CURRICULUM VITAE
Xiong MM, Ph.D.

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The University of Texas Health Science Center at Houston
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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 Human and Molecular Genetics
Program in Biostatistics, Bioinformatics & Systems Biology

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
	Panzhihua Steel Company, China
12/68-12/71	Assistant Engineer
	Panzhihua Steel Company, China

PROFESSIONAL ACTIVITIES

2005-	The International Society for Computational Biology
1994-	American Society of Human Genetics
2004-	Eastern North American Region/International Biometric Society
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

Google Scholar

Citation indices	All	Since 2011
Citations	10205	6316
h-index	43	27
i10-index	100	68

Research Gate Score: 43.77

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.
2. Jiang J, Lin N, Guo S, Chen J, Xiong MM. (2014). Methods for Joint Imaging and RNA-seq Data Analysis. arXiv: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.
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.
5. Zewdie G and Xiong MM. (2014). Fully Automated Myocardial Infarction Classification using Ordinary Differential Equations. aiXiv:1410.6984.
6. Li L and Xiong MM. (2014). A novel statistical method based on dynamic models for classification. aiXiv: 1410.7029.
7. Ma L, Lin N, Amos CI and Xiong MM. (2014). A General Statistic Framework for Genome-based Disease Risk Prediction. aiXiv:1410.7371 .
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

B. PAPERS IN REFEREED JOURNALS

12. 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.
13. 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.

14. Xu K, Jin L, Xiong M. (2017). Functional regression method for whole genome eQTL epistasis analysis with sequencing data. BMC Genomics. 18(1):385.
15. 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.
16. Chiu CY, Jung J, Wang Y, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Mills JL, Michael Boehnke M, Xiong MM, and Fan R. (2017). A Comparison Study of Multivariate Fixed Models and Gene Association with Multiple Traits (GAMuT) for Next-Generation Sequencing. Genetic Epidemiology. 41(1):18-34 .
17. 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.
18. 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).
19. 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.
20. Zhang F, Xie D, Liang M, Xiong M. (2016). Functional Regression Models for Epistasis Analysis of Multiple Quantitative Traits. PLoS Genet. 12(4):e1005965.
21. 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
22. 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].
23. 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.
24. 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.
25. 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.
26. Li L and Xiong MM. (2015). Dynamic Model for RNA-seq Data Analysis. BioMed Research International. Biomed Res Int. 2015:916352. PMCID: PMC4539434.
27. 1000 Genome Project Consortium. A global reference for human genetic variation. Nature (2015) 526(7571): 68-74.
28. 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.
29. Wang Y, Li Y, Cao H, Xiong M, Shuga.rt YY, Jin L. (2015). Efficient test for nonlinear dependence of two continuous variables. BMC Bioinformatics. 16(1):260. PMCID: PMC4539721
30. 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

31. 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.

32. 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

33. 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.

34. 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. PMCID: PMC4443751.

35. 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. PMCID: PMC4539419.

36. 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. PMCID: PMC4626363.

37. 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 PMCID: PMC4318209.

38. 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.

39. 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

40. 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

41. Zhang F, Boerwinkle E and Xiong MM. (2014). Epistasis Analysis for Quantitative Trait with Next-generation Sequencing Data. Genome Research. 24(6):989-98. PMCID: PMC4032862.

42. Delaneau O., Marchini J., McVeanh 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., Nemesh J., Poplin R., Schaffner S., Shakir K., Sabeti P., Grossman S., Tabrizi S., Tariyal R., Li H., Reich D., Durbin R., Hurles 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. PMCID: PMC4338501.

43. 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

44. 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. PMCID: PMC3632131.
45. 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
46. Xiong MM (2013). New Era for Health Care and Genomics. J Phylogen Evolution Biol. 1:e104.
47. 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
48. **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
49. Liang F and **Xiong MM**. (2013). Bayesian detection of causal rare variants under posterior consistency. PLos ONE. 8(7), e69633. PMC3724943.
50. Fan R, Zhang Y, Albert PS, Liu A, Wang Y, **Xiong MM**. (2012). Longitudinal Association Analysis of Quantitative Traits. Genet Epidemiol. 36: 856–869.
51. 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA (2012) An integrated map of genetic variation from 1,092 human genomes. Nature 491(7422):56-65. PMCID: PMC3498066 [Available on 2013/5/1]
52. Shugart YY, Zhu Y, Guo W, **Xiong MM** (2012) Weighted Pedigree-based Statistics for Testing the Association of Rare Variants. BMC Genomics, 13:667. PMCID: PMC3827928.
53. 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. PMCID: PMC3534768.
54. 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. PMCID: PMC3532851.
55. 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.
56. 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.
57. 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. PMCID: PMC3375640.
58. Zhu Y and **Xiong MM** (2012) Family-Based Association Studies for Next-Generation Sequencing. Am J Human Genet. 90(6):1028-1045. PMCID: PMC3370281
59. 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 . PMCID: PMC3499061.
60. 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. PMCID: PMC3291503

61. *Siu H, Jin L and **Xiong MM** (2012) Manifold Learning for Human Population Structure Studies. PLoS ONE, 7: e29901. PMCID: PMC3260176.

62. 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. PMCID: PMC3548254.

63. *Siu H, Zhu Y, Jin L and Xiong MM. (2011) Implication of Next-Generation Sequencing on Association Studies. BMC Genomics, 12:322. PMCID: PMC3148210

64. 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. PMCID: PMC3384547.

65. 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. PMC3137625.

66. 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.

67. *Fang S, *Fang X, **Xiong MM.** (2011) Psoriasis prediction from genome-wide SNP profiles. BMC Dermatol. 11(1):1. PMC3022824.

68. 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

69. *Luo L, Boerwinkle E and Xiong MM (2011) Association studies for next-generation sequencing. Genome Research, 21(7):1099-1108. PMCID: PMC3129252

70. *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. PMCID: PMC2944798.

71. *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. PMC3002314

72. *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. PMC2999346

73. *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. PMC2987176

74. *Luo L, *Peng G, *Zhu Y, *Dong H, Amos C, **Xiong MM.** (2010) Genome-wide gene and pathway analysis. Eur J Hum Genet. 18:1045-1053. PMCID: PMC2924916.

75. 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.

76. Xiong MM, Zhao Z, Arnold J, Yu F. (2010). Next-generation sequencing. J Biomed

Biotechnol. 2010:370710.

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78. *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.

79. *Wu X, Jin L**, Xiong MM**. (2009) Mutual information for testing gene-environment interaction. PLoS ONE. 4(2):e4578. PMC2642626**.**

80. 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) Poly-morphisms in the interleukin 3 gene show strong association with susceptibility to Graves' disease in Chinese population. Genes Immun. 10:260-266.

81. *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.

82. *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.

83. Seitsonen SP, Onkamo P, *Peng G, **Xiong M**, Tommila PV, Ranta PH, Holopainen JM, Moilanen JA, Palosaari T, Kaarniranta K, Meri S, Immonen IR, Järvelä IE. (2008) Multi-factor effects and evidence of potential interaction between complement factor H Y402H and LOC387715 A69S in age-related macular degeneration. PLoS One. 3(12):e3833. PMC2585793**.**

84. *Dong H, Xiao Y, Wang W, Jin L, **Xiong MM.** (2008) Symmetry of metabolic network JCSB 1: 1-20.

85. *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

86. Xiao Y, MacArthur BD, Wang H, **Xiong MM**, Wang W. (2008) Network quotients: Structural skeletons of complex systems. Physical Review E. 78: 046102.

87. 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.

88. Xiao Y, *Dong H, Wang W, **Xiong MM**, Shi B-L, Wu W. (2008) Structure based graph distance measures of high degree of precision. Pattern Recognition. 41: 3547-3561.

89. *Wu X, Jin L, **Xiong MM.** (2008) Composite measure of linkage disequilibrium for testing interaction between unlinked loci. Eur J Hum Genet. 16:644-651.

90. Xiao Y, Wu W, Wang H ,**Xiong MM,** Wang W. (2008) Symmetry-based structure entropy of complex networks. Physica A: Statistical Mechanics Applications. 387: 2611-2619.

91. **Xiong MM**, Arnett FC, Xiong H, Zhou XD. (2008) Differential dynamic properties of scleroderma fibroblasts in response to perturbation of environmental stimuli. Application of state-space model in studies of human complex disease. PLos ONE. 3(2): e1693. PMC2246014

92. *Zhao J, Boerwinkle E, **Xiong MM.** (2007) An entropy-based genome-wide transmission/ disequilibrium test. Hum Genet 121:357-367.

93. Xu S, Huang W, Wang H, He Y, Wang Y, Wang Y, Qian J, **Xiong MM**, Jin L. (2007) Dissecting linkage disequilibrium in African American genomes: Roles of markers and individuals. Mol Biol Evol. 24:2049-58.

94. Lee EB, Zhao J, Kim JY, **Xiong MM**, Song YW. (2007) Evidence of potential interaction of chemokine genes in susceptibility to systemic sclerosis. Arthritis Rheum. 56:2443-2448.

95. 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):3807-14

96. **Xiong MM**, Zhou X. (2007) Applications of systems biology. Cell Mol Life Sci. 64:1737-1738.

97. [*]Zhao J, Jin L, **Xiong MM.** (2006) Nonlinear tests for genome-wide association studies. Genetics. 174:1529-1538.

98. Zhou XD, **Xiong MM**, Tan FK, Guo XJ, Arnett FC. (2006) SPARC, an upstream regulator of CTGF in response to TGF-β stimulation. Arthritis Rheum. 54: 3885-3889.

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153. Zhao J, **Xiong MM**. (2003) Genetic analysis of function-valued traits. American Journal of Human Genetics 73:604.

154. **Xiong MM**. (2002) Modeling and identification of genetic networks. American Journal of Human Genetics 71: 390.

155. Zhang K, Akey JM, Wang N, **Xiong MM**, Chakraboty 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.

156. Sun M, **Xiong MM**. (2002) A mathematical programming approach for gene selection and tumor classification. American Journal of Human Genetics 71: 229.

157. 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.

158. Zhao J, **Xiong MM.** (2002) Unbiased quantitative population association test. American Journal of Human Genetics 71: 568.

159. Fan R, **Xiong MM**. (2002) Haplotype linkage disequilibrium mapping of quantitative trait loci. American Journal of Human Genetics 71: 572.

160. 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.

161. Fan R, Xiong MM. (2001) Combined linkage and association interval mapping of quantitative trait loci. American Journal of Human Genetics. 69: 1252.

162. Fang X, Xiong MM. (2001) Meta-learning for combining multiple classifiers. American Journal of Human Genetics. 69:1552.

163. Sun M, Xiong MM. (2001) A tabu search algorithm for gene selection in whole genome functional analysis. American Journal of Human Genetics. 69: 1671.

164. Zhao J, Xiong MM. (2001) The generalized T2 test for biomarker identification using gene expression data. American Journal of Human Genetics. 69: 1572.

165. 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.

166. Fornage M, Markgraff C, Xiong MM, Boerwinkle E, Doris PA. (2001) Gene expression

profiling and stroke susceptibility. Hypertension 38 (4): PE04.

167. 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.

168. 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.

169. 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.

170. 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.

171. Li W, Xiong MM. (2000) Computational Methods for Gene Expression Based Tumor Classification. American Journal of Human Genetics. 67: 78.

172. Zhang K, Xiong MM, Jin L, Rogers L, Amato R, Killary A, Lott S. (2000) Classification of Renal Cell Carcinoma with cDNA Microarray. American Journal of Human Genetics. 67: 96.

173. Akey JM, Jin L, Xiong MM. (2000) Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. American Journal of Human Genetics. 67: 227.

174. Xiao J, Akey JM, Xiong MM, Jin L. (2000) Linkage disequilibrium in isolated and outbred Chinese populations. American Journal of Human Genetics. 67: 225.

175. 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.

176. Chen H, Akey MJ, Xiong MM, Xu H, Xiao J, Jin L. (2000) Association of variation in the promoter of the Beta-2 Adrenergic Receptor and essential hypertension in an isolated Chinese population. American Journal of Human Genetics. 67: 228.

177. 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.

178. Xiong MM, Jin L. (2000) Extent of linkage disequilibrium in human populations and their implications in SNP mapping. Genetic. Epidemiology. 19: 277.

179. Xiong MM, Zhao J, Jin L, Boerwinkle E. (2000) Multiple point linkage disequilibrium fine-scale mapping of quantitative trait locus. Genetic. Epidemiology. 19: 277.

180. Xiong MM, Zhao J, Amos C, Boerwinkle E. (2000) Physiological and statistical genetic models of epistasis. Genetic. Epidemiology. 19: 278.

181. 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.

182. 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.

183. 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.

184. Xiong MM, Jin L. (1999) Admixture linkage disequilibrium mapping of quantitative trait

loci. American Journal of Human Genetics 65, A86.

185. 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.

186. 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.

187. 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.

188. 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.

189. 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.

190. 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.

191. 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, 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.

2. 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.

3. 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.

4. 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.

5. 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.
6. 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.
7. Integrative image and RNA-seq data analysis. Transcriptomics-2015. Orlando, FL, July 27-29, 2015.
8. Gene-gene interaction analysis for next-generation sequencing. ENAR, March 16-19, 2014, Baltimore, Maryland.
9. Topic contributed: Jiang J, Lin N and Xiong MM. (2014). Image RNA-seq data analysis in clouds. 2014 JSM, Boston, MA.
10. 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.
11. Classification analysis of big image data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.
12. QTL and Gene-gene Interaction Analysis for Next-generation Sequencing, ENAR, March 10-13, 2013 Spring Meeting - Orlando, Florida.
13. Alternative Direction Minimization Methods for Phenotype Prediction and variable Selection. Biometrics-2013, June 10-12, Chicago.
14. (Keynote Speaker) International Conference and Exhibition on Biometrics and Biostatistics 5-7 March 2012, Omaha.
15. Genetic and Epigenetic Analysis for Next-Generation Sequencing. March 22, 2012, Department of Epidemiology, MD Anderson Cancer Center.
16. Genetic Studies of Complex Diseases in the Sequence Era. October 5, 2012. Department of Statistics, Texas A&M University.
17. Statistical Challenges Arising from Next-generation Sequencing. December, 14, 2011, Department of Bioinformatics and Computational Biology, Anderson Cancer Center.
18. Association studies for next-generation sequencing. May 30, 2011, National Institute of Mental Health.
19. Mathematical challenges in data analysis raised by next-generation sequencing. School of Mathematics Science, Fudan University, China, November 2, 2011.
20. Data analysis for next-generation sequencing. School of Finance and Statistics, East China Normal University, November 4, 2011.
21. Gene and pathway-based association studies. China-UK Statistical Genetics, Population Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
22. Implication of next-generation sequencing on association studies. China-UK Statistical Genetics, Population   Genetics and Genetic Epidemiology Workshop, Shanghai, China, June 25-27, 2010.
23. Integrated genetic and epigenetic analysis in cancer studies. The Second International Conference on Statistical Genetics and Systems Biology, Kunming, China, July 22-25, 2009.
24. Dynamic Pathway Analysis, The First International Conference on Statistical Genetics and Systems Biology, Qingdao, China, June 14-16, 2007.
25. State Space Equations for Modeling Gene Networks. The First International Conference on

Computational Systems Biology. Shanghai, July 20-23, 2006

26. Genetic interaction networks and regulatory networks for genetic studies of complex diseases. Computational Biology 2005 – Challenges and Visions. Shanghai, October 13-16.
27. Nonlinear approach to dissecting genetic structure of complex diseases, The International Symposium on Genomic Medicine, June 28-30, 2005. Shanghai, China.
28. A Systems Biology Approach to Genetic Studies of Complex Diseases, March 2, 2004, Yale University.
29. An example of application of bioinformatics to systems biology, Eastern Forum of Science and Technology. July 11-12, 2004, Shanghai, China.
30. Network Biology, July 18, 2004, Shanghai Second Medical University, China.
31. Differentially expressed genetic networks, the 7th World Multiconference on Systemics, Cybernetics and Informatics, July 27-30, 2003, Orlando, Florida.
32. Perspective in Systems Biology, December, 24, 2003, Fudan University, Shanghai, China.
33. Large-scale gene expression data analysis and disease diagnosis, August 26-27, 2002. International Biopharmaceutical Technology Conference, Fujian, China.
34. Gene expression-based tumor classification, December 22, 2002, Department of Statistics, Beijing University, China.
35. Bioinformatics and genomic science research, December, 19, 2001, National Genomic Center at Shanghai, China.
36. Generalized T^2 test for whole genome linkage disequilibrium profile analysis, May 23-26, 2001, International conference for mapping complex disease genes, Changsha, China.
37. Biomarker Identification by feature selection. May 21, 2001, Institute of System Science and Mathematics, Chinese Academy of Science, Beijing.
38. Advances in Bioinformatics, May 27, 2001, Department of Genetics, Fudan University, China.
39. Cancer functional genomic analysis, May 30, 2001, Zhejiang University, Hangzhou, China
40. Mapping complex trait loci. Feb. 3, 2000, Workshop at NIH.
41. Neural networks for gene expression based tumor classification, Feb. 21, 2000, Division of Biostatistics, Saint Louis Washington University, Saint Louis, Missouri.
42. 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.
43. Gene selection in gene expression based tumor classification, April 23, 2000, Department of Computer Science, University of South West Louisiana.
44. Linkage disequilibrium mapping for complex disease, May, 2000, National Institute of Dental and Craniofacial Research Genetics Work Group.
45. Microarray and tumor classification, June 29, 2000, Darlian Institute of Chemistry, Darlian, China.
46. Combined linkage and linkage disequilibrium, July 4, 2000, Department of Statistics Beijing University, China.
47. Microarray and tumor diagnosis, July 5, 2000, Beijing General Hospital, Beijing, China.
48. Genomic circuits and cardiac diseases, July 6, 2000, Chinese Academy of Medical Science, Beijing, China.
49. Pathway identification, July 10, 2000, Chinese Institute of Biochemistry, Shanghai, China.
50. Statistical and computational methods for gene expression based tumor classification, Jan. 9, 2000, Department of Mathematics, University of Southern California, Los Angeles.

51. Linkage and linkage disequilibrium analysis for genetic studies of complex diseases, April, 1999, Chinese Academy of Medical Science, Beijing, China.
52. Advances in cancer genomics, April, 1999, Beijing Institute of Cancer, Beijing, China.
53. Advances in plant genetics, April, 1999, Institute of Plant, Chinese Academy of Science, Beijing, China.
54. Functional genomics in plant science, August, 1999, Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China.
55. Linkage disequilibrium based regression methods for mapping quantitative trait loci, August, 1999, Institute of Genetics, Fudan University, China.
56. Statistical analysis of mapping quantitative trait loci, February, 1997, Department of Statistics, Columbia University, New York.
57. Linkage disequilibrium for fine scale mapping, March, 1997, Department of Biology, Georgia Tech, Atlanta, Georgia.
58. Fine-scale mapping: theory and application, September, 1996, McGill University, Canada.
59. Fine-scale mapping of quantitative trait loci, September, 1996, University of Montreal, Canada.
60. Strategy for mapping complex trait loci, July, 1996, Sequana Therapeutics, Inc., La Jolla, California.

Presentations

1. 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.
2. 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.
3. 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.
4. 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.
5. 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.
6. Lin Nan, Wang P, Zhu Yun 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
7. 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.
8. 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.
9. Li L and Xiong MM. (2014). An Ordinary Differential Equation Model for Gene Regulation with RNA-seq Data. 2014 JSM, Boston, MA.

10. Zhang, F, Boerwinkle E and Xiong MM. (2013). Epistasis analysis for quantitative trait with next-generation sequencing data (Plat form). 63th annual meeting of The American Society of Human Genetics. October 22-26, 2013, Boston, Massachusetts.

11. 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.

12. Family-based association studies for next generation sequencing. 30 Years of Computational Biology at USC. March 30-April 1, 2012. Los Angeles, California.

13. 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.

14. 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.

15. 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.

16. Population structure analysis for next-generation sequencing. 2011 IEEE World Congress on Engineering and Technology. Shanghai, China. October 28-Novemeber 2, 2011,

17. A novel genome continuum model for sequence-based association studies. 2010 Joint Statistical Meetings, July 31-August 5, 2010, Vancouver, Canada.

18. Association Studies for Next-Generation Sequencing. 60th annual meeting of The American Society of Human Genetics, Nov. 2-6, 2010, Washington DC.

19. 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.

20. 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.

21. Genome-wide Gene and Pathway Analysis. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.

22. Genome-wide interaction analysis of coronary artery disease. 59th annual meeting of The American Society of Human Genetics, Oct. 20-24, 2009, Honolulu.

23. Information Geometry, Gene-Gene, Gene-Environment Interaction, and Pathway Association. 2008 Joint Statistical Meetings, Colorado, August 3-7, 2008.

24. 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.

25. 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.

26. Do Genetic Networks Obey Kirchhoff's and Ohm's Laws? The IASTED International Conference on Computational Systems Biology. November 13-14, 2006, Dallas.

27. Genetic Interaction Networks in Association Studies of Complex Diseases. The 2006 Joint Statistical Meeting, August 6-10, Seattle, Washington.

28. State-space approach to modeling dynamics of gene regulation in networks. 2005

International Conference on Bioinformatics. September 22-24, Busan, Korea.
29. Nonlinear Tests for Categorical Data. ENAR, Austin Texas, March 20-23, 2005.
30. Systems Biology Approaches to Genetic Studies of Complex Diseases. Pathway analysis for Target and Compound Evaluation. San Francisco, CA, April 20-22, 2005.
31. Generalized Circuit Analysis of Biological Networks. 2004 International Conference on Complex Systems, Boston, May 16-21, 2004.
32. Statistical model for function valued traits. Genetic Analysis of Complex Diseases & Human Population, September, 19-21, 2003, Chicago, Illinois.
33. Modeling and identification of genetic networks. ASHG 52th Annual Meeting, Baltimore, 2002.
34. Randomly distributed recombination may generate block-like pattern of linkage disequilibrium: An act of genetic drift. ASHG 52th Annual Meeting, Baltimore, 2002.
35. Differentially regulated genetic networks. 2002 NCRR Bioinformatics Conference. September 27-29, 2002. Boston.
36. The effect of ascertainment bias on estimates of linkage disequilibrium. ASHG 51th Annual Meeting, San Diego, 2001.
37. Dynamic models for mapping quantitative trait with time-dependent genetic effect. ASHG 51th Annual Meeting, San Diego, 2001.
38. Structural equation models for pathway identification. Oncogenomics Conference. January 25-27, 2001, Tucson, Arizona.
39. Population genomic models and their applications to genetic studies of complex traits. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Geogia.
40. Linkage and association studies of QTL for nuclear families by mixed models. 2001 Joint Statistical Meetings. August 5-9, 2001. Atlanta, Georgia.
41. Multiple trait-locus model for quantitative trait analysis, 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
42. Linkage disequilibrium mapping of quantitative trait loci: multiple trait analysis, 27th Annual Meeting of the Texas Genetics Society, March 23-25, 2001, Houston.
43. 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.
44. The haplotype disequilibrium test for genome-wide screen: Its power and study design. an. 2000. Pacific Symposium of Biocomputing 2000. Maui, Hawaii.
45. Fine-Scale Mapping of Quantitative Traits Loci by Interval Mapping in Human Population. At ASHG 50th Annual Meeting, Philadelphia, Oct.3-7, 2000.
46. Linkage Disequilibrium mapping of quantitative trait loci: multiple trait analysis. ASHG 50th Annual Meeting, Philadelphia, Oct. 3-7, 2000.
47. 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.
48. Gene expression in myositis biopsies. 64th Annual Scientific Meeting of Rheumatology, October 29 - November 2, Philadelphia.
49. Gene expression profile of muscle biopsies from patients with inflammatory myopathies. 64th Annual Scientific Meeting of Rheumatology, October 29-November 2, Philadelphia.
50. 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.

51. Gene expression based tumor classification, IBC's 6th Annual Biochip Technologies Conference, 1999, Nov. 2-5, Berkeley, CA.
52. 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.
53. Mapping QTL by linkage disequilibrium. Joint Statistical Meetings, August 9-13, 1998, Dallas, Texas.
54. 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.
55. 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.
56. Modeling the population dynamics of simple sequence repeats. 46th Annual Meeting of the American Society of Human Genetics,1995.
57. Neural Networks with Hidden Markov Processes. Artificial Neural Networks in Engineering Conference, Nov. 13-16, 1994, St. Louis.
58. Weighted neural network models for nonlinear regression with fixed and random effects. World Congress on Neural Networks, June 5-9, 1994, San Diego.
59. An O (n^3) Neural Network Model for Linear Programming. World Congress on Neural Networks, Portland, July 11-15, 1993.
60. 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.
61. 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.
62. Learning potential functions and differential inclusion. Proceedings of IJCNN '92, Baltimore, June 7-11, 1992.

ACTIVE GRANTS

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

Principal Investigator (40%) 1R01GM104411-01
                        Unified Statistical Methods for Sequence-Based Association Studies.
                        NIGMS
                        Total Cost: $1,737,913
                        04/01/2013-01/31/2017

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

Understanding the genetic architecture of schizophrenia in Chinese population
NIMH
Total Costs: $599,933
08/01/2013-07/31/2016

Investigator (15%) #81373100
Develop statistical methods for genome-wide gene-environment interaction analysis with next-generation sequencing data.
NSF, China
Total Cost: 700,000 Yuan
01/2014-12/2017

PENDING GRANTS

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

SUBMITTED, BUT NOT FUNDED

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%) 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

Investigator (5%)	2 U54 HG003273-09
The Human Genome Sequencing Center
NIH
Total Costs: $1,249,377
11/01/2011-10/31/2015

Co-Investigator (15%)	1U01HG005728-01
Detecting Natural Selection for the 1000 Genomes Dataset
NIH – National Human Genome Research Institute
Total Costs: $777,305
5/28/10 - 4/30-2012

Principal Investigator (30%): 1R01AR057120-01
Network Approach to GWAS of Rheumatoid Arthritis (RA),
Ankylosing Spondylitis (AS) and Psoriasis.
NIAMS
Total Costs: $556,353
09/01/2009 -08/31/2011

Principal Investigator (25%) P01 AR052915-01A1
Genetics and Ankylosing Spondylitis (AS) Pathogenesis
Project 4: Analysis of Genetic-Environmental Networks in
Spondyloarthritis
National Institute of Health
Total Costs: $7,417,127
07/01/2006-06/30/2011

Co-Investigator (15%)   NIAMS P50 AR054144-01 CORT
National Institute of Health
Center of Research Translation in Systems Sclerosis
National Institute of Health
Total Costs: $7,382,620
09/01/2006 - 08/31/2011

Co-Investigator (5%)   1 R01 HL084099-01A1
National Institute of Health
Genes of the CYP450-Derived Eicosanoid Pathway in Subclinical
Atherosclerosis
Total Costs: $2,872,877
1/1/2007 - 03/30/2011

Co-Investigator (5%)   PR064803
Department of Defense
The Integrative Studies of Genetic and Environmental factors in
Systemic Sclerosis
Total Costs: $928,125
1/1/2007 - 03/30/2011

Co-Principal Investigator: Development of Statistical Methods and Software for Testing
Gene-Environment Interaction and Construction of Genetic
Interaction Networks in Complex Diseases.
Ministry of Science & Technology, China
Total Costs: 1,000,000 Yuan
09/01/2007 - 08/31/2011

Co-Investigator (40%):   R01 HL74735-01
National Institute of Health
Antihypertensive Pharmocogenomics
Total Costs: $1,162,816
04/01/2004 - 03/30/2008

Co-Principal Investigator: Study of Dynamics and Network Structure of Biological Systems
of Complex Diseases
Science & Technology Commission of Shanghai Municipality,
China
Total Costs: 8,000,000 Yuan
11/30/04 - 10/30/07

Consultant: 1R03AR050517-01A2
Study of SPARC in scleroderma skin fibroblasts.
National Institute of Health
Total Costs: $223,062
4/1/05 - 3/31/08

Co-Investigator (10%):   5P50-AR44888-03
Mapping Scleroderma Susceptibility Genes in the Choctaw
National Institute of Health
Total Costs: $4,338,583
09/16/2001 - 09/14/2006

Co-Investigator (15%):   U01-HL054481
Genetic Determinants of High BP in Three Racial Groups
(Network)
National Institute of Health
Total Costs: $ 437,846
09/05/1995 - 06/30/2005

Co-Investigator (5%):   5 R01 HL069125-03
Gene-Environment Interactions and Stroke Susceptibility.
National Institute of Health
Total Costs $422,749
09/30/2001 - 09/29/2005

Principal Investigator of subcontract to UT-SPH (50%):
NIH R01 GM5651-03
Statistical Models in Population and Quantitative Genetics
National Institute of Health
Total Cost: $423,791
01/01/1997 - 12/31/2001

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

NIH ES09912
Linkage and Linkage disequilibrium for Quantitative Traits
National Institute of Health
Total Cost: $1,267,766
01/01/1999 - 12/31/2001

Co-Investigator (20%):   NIH HG0 1833-02 A1
Construction and Application of a U. S. Admixture Map
National Institute of Health
Co-Investigator (20%)
Total Cost: $482,961
09/24/1999 - 05/31/2002

ACADEMIC ACTIVITIES

COURSES TAUGHT

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 SUPERVI Graduate 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. GE Qiyang	09/2017-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

Name	*Discipline/Module*	*Degree*	*Role*	*Graduation*
1. Lerong Li	Biostatistics	Ph. D.	Advisor	08/2013-12/2014

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

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

Dissertation Title: Functional linear model with functional response and predictor for temporal quantitative traits in sleep apnea
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, Tulane Univrsity

10..Akey, Joshua,   GSBS   Ph.D.   On-line Supervisor   09/1998-12/02
Professor, Department of Genomic Science, University of Washington

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

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

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

14. Lian Lin   Biostatistics   Ph.D.   Advisor   08/2009-Present
15. Pengyi Gu   Biostatistics   Ph.D.   Advisor   09/2013-Present
16. 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

PhD dissertation committee

1. Xia Wang	Baylor College of Medicine, Ph. D		Mentor	07/2012-Present
2. Zachry Tore Soens	Baylor College of Medicine, Ph. D		Mentor	09/2014-Present
3. Ho-Lan Peng	Biostatistics	Ph.D.	Member	04/2016-Present
4. Pervin, Hannah E	Biostatistics	Ph.D.	Member	03/2016-Present
5.Yulun Liu	Biostatistics	Ph.D.	Member	06/2014-04/2016
4. Chuan Hong	Biostatistics	Ph.D.	Member	01/2014-04/2016
5. Jin Su	Biostatistics	Ph.D.	Member	11/2010-04/2016
6. Hui Peng	Biostatistics	Ph.D.	Member	11/2010-Present
7. Xiang Shu	Biostatistics	Ph.D.	Member	12/2014-Present
8. Xuan Zhang	Biostatistics	Ph.D.	Member	06/2010-Present
9. Hong Wei Tang	Biostatistics	Ph.D.	Member	05/2010-Present
10.Caimiao Wei	Biostatistics	Ph.D.	Member	09/2008-05/2015
11. Jiabu Ye	Biostatistics	Ph.D.	Member	05/2015-Present
11. E Lin	Biostatistics	Ph.D.	Member	10/2010-11/2014
12. Taebeom Kim	Biostatistics	Ph.D.	Member	10/2012-11/2014
13.Wei Qiao	Biostatistics	Ph.D.	Member	05/2010-11/2014
14. Renke Zhou	Biostatistics	Ph. D.	Member	10/2008-12/2014
15.Vineetkumar Kharat	Epidemiology	Ph.D.	Member	03/2013-05/2014
16. Manandhar, Pratik	Biostatistics	Ph.D.	Member	09/2013-05/2014
15. Nianxiang Zhang	Biostatistics	Ph.D.	Member	08/2010-08/2013
16. Suyu Liu	Biostatistics	Ph.D.	Member	09/2009-08/2013
17. Yi-Ju Chiang	Biostatistics	Ph.D.	Member	09/2009-08/2013
18. Min Yi	Biostatistics	Ph.D.	Member	09/2009-08/2012
19. Shangying Liang	Biostatistics	Ph.D.	Member	10/2009-08/2013
20. Yung Fei Wang	Biostatistics	Ph.D.	Member	10/2008-08/2012
21. Lin Huo	Biostatistics	Ph.D.	Member	10/2008-02/2009
22. Jun Liu	Biostatistics	Ph. D.	Member	10/2008-04/2012
23. Yu-Li Ling	Biostatistics	Ph.D.	Member	07/2008-04/2012
24. Furong Huang	Biostatistics	Ph.D.	Member	09/2006-08/2012
25. Jacy Crosby	Biostatistics (GSBS)	Ph.D.	Member	06/2008-09/2010
26. Bo He	Biostatistics	Ph.D.	Member	09/2008-08/2013
27. Ho, Chung-Han	Biostatistics	Ph.D.	Member	10/2008-08/2013
28. Xuemin Gu	Biostatistics	Ph.D.	Member	09/2009-08/2012
29. Jang H Yun	Biostatistics	Ph.D.	Member	06/2008-08/2013
30.Yaji Xu	Biostatistics	Ph.D.	Member	09/2005-05/2010
31. Ping Liu	Biostatistics	Ph.D.	Member	09/2009-08/2012
32. Yufeng Zhang	Biostatistics	Ph.D.	Member	08/2008-08/2012
32. Sijin Wen	Biostatistics	Ph.D.	Member	2005-05/09
33.Qing Zhang	Biostatistics	Ph.D.	Member	2000-05/09
34. Hui Zhao	Biostatistics	Ph.D.	Member	2003-05/2007
36. Yiqun Zhang	Biostatistics	Ph.D.	Member	2004-2011
37. Liu, Xiaoming	GSBS	Ph.D.	Member	09/2002-08/06
Assistant Professor, SPH				
38. Mak, Solida	GSBS	Ph.D.	Member	09/2003-06/08
39. Chung, Charles	GSBS	Ph.D.	Member	09/2003-05/07
40. Dayna Tirpak	GSBS	Ph.D.	Member	09/1998-12/02

41. Kun Zhang	GSBS	Ph.D.	Member	09/1999-05/03
Associate Professor, University of California at San Diego				
42. Alanna Morrison	GSBS	Ph.D.	Member	09/1997-05/01
Professor, UTSPH				
43. Zhongming Zhao	GSBS	Ph.D.	Member	2000
Associate Professor, Vanderbilt University.				
44. Andrei Rodin	GSBS	Ph.D.	Member	Fall, 1999
45. Grier P. Page	GSBS	Ph.D.	Member	Fall, 1998
Associate Professor, University of Alabama				
46. Hong Yan Xu	GSBS	Ph.D.	Member	2001-2003
Associate Professor, Georgia Medical College				
47. Qiqing Wang	GSBS	Ph.D.	Member	2001-2003
48. Xi Zhou	GSBS	Ph.D.	Member	2001-2003
49. John C. Huber Jr.	Biological Science	Ph.D.	Member	2000-2004
Associate Professor, Texas A&M University				

Primary MS thesis advisor

1. Shudi Li	Biostatistics	M.S	Advisor	08/2015-2016
2. Yuefei Wang	Biostatistics	M.S.	Advisor	09/2016-Pesent
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

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

2017/2. Healthcare Delivery and Methodologies- Member Conflict Special Emphasis Panel: Biostatistical Methods and Research Design (BMRD) (HDM ZRG1 (05).
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

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
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

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 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

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-Present)
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)