Department of Mathematical Science
Michigan Technological University
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Houghton MI 49931

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Education

Ph.D. in Statistics, July 1999
Peking University, Beijing, China
Supervisor: Professor Zhongguo Zheng
Dissertation: Non-parametric function estimation based on wavelet method

M.S. in Statistics, July 1988
Northeast Normal University, Changchun, China
Supervisor: Professor Xianhai Zhu and Mingwen Wang
Dissertation: Admissible estimators in linear model

BSc. in Mathematics, July 1983
Hebei Normal University, Shijiazhuang, China

Positions

Professor (August 2008-present)
Department of Mathematical Sciences
Michigan Technological University
Associate Professor (August 2004-July 2008)
Department of Mathematical Sciences
Michigan Technological University
Assistant Professor (August 2001—July 2004)
Department of Mathematical Sciences
Michigan Technological University
Affiliated Faculty Member (August 2002-present)
Biotech Research Center
Michigan Technological University
Postdoctoral Associate (July 1999 − August 2001)
Department of Epidemiology and Public Health
Yale University, School of Medicine
Lecturer/Associate Professor (1988 − 1999)
Department of Mathematics
Heilongjiang University, Harbin, China
Visiting Research Fellow (Oct. 1993 − Jan. 1995)
Department of mathematics
Budapest Technical University, Budapest, Hungary
Assistant Teacher (1983-1985)
Department of Mathematics

Hebei Normal University, Shijiazhuang, China

Honors

2008 Michigan Technological University Research Award
Outstanding Research Award
Department of Mathematical Sciences
Michigan Technological University, 2002, 2004, 2005, 2006
Outstanding Research Award
Heilongjiang University, Harbin, China, 1994, 1995, 1996

Research Interests:

1. **Statistical Genetics:** Developing statistical methods and computational tools to map complex disease genes both based on pedigree data and population data; developing statistical methods used in population genetics, computational biology, and microarray data analysis.

2. **Theoretical Statistics:** Nonparametric estimation of density function, regression function and variance function; Profile likelihood based methods; semi-parametric models; multivariate analysis.

Publications (* denote senior corresponding author)

1. Wang X, **Zhang SL**, Sha Q. A new association test to test multiple-marker association (Accepted for publication by *Genetic Epidemiology)*
2. Zhang Z, **Zhang SL,** Wong MY, Wareham NJ, Sha Q (2008) Ensemble learning approach jointly modeling main and interaction effects in genome-wide association studies. *Genetic Epidemiology,* 32:285-300.
3. Qin H, Feng T, Harding S, Tsai CJ and ***Zhang SL** (2008) An efficient method to identify differentially expressed genes in microarray experiments. *Bioinformatics*, 24: 1583-1589.
4. ***Zhang SL**, Sha Q. Association tests for complex disease genes while controlling population stratification. CURRENT TOPICS IN HUMAN GENETICS -Studies in Complex Diseases, by World Scientific Publishing Company; Imperial College Press. ISBN 978-981-270-472-6. Pub. date: Nov 2007.
5. Zhang Z, **Zhang SL**, Sha Q (2007) A multi-marker test based on family data in genome-wide association study. BMC Genetics, 8:65.
6. Feng T, **Zhang SL**, Sha Q (2007) Two-Stage Association Tests for Genome-wide Association Studies Based on Family Data with Arbitrary Family Structure. *European Journal of Human Genetics*, *15: 1169–1175.*
7. Sha Q, Chen H, **Zhang SL** (2007) New association tests based on haplotype similarity. *Genetic Epidemiology*, 31(6):577-93.

8. Tang R, Wang F, Sha Q, **Zhang SL**, Chen HS (2007) Genome-wide association tests by using block information in family data, *BMC Genetics*, 1(Suppl 1)**:**S149.
9. Wang X, Zhang Z, **Zhang SL**, Sha Q (2007) Genome-wide association tests by two-stage approaches with unified analysis of families and unrelated individuals. *BMC Genetics*, 1**(**Suppl 1)**:**S140.
10. Feng T, **Zhang SL**, Sha Q (2007) A method dealing with a large number of correlated traits in a linkage genome scan. *BMC Genetics*, 1(Suppl 1)**:**S84.
11. Naranjo F, Márquez I, Gendzekhadze K, **Zhang SL**, Fernández-Mestre M, Yegres F, Richard-Yegres N, Navas T, Montagnani S, Ogando V, Layrisse Z (2006) Human leukocyte antigen class I and MICA haplotypes in a multicase family with Cladophialophora carrionii chromoblastomycosis. *Tissue Antigens* 68 (4), 287–292.
12. Zhu X, **Zhang SL**, Tang H, Cooper R (2006) A classical likelihood based approach for admixture mapping using EM algorithm. *Human Genetics* 120(3): 431-445.
13. Sha Q, Zhang X, Zhu X, ***Zhang SL** (2006) Analytical correction for multiple testing in admixture mapping. *Human Heredity 62: 55-63*.
14. Sha Q, Zhu X, Zuo Y, Cooper, R, ***Zhang SL** (2006) A combinatorial searching method for detecting a set of interacting loci associated with complex traits. *Annals of Human Genetics* 70 (5), 677-692
15. Sha Q, Dong J, Jiang R, ***Zhang SL (**2005) Test of association between quantitative traits and haplotypes in a reduced-dimensional space. *Ann Hum Genet.* 69(6):715-732
16. Sha Q, Dong J, Jiang R, Chen HS, ***Zhang SL (**2005) Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. *Genetic Epi.* 28(4):341-351
17. Yu K, **Zhang SL**, Boreck I, Kraja D, Xiong C, Myers R, Province M (2005) Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. *Ann Hum Genet* 69(4):455-467
18. Jiang H, Deng Y, Chen H, Tao L, Sha Q, Chen J, Tsai CJ, ***Zhang SL** (2004) Joint analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. *BMC Bioinformatics* 5 (1):81
19. ***Zhang SL**, Sha Q, Chen HS, Dong J, Jiang R (2004) Impact of genotyping error on type I error rate of the haplotype-sharing transmission /disequilibrium test (HS-TDT): reply to Knapp and Becker. *Am J Hum Genet 74*: 591-593.
20. Zhu X, **Zhang SL**, Kan D, Cooper R (2004) Haplotype block definition and its application. *Pacific Symposium on Biocomputing 9:152-163*
21. ***Zhang SL**, Sha Q, Chen HS, Dong J, Jiang R (2003) Transmission/disequilibrium test based on haplotype sharing for tightly linked markers. *Am J Hum Genet 73:566–579*
22. Li WD, Li D, Wang S, **Zhang SL**, Zhao H, Price RA (2003) Linkage and linkage disequilibrium mapping of genes influencing human obesity in chromosome region 7q22.1–7q35. *Diabetes* 52(6):1557-1561.
23. Chen HS, **Zhang SL** (2003) Haplotype inference for multiple tightly linked multilocus phenotypes including nuclear family information. *METMBS* 165-171

24. Dong J, **Zhang SL**, Jiang R(2003) Multipoint fine-scale mapping susceptibility genes with multiple ancestral haplotypes. *METMBS* 66-71
25. Chen HS, Zhu X, Zhao H, ***Zhang SL** (2003) Qualitative semi-parametric test for genetic associations in case-control designs under structured populations*. Ann Hum Genet* 67:250-264
26. **Zhang SL**, Wong M (2003) Wavelet threshold estimation in additive regression model. *Ann Statist* 31(1):152-172
27. **Zhang SL**, Zhu X., Zhao H (2003) On a semi-parameter test to detect associations between quantitative trait and candidate genes using unrelated individuals. *Genetic Epi* 24:45-56
28. **Zhang SL**, Zheng Z (2002) Nonlinear wavelet density estimation for correlated observations. *J System Sci Math Sci* 10:497-506
29. Zhu X, **Zhang SL**, Zhao H, Cooper RS (2002) Association mapping using a mixture model for complex traits. *Genetic Epi* 23(2):181-196
30. **Zhang SL**, Wong M, Zheng Z (2002) Wavelet threshold estimation of regression function with random design. *J Multivariate Anal* 80(2): 256-284
31. **Zhang SL**, Kidd KK, Zhao HY (2002) Detecting genetic association in case-control studies using similarity-based association tests. *Statistica Sinica* 12(1):337-359
32. **Zhang SL**, Zhao H (2002) Linkage disequilibrium mapping with genotype data. *Genetic Epi* 22(1):66-77
33. **Zhang SL**, Zhang K, Li J, Zhao H. (2002) On a family-based haplotype pattern mining method for linkage disequilibrium mapping. *Pacific Symposium on Biocomputing 7* p.100-111
34. **Zhang SL**, Zhao H (2001) Quantitative similarity-based association tests using population samples. *Am J Hum Genet* 69:601-614
35. **Zhang SL**, Pakstis AJ, Kidd KK, Zhao H (2001) Comparisons of two methods for haplotype construction and haplotype frequency estimates from population data. *Am J Hum Genet.* 69: 906-912
36. **Zhang SL**, Zhang K, Li J, Sun FZ, Zhao H (2001) Test of linkage and association for quantitative traits in general pedigree: the quantitative pedigree disequilibrium test. *Genetic Epi* 18 (Supp 1):370-375
37. Li J, Wang D, Dong J, Jiang R, Zhang K, **Zhang SL**, Zhao H, Sun F (2001) The power of transmission disequilibrium tests for quantitative traits. *Genetic Epi* 18 (Supp 1): 632-63
38. Wong MY, **Zhang SL** (2001) Degree of freedom and the likelihood ratio test for the generalized Behrens-Fisher problem*. J Appl Statist* 28(8): 1067-1074
39. **Zhang SL**, Sha Q, Zhou W (2001) Uniformly most powerful invariant test and its' application. *Northeast Math* 17(1):13-20
40. Zhao H, **Zhang SL**, Merikangas KR, et al (2000) Transmission/disequilibrium tests using multiple tightly linked markers*. Am J Hum Genet* 67(4):936-946
41. **Zhang SL**, Zhao H (2000) Linkage disequilibrium mapping using the decay of haplotype sharing method with step-wise mutation model and variable population size. *Genetic Epi* 19(Suppl 1) 99-105

42. **Zhang SL**, Sha Q, Cheng M (2000) The strong consistency of nonlinear wavelet regression Estimation. *Chinese J Appl Prob Statist* 15(4):375-380
43. Dong J, **Zhang SL** (2000) Wavelet threshold estimator of regression function with random design. *Advances Math* 28(5):471-472
44. **Zhang SL**, Zheng Z (2000) On the consistency of cross-validation in non-linear wavelet regression estimation. *Acta Mathematica Scientia* 20(1):1-11
45. **Zhang SL**, Zheng Z (1999) Convergence rate of cross-validation in nonlinear wavelet regression estimation. *Chinese Sci Bull* 44(10):898-901
46. **Zhang SL**, Zheng Z (1999) Limiting distribution of quadratic deviation of two wavelet density estimator with application. *Chinese Ann Math* 22(A):151-162
47. **Zhang SL**, Zheng Z (1999) Asymptotic normality of linear wavelet density estimator with application. *Commu. Statist-Theory Meth* 28(5):1093-1104
48. **Zhang SL**, Zheng Z (1999) Nonlinear wavelet regression estimation with random design. *Science in China (A)* 29(4):311-319
49. **Zhang SL**, Sha Q, Ma W, Wang L (1999) The best equivariant estimate of parameters in normal population. *J Engineering Math* 16(3):19-24
50. **Zhang SL**, Sha Q (1997) On the best equal-variant estimator of covariance matrix of multivariate normal population. *Communication in Statist-Theory Meth* 26(8):2021-2023
51. **Zhang SL** (1997) Strong consistency of regression function estimation for Randomly missing data. *Chinese J Appl Prob Statist* 13(2):204-210
52. **Zhang SL**, Chen C (1997) Testing the equality of linear regression models. *Heilongjiang Daxue Ziran Kexue Xuebao* 14(1):1-4
53. **Zhang SL**, Sha Q, Zhu X (1995). Test whether K groups of intra-class data belong to same linear model. *Acta Appl Math Sinica* 18(4):518-527
54. **Zhang SL** (1995) Strong consistency of regression function estimates. *Kybernetica* 31(4):375-384.
55. **Zhang SL** (1994) Linear admissible estimator in linear model with respect to restricted parameter set. *Acta Appl Math Sinica* 17(3):470-472
56. **Zhang SL**, Liu YQ (1994) An optimality property of generalized Gauss-Markov estimators. *Heilongjiang Daxue Ziran Kexue Xuebao* 11(4):14-17
57. Cai JZ, **Zhang SL** (1993) Estimation problems of covariance matrices of multivariate normal distributions. *Heilongjiang Daxue Ziran Kexue Xuebao* 10(2):22-27
58. Wu QK, **Zhang SL**, Guan JW (1993) Testing the equality of variances and regression coefficients of multi-linear models. *Heilongjiang Daxue Ziran Kexue Xuebao* 10(1):22—27
59. **Zhang SL**, Xin HX, Wu QK (1993) Singular perturbations of boundary value problems for two parameters Volterra integro-differential equations. *Heilongjiang Daxue Ziran Kexue Xuebao* 10(4): 16-20
60. **Zhang SL** (1991) Admissibility of quadratic estimators of the variance and simultaneous estimation of regression coefficients and the variance in restricted linear models. *Heilongjiang Daxue Ziran Kexue Xuebao* 8(4):19-25

61. Zhu X, **Zhang SL** (1989) Admissibility of linear estimators in linear model. *Chinese Sci. Bull* 34(11):805-808

Published Abstract:

1. Nickolov RZ, Milanov VB, **Zhang S**. Association Tests for Candidate Genes Based on Gibbs Random Fields Models. GENETIC EPIDEMIOLOGY 31(5); 491 July 2007.
2. **Zhang S**, Zhang Z, Sha Q, Wong MY. An Ensemble Learning Approach for Identifying a Set of Interacting Loci with Complex Traits. GENETIC EPIDEMIOLOGY 31(5); 506-507 July 2007.
3. Zhang Z, Sha Q, **Zhang S**. A Two-stage Multi-marker Test using the Same Date Set in Genome-wide Association Study based on Family Data. GENETIC EPIDEMIOLOGY 31(5); 506 July 2007.
4. Chen HS, Sha Q, **Zhang S**. Multi-marker association test while controlling population stratification. GENETIC EPIDEMIOLOGY 31(5); 466 July 2007.
5. **Zhang S**, Sha Q, Zhu X. Analytical correction for multiple testing in admixture mapping, including genome-scan. GENETIC EPIDEMIOLOGY 29 (3): 291-291 193 NOV 2005.
6. Zhu X, **Zhang S**, Tang H, et al. A classical likelihood based approach for admixture mapping using EM algorithm. GENETIC EPIDEMIOLOGY 29 (3): 291-292 198 NOV 2005.
7. Jiang R, Dong J, **Zhang S**, Sha Q. A multilocus association analysis method based on projection pursuit discriminant analysis. GENETIC EPIDEMIOLOGY 29 (3): 257-258 81 NOV 2005.
8. Sha Q, Chen HS, **Zhang S**. New association tests based on haplotype similarity. GENETIC EPIDEMIOLOGY 29 (3): 277-277 145 NOV 2005.
9. Chen HS, Sha Q, **Zhang S**. A sequential association test in family-based analysis with parental phenotypes. GENETIC EPIDEMIOLOGY 29 (3): 240-240 21 NOV 2005.
10. **Zhang S,** Sha Q, Zhu X. Analytical correction for multiple testing in admixture mapping, including genome-scan. GENETIC EPIDEMIOLOGY 29 (3): 291-291 193 NOV 2005.
11. **Zhang S**, Sha Q, Cooper R, et al. A combinatorial searching method for detecting a set of interacting loci associated with complex traits. AMERICAN JOURNAL OF HUMAN GENETICS 73 (5): 2593 NOV 2003.

Paper Submitted

1. Sha Q, Zhang Z, Schymick JC, Traynor BJ, **Zhang SL**. Genome-wide association reveals three SNPs associated with sporadic amyotrophic lateral sclerosis through their interactions (submitted to *European Journel of Human Genetics*)
2. Z Zhang, H Qin, **S Zhang,** Q Sha. A localized expectation-maximization algorithm for imputing the genotypes at untyped loci in genome-wide studies (submitted to *Bioinformatics*)

3. H Qin, T Feng, **S Zhang,** Q Sha. Genome-wide Data-driven Weighted Association Testing Boosted by Founder Information (submitted to *European Journel of Human Genetics*)

Papers in preparation:

1. T Feng, Q Sha, **S Zhang**. Using the mixture of multiple methods to reduce SNPs for genome-wise studied.
2. Chen HS**,** Sha Q, **Zhang S**. Multi-marker association test while correcting population stratification.
3. Z Zhang, **S Zhang**. Q Sha. Genome-wide association studies for mapping complex disease genes using association rules and their unions.
4. T Feng, **S Zhang,** Q Sha**.** Odds Ratio Estimates Based on Case-Control Data from Genome-Wide Association Studies.
5. R Tang, F Tao, Q Sha, **S Zhang**. A New Sliding-Window Test via Principal Component Analysis.
6. Z Zhang, A Niu, **S Zhang**, Q Sha. Identify joint effects of genes in Genome-wide association studies.

Computing and Software

Language/Package: Fortran, C, C++, S-plus, R, and SAS.
Software produced: (free available for research community through website http://www.math.mtu.edu/~shuzhang or http://bioinformatics.med.yale.edu**)**

[1] LDMhap: Mapping disease gene with haplotype data
[2] LDMgen: Mapping disease gene with genotype data
[3] MultiTDT: TDT type test by using tightly linked multiple markers
[4] SAT: Association test based on case-control sample which allow population structure
[5] QSAT: The quantitative version of SAT.
[6] **HS-TDT**: Haplotype-sharing TDT
[7] **ELA**: Ensemble learning approach to detect gene-gene interactions

Talks and Presentations

1. Association Tests for Candidate Genes Based on Gibbs Random Fields Models(poster). 15th Annual Meeting of the International Genetic Epidemiology Society, Tampa Bay, FLA, 2006.
2. A two-stage multi-marker test using the same date set in genome-wide association study based on family data (poster). 15th Annual Meeting of the International Genetic Epidemiology Society, Tampa Bay, FLA, 2006.

3. Multi-marker association test while correcting population stratification (poster). 15th Annual Meeting of the International Genetic Epidemiology Society, Tampa Bay, FLA, 2006.
4. Genome-wide association tests by two-stage approaches with unified analysis of families and unrelated individuals (poster). 15th Genetic Analysis Workshop, Tampa Bay, FLA, 2006.
5. Genome-wide association tests by using block information in family data (poster). 15th Genetic Analysis Workshop, Tampa Bay, FLA, 2006.
6. A method dealing with a large number of correlated traits in a linkage genome scan (poster). 15th Genetic Analysis Workshop, Tampa Bay, FLA, 2006.
7. A multiple test procedure controlling Type I error for genome scan association studies using HapMap data. Joint Statistical Meetings, Section on Statistics in Epidemiology, Biometrics, ENAR, 2006.
8. Ensemble Learning for Set-Association (ELSA). University of Michigan, April, 2006.
9. New association tests based on haplotype similarity (poster). 14th Annual Meeting of the International Genetic Epidemiology Society. Salt Lake City, UT, 2005.
10. A sequential association test in family-based analysis with parental phenotypes (poster). 14th Annual Meeting of the International Genetic Epidemiology Society. Salt Lake City, UT, 2005.
11. A multilocus association analysis method based on projection pursuit discriminant analysis (poster). 14th Annual Meeting of the International Genetic Epidemiology Society. Salt Lake City, UT, 2005.
12. Disease gene location estimation using admixture population (poster). 55th Annual Meeting of American Society of Human Genetic, Salt Lake City, Utah. Oct., 2005
13. Analytical correction for multiple testing in admixture mapping, including genome-scan (poster) 14th Annual Meeting of International Genetic Epidemiology Society, Park City, Utah. Oct. 2005
14. Current statistical methods in genetic epidemiology (invited) Heilongjiang University, Harbin china. July, 2005
15. Statistical Methods in detecting gene-gene interaction. Northeast Normal University. Changchun, China. July 2005
16. A Combinatorial searching method for detecting a set of interacting loci associated with complex traits. The Hong Kong University of Science and Technology. June, 2005
17. Non-parametric method in genetic association studies. The Hong Kong University of Science and Technology. June, 2005
18. Statistical and computational methods in statistical genetic. Department of Computer Science, Michigan Technological University, Houghton, MI, 2004
19. A Combinatorial searching method for detecting a set of interacting loci associated with complex traits. Michigan State University, July, 2004
20. Association studies in structured population (invited). Chinese Academy of Science, Nov. 2003.
21. Statistical methods in mapping complex disease genes (invited).Heilongjiang University, China, Nov., 2003.
22. Detecting genetic association in case-control studies using similarity-based association tests (invited). Joint Statistical Meetings. New York, Aug., 2002.

23. Population-based association studies (invited). *Northeast Normal University*, China, 2002.
24. Linkage disequilibrium mapping for complex trait by haplotype/genotype sharing. *Annual Meeting of American Society of Human Genetics.* San Diego, Oct., 2001.
25. Linkage disequilibrium mapping with genotype data. *Annual Meeting of the International Society of Genetic Epidemiology.* San Antonio, Oct., 2000.
26. Convergence rate of cross-validation for threshold wavelet regression estimator. *Fifth Beijing and Tianjing Conference on Statistics*. Beijing, China, 1999.
27. Function estimation based on wavelet methods (invited). *Chinese University, Hong Kong*, 1999.
28. Nonlinear wavelet regression estimation with random design. *Fourth China-Japan Conference on Statistics*. Xian, China, 1998.
29. Wavelet threshold estimation in additive regression model. *Annual Meeting of Chinese Society of Probability and Statistics. Beijing, China, 1998.*
30. Threshold wavelet density estimation for correlated data. *Fourth Beijing and Tianjing Conference on Statistics*. Beijing, China, 1998.
31. Application of wavelet methods in Statistics. *Annual Meeting of Chinese Society* of *Probability*

Funding

1. MTU Research Excellence Fund (PI). Award amount $ 35,000, Period covered 6/1/02-5/31/03.

2. 1 R01 GM069940-01A2 (PI; Co-PIs: HS Chen, R Jiang, J Dong)
Statistical Methods for Mapping Complex Disease Genes
Award amount: $700,000.
Period covered: 08/01/2005 – 7/31/2008
Source: NIH/NIGM

3. 1 R03 HG 003613 -01 (PI; Co-PI: HS Chen)
Statistical Methods for Admixture Mapping
Award amount: $228,000.
Period covered: 9/26/2005 – 8/31/2008
Source: NIH/HGRI

4. 1R01HG003054-01A1(PI of subcontract; PI of whole project: X. Zhu in Loyola University)
LD Mapping Using Haplotype Block: Methods & Application
Award amount: $800,000 (Award of subcontract: $110,000)
Period covered: 4/1/2005 – 3/31/2009
Source: NIH

5. 1R03AG024491-01 (PI: Huann-Sheng Chen)
Mapping Complex Disease Genes Incorporating Age-at-Onset
Award amount: $140,200.
Period covered: 9/1/2004 – 8/31/2006

Source: NIH

6. NSF 0421756 (PI: Chung-Jui Tsai)
A functional genomics approach to investigate regulation of phenolic glycoside metabolism in populus
Award amount: $2,014,200.
Period covered: 9/1/2004 – 8/31/2008
Source: NSF

Proposal not funded:

Identification of interaction genes for sporadic ALS, NIH, (submitted on June, 2007), 04/15/08-04/14/10, $156,000, co-PI (PI: Qiuying Sha. co-PI: Huann-Sheng Chen).

Identification of interaction genes for sporadic ALS, NIH, (revised on Nov, 2007), 07/15/08-07/14/10, $156,000, co-PI (PI: Qiuying Sha, co-PI: Huann-Sheng Chen).

Identify gene-gene interactions in genome-wide association studies, REF (RS), MTU, co-PI (Submitted on Feb, 2008), 06/01/08-05/30/09, $38,000, (PI: Qiuying Sha).

Courses Taught in Recent Years:

Fall Semester (2006) Statistical Genetics
Fall Semester (2005) Computational Statistics
Spring Semester (2004) Statistical Genetics, and Engineering Statistics
Fall Semester (2004) Mathematical Statistics II, and Engineering Statistics
Spring Semester (2003) Mathematical Statistics I
Fall Semester (2003): Engineering Statistics
Fall Semester (2002): Statistical Genetics, and Engineering Statistics
Fall Semester (2001): Probability
Fall Semester (2000): Generalized Linear Model
Fall Semester (1999): Advanced Probability
Spring Semester (1998): Multivariate Statistics

Mentor of Postdoctoral Fellows:

2005-present: Zhaogong Zhang (Statistical Genetics and Data Mining)
2006-Jan. 2008: Tao Feng (Statistical Genetics)

Advisor of Ph.D Students:

2001-2004: Radoslav Nickolov (Statistical Genetics, MTU)
2005-present: Zhan Ye (Statistical Genetics, MTU)
2004-present: Huaizhen Qin (Statistical Genetics, MTU)
2005-present: Xuexia Wang (Statistical Genetics, MTU)
2006-present: Rui Tang (Statistical Genetics, MTU)

Advisor of Master Students:

2003-2005: Raymond Molzon (Statistical Genetics, MTU)
2003-2005: Zhan Ye (Statistical Genetics, MTU)
2002-2004: Haihua Li (Statistical Genetics, MTU)
2002-2004 Yanyan Lu (Statistical Genetics, MTU)
2001-2003: Hong Li (Statistical Genetics, MTU)
1995-1998 Weijun Ma (Statistics, Heilongjiang University)
1995-1998 Yinmei Liu (Statistics, Heilongjiang University)
1995-1998 Wenyuan Chen (Statistics, Heilongjiang University)
1995-1998 Tao Feng (Statistics, Heilongjiang University)
1995-1998 Wenhai Zhou (Statistics, Heilongjiang University)

Committee Member of the Following Graduate Students:

Liu Yuanxin (MA); Shuang Du (MA); Lin Tao (MA); Valentin Milanov (MA); Fang Guo (ME); Xiaorui Fan (ME); Xinli Wang (CS); Priya Ranjan (FRES); Li Li (MA) MS; Xiaoqi Cui (MA); Kumari Sapna (MA)

As a Reviewer for Following Journals:

American Journal of Human Genetics; Annuals of Statistics; Annuals of Human Genetics; Genetic Epidemiology; Bioinformatics; Annals of Institute mathematical Statistic; BMC Bioinformatics; BMC Genetics; Statistical Applications in Genetics and Molecular Biology; Human Heredity; Journal of Agricultural, Biological, and Environmental Statistics; Journal of Multivariate Analysis; Human Genomics; Human Genetics.

Committees Services:

Statistics recruitment committee (2007)
Graduate Committee (2006)