000.
 50. Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. ASHG 50th Annual Meeting, Philadelphia, Oct. 3-7, 2000.
 51. 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.
 52. Gene expression in myositis biopsies. 64th Annual Scientific Meeting of Rheumatology, October 29 - November 2, Philadelphia.
 53. Gene expression profile of muscle biopsies from patients with inflammatory myopathies. 64th Annual Scientific Meeting of Rheumatology, October 29-November 2, Philadelphia.
 54. 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.
 55. Gene expression based tumor classification, IBC's 6th Annual Biochip Technologies Conference, 1999, Nov. 2-5, Berkeley, CA.
 56. 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.
 57. Mapping QTL by linkage disequilibrium. Joint Statistical Meetings, August 9-13, 1998, Dallas, Texas.
 58. 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.
 59. 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.
 60. Modeling the population dynamics of simple sequence repeats. 46th Annual Meeting of the American Society of Human Genetics, 1995.
 61. Neural Networks with Hidden Markov Processes. Artificial Neural Networks in Engineering Conference, Nov. 13-16, 1994, St. Louis.
 62. Weighted neural network models for nonlinear regression with fixed and random effects. World Congress on Neural Networks, June 5-9, 1994, San Diego.
 63. An $O(n^3)$ Neural Network Model for Linear Programming. World Congress on Neural Networks, Portland, July 11-15, 1993.
 64. 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.
 65. 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.
 66. Learning potential functions and differential inclusion. Proceedings of IJCNN '92, Baltimore,

June 7-11, 1992.

ACTIVE GRANTS

Investigator (5%) #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

PENDING GRANTS

Investigator The Serum Metabolome and Successful Aging
NIH
Total Cost: \$2,602,477.00
04/01/2019 - 03/31/2023

Co-PI Dissecting tumor-immune cell interactions in melanoma
Progression
CPRIT
Total cost: \$142,265.00
03/01/2019 - 02/28/2022

SUBMITTED, BUT NOT FUNDED

Principal Investigator (60%) R35GM127039
Deep learning and causative inference in heterogeneous populations
Total Cost: \$3,077,680.00
05/01/2018 - 04/30/2023

Investigator (5%) Metabolomic Predictors of Heart Failure in a Biracial Population
NIH
Total Cost: \$2,453,453
07/01/2017 - 06/30/2021

Investigator (5%) Metabolic Signatures Underlying Cardiac Function for Heart Failure in Multi-Ethnic Populations
NIH
Total Cost: 3,129,802
04/01/2018 - 03/31/2022

Principal Investigator (40%) Deep Genetic Analysis of Complex Disease
Templeton FOUNDATION
Total Cost: \$567,129.00

Principal Investigator (40%) 01/01/2017 - 12/31/2019
 Deep causal network analysis for precision medicine
 NIH
 Total Cost: \$1,302,938.00

Investigator (15%) 04/01/2017 - 03/31/2020
 Multi-ethnic Pleiotropic Gene Mapping for Alcohol and Nicotine
 Co-addiction
 NIH
 04/01/2017 - 03/31/2021

Principal Investigator (30%) 1R01CA206141-01
 Combined Image and Biomarker Approach to Early Detection of
 Pancreatic Cancer
 NCI
 Total Costs: \$3,595,210.00
 04/01/2016 - 03/31/2021

Principal Investigator (40%) Deep Genetic Analysis of Complex Disease
 Templeton FOUNDATION
 Total Cost: \$567,129.00
 01/01/2017 - 12/31/2019

Principal Investigator (40%) Deep causal network analysis for precision medicine
 NIH
 Total Cost: \$1,302,938.00
 04/01/2017 - 03/31/2020

Investigator (15%) Multi-ethnic Pleiotropic Gene Mapping for Alcohol and Nicotine Co-
 addiction
 NIH
 04/01/2017 - 03/31/2021

Principal Investigator (40%) 1R01MH109884-01
 Causal Psychiatric Networks for Integrative Genomics,
 Epigenomics, Transcriptomic, Imaging and Phenotype Data
 Analysis
 NIH
 Total Costs: \$3,157,631.00
 03/01/2016 - 02/28/2021

Principal Investigator (30%)
 Causal Networks for Integrative Genomics, Transcriptomes',
 Imaging and Phenotype Data Analysis
 NIH
 Total Costs: \$1,104,048.00
 09/01/2015 - 08/31/2018

Principal Investigator (40%)
 Gene-gene and Gene-environment Interaction Analysis of Multiple
 Complex Traits
 NIH
 Total Costs: \$1,572,640.00

01/01/2016 - 12/31/2020

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

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

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

Principal Investigator (30%) 5R01HL106034-02 (0008215)
Statistical Methods for Finding Missing Heritability
NHLBI
Total Costs: \$ 1,582,967
1/10/2011 - 12/31-2014

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 (5%)	<p>2 U54 HG003273-09 The Human Genome Sequencing Center NIH Total Costs: \$1,249,377 11/01/2011-10/31/2015</p>
Co-Investigator (15%)	<p>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</p>
Principal Investigator (30%):	<p>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</p>
Principal Investigator (25%)	<p>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</p>
Co-Investigator (15%)	<p>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</p>
Co-Investigator (5%)	<p>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</p>
Co-Investigator (5%)	<p>PR064803 Department of Defense The Integrative Studies of Genetic and Environmental factors in Systemic Sclerosis</p>

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 Pharmacogenomics
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

2016

Spring Individual Studies in Biostatistics, PH 1999-110 (1)
Dissertation Research, PH9999-413 (1)
Thesis Research, PH 9998-304 (1)
Summer Data Science 2
Fall Introduction to Genomics and Bioinformatics, PH1980L, GS110032 (Course
organizer and Lead Instructor)
Statistical Genetics, PH1986L, GS110072 (Lecturer).
Dissertation Research, PH9999-413 (2)
Thesis Research, PH 9998-304 (1)

2015 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 (1)
Dissertation Research, PH9999-413 (1)

Spring Population Genetics, PH1984L, GS110042 (Lecturer)

Individual Studies in Biostatistics, PH 1999-110 (4)
Dissertation Research, PH9999-413 (1)
Thesis Research, PH 9998-304 (4)

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

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-150 (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 and GS110053 (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 and GS110053 (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

2008 Spring

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 and GS110053 (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 and GS110053 (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 and GS110053 (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 SUPERVIGraduate School of Biomedical Sciences (GSBS) and School of Public Health

Postdoctoral Fellow

1. Hong Zhang	08/2015-08/2016
2. Azam Yazdani	04/2013-05/2014

3. Futao Zhang, Lecturer, Dept of Computer Science, Hohai University 08/2012-12/2013
4. Dan Xie, Associate Professor, Hubei University of Chinese Medicine 04/2011-05/2012
5. Xuesen Wu 12/2009-06/30/2010
Professor, Char of Department of Public Health, Bengbu Medical College at Bengbu
6. Xiangzhong Fang, Professor, Chair of Dept of Biostatistics, Beijing University, China
01/2008-07/2008
01/2000-01/2001
7. Winston Wa Shing Lau 07/2007-10/2007
8. Jinying Zhao 05/2005- 12/2005
Professor, Department of Epidemiology, Tulane University
9. Jun Li 01/2001-01/2003

Research Fellow

1. Wen-jia Peng 07/2017-Present
2. QiyangGe 09/2017-Present
3. Zhouxuan Li 03/2018-Present
3. Zixing Hu 10/2015-06/2017
4. Jingqi Zhou 11/2015-03/2016
5. Panpan Wang 09/2013-12/2015
6. Shicheng Guo 01/2013-03/2015
Postdoctoral Fellow, University of California at San Diego
7. Keling Xu 08/2014-08/2015
8. Minyi Chen 04/2012-06/2013
9. Yan Cui 05/2011-12/2012
10. Yun Zhu 12/2009-08/2011
Ph. D., Department of Epidemiology, Tulane University
11. Shengjun Hong 09/2010-08/2012
Postdoctoral Fellow, CAS-MPG Partner Institute for Computational Biology
12. Pengfei Hu 09/2009-08/2011
Research Associate, School of Life Science, Fudan University, China
13. Hoicheong Siu 01/2010-01/2012
Postdoctoral Fellow, Hong Kong University
14. Hua Dong 09/2007-10/2009
15. Xiaodian Sun 10/2008-04/2009
Postdoctoral Fellow, Department of Statistics, Penn State University
16. Qian Hao 11/2006-06/2007
17. Wuju Li 1998-2000
Professor, Center of Bioinformatics, Institute of Basic Medical Science, China

Graduate Student Advisor and Committees:

Primary PhD Student Advisor

<u>Name</u>	<u>Discipline/Module</u>	<u>Degree</u>	<u>Role</u>	<u>Graduation</u>
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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 02/2013-04/2015
Dissertation Title: Functional linear model with functional response and predictor for temporal quantitative traits in sleep apnea
Biostat Solution, Washington DC, MD

3. Long Ma Biostatistics Ph. D. Advisor 09/2011-04/2015
Dissertation Title: general statistics framework for disease risk prediction by genetic variants, gene expression and image
Gilead Sciences, Inc, Foster City, CA

4. Mohammad Rahman Biostatistics Ph. D. Advisor 08/2013-04/2015
Dissertation Title: Sparse structural equation models for genotype-phenotype networks
Bristol Myers Squibb Pharmaceutical located in Princeton, New Jersey.

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, University of Florida

- 10..Akey, Joshua, GSBS Ph.D. On-line Supervisor 09/1998-12/02
Professor, Lewis-Sigler Institute for Integrative Genomics, Princeton University
11. Nan Lin Biostatistics Ph. D. Advisor 05/2013-05/2018

12. Xuehan Ren Biostatistics Ph. D. Advisor 08/2013-03/2016

13. Junhai Jiang Biostatistics Ph. D. Advisor 08/2013-01/2015

14. Lian Lin	Biostatistics	Ph.D.	Advisor	08/2009-
15. Pengyi Gu	Biostatistics	Ph.D.	Advisor	09/2013-Present
16. Shudi Li	Biostatistics	Ph. D.	Advisor	08/2016-Present
17. Shi Pu	Biostatistics	Ph. D.	Advisor	08/2007-05/2008
18. Tao Xu	Biostatistics	Ph. D.	Advisor	09/2016-Present
19. Rong Jiao	Biostatistics	Ph. D.	Advisor	10/2016-Present
20. Helen Engle	Biostatistics	Ph. D.	Advisor	09/2018-Present
21. Michael W Newlin	Biostatistics	Ph. D.	Advisor	09/2018-Present
22. Jingyan Wang	Biostatistics	Ph. D.	Advisor	09/2018-Present
23. Yuanyuan Liu	Biostatistics	Ph. D.	Advisor	09/2017-Present

PhD dissertation committee

1. Xia Wang	Baylor College of Medicine, Ph. D		Mentor	07/2012-08/2014
2. Zachry Tore Soens	Baylor College of Medicine, Ph. D		Mentor	09/2014-08/2016
3. Jun Zhang	Biostatistics	Ph.D.	Member	09/2016-11/2018
4. Kan Li	Biostatistics	Ph.D.	Member	09/2016-03/2018
5. Yunxi Zhang	Biostatistics	Ph.D.	Member	09/2016-08/2018
6. Yi, Misung	Biostatistics	Ph.D.	Member	08/2017-Present
7. Ho-Lan Peng	Biostatistics	Ph.D.	Member	04/2016-Present
8. Pervin, Hannah E	Biostatistics	Ph.D.	Member	03/2016-Present
9. Yulun Liu	Biostatistics	Ph.D.	Member	06/2014-04/2016
10. Chuan Hong	Biostatistics	Ph.D.	Member	01/2014-04/2016
11. Jin Su	Biostatistics	Ph.D.	Member	11/2010-04/2016
12. Hui Peng	Biostatistics	Ph.D.	Member	11/2010-Present
13. Xiang Shu	Biostatistics	Ph.D.	Member	12/2014-Present
14. Xuan Zhang	Biostatistics	Ph.D.	Member	06/2010-Present
15. Hong Wei Tang	Biostatistics	Ph.D.	Member	05/2010-Present
16. Caimiao Wei	Biostatistics	Ph.D.	Member	09/2008-05/2015
17. Jiabu Ye	Biostatistics	Ph.D.	Member	05/2015-Present
18. E Lin	Biostatistics	Ph.D.	Member	10/2010-11/2014
19. Taebeom Kim	Biostatistics	Ph.D.	Member	10/2012-11/2014
20. Wei Qiao	Biostatistics	Ph.D.	Member	05/2010-11/2014
21. Renke Zhou	Biostatistics	Ph. D.	Member	10/2008-12/2014
22. Vineetkumar Kharat	Epidemiology	Ph.D.	Member	03/2013-05/2014
23. Manandhar, Pratik	Biostatistics	Ph.D.	Member	09/2013-05/2014
24. Nianxiang Zhang	Biostatistics	Ph.D.	Member	08/2010-08/2013
25. Suyu Liu	Biostatistics	Ph.D.	Member	09/2009-08/2013
26. Yi-Ju Chiang	Biostatistics	Ph.D.	Member	09/2009-08/2013
27. Min Yi	Biostatistics	Ph.D.	Member	09/2009-08/2012
28. Shangying Liang	Biostatistics	Ph.D.	Member	10/2009-08/2013
29. Yung Fei Wang	Biostatistics	Ph.D.	Member	10/2008-08/2012
30. Lin Huo	Biostatistics	Ph.D.	Member	10/2008-02/2009
31. Jun Liu	Biostatistics	Ph. D.	Member	10/2008-04/2012

32. Yu-Li Ling	Biostatistics	Ph.D.	Member	07/2008-04/2012
33. Furong Huang	Biostatistics	Ph.D.	Member	09/2006-08/2012
34. Jacy Crosby	Biostatistics (GSBS)	Ph.D.	Member	06/2008-09/2010
35. Bo He	Biostatistics	Ph.D.	Member	09/2008-08/2013
36. Ho, Chung-Han	Biostatistics	Ph.D.	Member	10/2008-08/2013
37. Xuemin Gu	Biostatistics	Ph.D.	Member	09/2009-08/2012
38. Jang H Yun	Biostatistics	Ph.D.	Member	06/2008-08/2013
39. Yaji Xu	Biostatistics	Ph.D.	Member	09/2005-05/2010
40. Ping Liu	Biostatistics	Ph.D.	Member	09/2009-08/2012
41. Yufeng Zhang	Biostatistics	Ph.D.	Member	08/2008-08/2012
42. Sijin Wen	Biostatistics	Ph.D.	Member	2005-05/09
43. Qing Zhang	Biostatistics	Ph.D.	Member	2000-05/09
44. Hui Zhao	Biostatistics	Ph.D.	Member	2003-05/2007
45. Yiqun Zhang	Biostatistics	Ph.D.	Member	2004-2011
46. Liu, Xiaoming	GSBS	Ph.D.	Member	09/2002-08/06
Assistant Professor, SPH				
47. Mak, Solida	GSBS	Ph.D.	Member	09/2003-06/08
48. Chung, Charles	GSBS	Ph.D.	Member	09/2003-05/07
49. Dayna Tirpak	GSBS	Ph.D.	Member	09/1998-12/02
50. Kun Zhang	GSBS	Ph.D.	Member	09/1999-05/03
Professor, Chair, Dept of Bioengineering, University of California at San Diego				
51. Alanna Morrison	GSBS	Ph.D.	Member	09/1997-05/01
Professor, Chair, UTSPH				
52. Zhongming Zhao	GSBS	Ph.D.	Member	2000
Professor, University of Texas Health Science Center at Houston.				
53. Andrei Rodin	GSBS	Ph.D.	Member	Fall, 1999
54. Grier P. Page	GSBS	Ph.D.	Member	Fall, 1998
Associate Professor, University of Alabama				
55. Hong Yan Xu	GSBS	Ph.D.	Member	2001-2003
Associate Professor, Georgia Medical College				
56. Qiqing Wang	GSBS	Ph.D.	Member	2001-2003
57. Xi Zhou	GSBS	Ph.D.	Member	2001-2003
60. John C. Huber Jr.	Biological Science	Ph.D.	Member	2000-2004
Associate Professor, Texas A&M University				

Primary MS thesis advisor

1. Shudi Li	Biostatistics	M.S	Advisor	08/2015-2016
2. Yuefei Wang	Biostatistics	M.S.	Advisor	09/2016-05/2017
2. Wenqian Liang	Biostatistics	MS.	Advisor	09/2015-04/2016
Thesis Title: Image classification using segmentation, functional principal component analysis and sparse sufficient dimension reduction				
3. Jin Yu	Biostatistics	M.S.	Advisor	08/2013-05/2015
Thesis Title: Construct gene correlation network with NGS by cloud computing				

3. Ruling Liu	Biostatistics	M.S.	Advisor	08/2012-05/2015
4. Jialing Zhu	Biostatistics	M.S.	Research Supervisor	01/2011-07/2014
Thesis Title: GIS mapping and gene-environment interaction.				
5. Jin Li	Biostatistics	M.S.	Advisor	11/2010-12/2012
6. 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.				
7. 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.				

8. Yun Zhu	Biostatistics	M.S.	Advisor	08/2010-12/2011
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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 Holmes	MPHINF	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

2018 The Research Grants Council (RGC) of Hong Kong
2017 IMST-F(40)P study section , ZRG1 (NIH)
2017/2. Healthcare Delivery and Methodologies- Member Conflict Special Emphasis Panel: Biostatistical Methods and Research Design (BMRD), HDM ZRG1 (NIH).
2017/3. The Research Grants Council (RGC) of Hong Kong.
2017/5. CNSF Grant Review.
2017/6. Health and Medical Research Fund (Hong Kong)
2016/10. The Program Project: Statistical Genetics [ZRG1 IMST-R (40) P] study section.
2016/06. The NIH Infectious Disease, Reproductive Health, and Asthma/Pulmonary Conditions (IRAP) study section.
CNSF Grant Review (2016)
The Research Grants Council (RGC) of Hong Kong (2016)
2015/04/ CDC/CGH/OD (GH15-005) Conducting Public Health in China
2015/04/ CDC/CGH/OD (GH14-002)
2015/05 ZRG1 GGG-L, AREA: Genes, Genomes and Genetics
The Research Grants Council (RGC) of Hong Kong (2015)
CNSF Grant Review (2015)
Estonian Research Council (2014)
CNSF Grant Review (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

University of Arkansas for Medical Sciences
University of Nebraska
Indiana University at Bloomington

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
PLoS Computational Biology
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
 Guest Editor Shift the Current Paradigm of Genetic Studies of Complex Diseases from Association to Causation, Frontiers in Genetics
 Leading Guest Editor: Special Issue on Next-Generation Sequencing. 2009-2010. Journal of Biomedicine and Biotechnology
 2009- Academic Editor: PLoS ONE
 Associate Editor: BioMed Research International
 2007- Associate Editor: Recent Advances in DNA & Gene Sequences (Recent Patents in DNA and Gene Sequences)
 2010- Associate Editor: International Journal of Computational Bioscience
 2014- Associate Editor: Statistics and Its Interface
 2007- Editorial Board Member: Current Genomics
 2011- Editorial Board Member: Frontiers in Genetics / Evolutionary and Population Genetics
 2012- Editorial Board Member: Journal of Genetic Disorders & Disease Information (JGDDI)
 2012- Editorial Board Member: Cancer Medicine
 2012- Editorial Board Member: International Journal of Statistics in Medical Research
 2013- Editorial Board Member: Journal of Phylogenetics & Evolutionary Biology
 2015- Editorial Board Member: Statistics in Biomarkers
 2015- Editorial Board Member: SM Journal of Engineering Sciences
 2016- Editorial Board Member: Journal of Clinical Epigenetics
 2015- 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

Organizing Committee Member, 2nd International Hematologists Summit (HIS-2019), May 30-31, 2019 at Nice, France.

Organizing Committee and Leadership Committee, Genome San Diego 2018, Nov 26-28, 2018, San Diego, USA

Program Committee, 4th International Conference on Big Data and Information Analytics, December 17-19, 2018, Houston, Texas

Organizer, Session in New Generation of genomic, epigenomic, and imaging data analysis in mental disorder studies. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.

Organizer, Session in Intelligent Learning and Integrative Analysis in Cancer Research. The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, December 19-22, 2016, Shanghai, China.

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.

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 big genomic and epigenomic data analysis and its application to precision medicine (July 2-9, 2017, Chengdu, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (June 20-25, 2016, Shanghai, China).

Co-Organizer and Lecturer, National Workshop on Statistical Genetics, Systems Biology and Molecular Evolution (June 1-9, 2015, Xining, China).

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 on Large 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

Data Science Faculty Search Committee (2017-present)

Methodology Committee (2017-present)

GSBS poster judge

3 Year Review Committee (2017)

GSBA, Student Scholarship Committee (2015-2017)

Six Year Review Committee (2015- 2016)

IFC the Administrative Affairs Subcommittee (2014-2016)

IFC Faculty Status, Rights & Responsibilities Committee (2013)

GSBA, Student Scholarship Committee (2015-2016)

GSBA, Biostatistics and Bioinformatics Admission Committee (2012-2016)

Admission Committee in Division of Biostatistics (2012-2014)

Big Data Analysis Faculty Search Committee (2013-2015)

Faculty Development Leave Committee (2012)

Burks Scholarship Selection Committee (2011-2016)

Faculty Council Representative in the SPH (2009-2015)

Inter Faculty Council (IFC) Representative (2010-2016)

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)