

The Department of Mathematical Sciences  
Michigan Technological University  
1400 Townsend Drive  
Houghton MI 49931

Phone: (906)-487-2146  
Fax: (906)-487-3133  
Email: [qsha@mtu.edu](mailto:qsha@mtu.edu)

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## Education:

Ph.D. in Statistics, May 2005. Michigan Technological University, Houghton, MI  
M.S. in Mathematics, July 1988. Heilongjiang University, Harbin, China  
B.S. in Mathematics, July 1985. Heilongjiang University, Harbin, China

## Professional experience:

Assistant Professor at Michigan Technological University, Houghton, 2005 – present  
Affiliated Faculty Member , Biotech Research Center, Michigan Technological University.  
August 2007—present  
Teaching Assistant Instructor at Michigan Technological University, 2002-2004  
Research Assistant at Michigan Technological University, 2001-2002  
Associate Professor at Heilongjiang University, Harbin, China 1997 - 1999  
Assistant Professor at Heilongjiang University, Harbin, China 1990 - 1997  
Lecturer at Heilongjiang University, Harbin, China 1988 – 1990

## Research interests: Statistical Genetics

- Developed statistical methods and computational tools to map complex disease genes both based on pedigree data and population data.
- Developed statistical methods used in microarray data analysis.

## Honors:

Outstanding faculty research award (junior level), Department of Mathematical Sciences, Michigan Technological University, 2007.  
Graduate Dean's Award for Academic Achievement, Michigan Technological University, 2004.  
Outstanding Academic Achievement Award, Department of Mathematical Sciences, Michigan Technological University, April, 2002.  
Outstanding Academic Achievement Awards in the following courses (for top 2 students): Mathematical Statistics I, II, Experimental Design, Regression Analysis, Categorical Data Analysis, Mathematical Modeling, and Complex Variables. (Department of Mathematical Sciences, Michigan Technological University, 2002 – 2004).  
Outstanding Research Award, Heilongjiang University, Harbin, China, 1998.  
Outstanding Teaching Award, Heilongjiang University, Harbin, China, 1997.  
Outstanding Teaching Award, Heilongjiang Province, Harbin, China, 1991.

## Computer skills:

Programming in C, C++, UNIX, SAS, S-Plus, and Mathematica.

## Activity:

PHI KAPPA PHI Honor Society member, since 2003

American Mathematical Society member, since 2002

## Peer-reviewed publications (\* denotes senior corresponding author):

1. Wang X, Zhang SL, **Sha Q\*** (2008) 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. Zhang Z, Zhang S, **Sha Q\*** (2007) A multi-marker test based on family data in genome-wide association study. *BMC Genetics*, 8:65.
4. Feng T, Zhang S, **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.
5. **Sha Q\***, Chen H, Zhang S (2007) New association tests based on haplotype similarity. *Genetic Epidemiology*, 31(6):577-93.
6. Feng T, Zhang S, **Sha Q\*** (2007) A method dealing with a large number of correlated traits in a linkage genome scan. *BMC Proceedings*, 1(Suppl 1):S84.
7. Tang R, Wang F, **Sha Q**, Zhang S, Chen HS (2007) Genome-wide association tests by using block information in family data. *BMC Proceedings*, 1(Suppl 1):S149.
8. Wang X, Zhang Z, Zhang S, **Sha Q\*** (2007) Genome-wide association tests by two-stage approaches with unified analysis of families and unrelated individuals. *BMC Proceedings*, 1(Suppl 1):S140.
9. Zhang S, **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.
10. **Sha Q**, Zhang X, Zhu X, Zhang S (2006). Analytical correction for multiple testing in admixture mapping. *Human heredity* 62: 55-63.
11. **Sha Q**, Zhu X, Cooper R, Zhang S (2006). A combinatorial searching method for detecting a set of interacting loci associated with complex traits. *Annals of Human Genetics* 70(5):677-692.
12. **Sha Q**, Dong J, Jiang R, Zhang S (2005). Tests of association between quantitative traits and haplotypes in a reduced-dimensional space. *Annals of Human Genetics* 69, 715-732.
13. **Sha Q**, Dong J, Jiang R, Chen HS, Zhang S (2005). Haplotype sharing transmission/disequilibrium test that allows for genotyping error. *Genetic Epidemiology* 28(4): 341-351.

14. Jiang, H., Y. Deng, H-S. Chen, L. Tao, **Sha Q**, J. Chen, C-J Tsai and S. Zhang (2004). Joint analysis of multiple microarray gene-expression data sets to select lung adenocarcinoma marker genes. *BMC Bioinformatics* 5(1):81.
15. Zhang S, **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.
16. Zhang S, **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.
17. Zhang S, **Sha Q**, Zhou W (2001). Uniformly most powerful invariant test and its application. *Northeast Math* 17(1): 13-20.
18. Zhang S, **Sha Q**, Cheng M (2000). The strong consistency of nonlinear wavelet regression estimation. *Chinese J Appl Prob Statist* 15(4): 375-380.
19. Zhang SL, **Sha Q**, Ma W, Wang L (1999). The best equal-variant estimate of parameters in normal population. *J Engineering Math* 16(3): 19-24.
20. **Sha Q**, Xiao C, (1999). Strong consistency of wavelet estimators of regression functions. *J. of Natural Science of Heilongjiang University* 16(1), 9-13.
21. Zhang S, **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.
22. **Sha Q**, (1996). The relations of three topologies in the space of set-value mappings. *J. Harbin Univ. Sci. & Tech.* 20(2), 115-116.
23. **Sha Q**, Zheng D, Zhang J (1996). Admissible linear estimators of parameter functions which may be non-estimable in Gauss-Markov model. *Heilongjiang Daxue Ziran Kexue Xuebao* 13(3): 5-9.
24. **Sha Q**, (1996). Strong consistency of partitioning estimates of regression function for randomly missing data. *J. of Natural Science of Heilongjiang University* 13(1), 10-15.
25. Lu C, **Sha Q**, and Li W (1996). Admissibility of a simultaneous nonnegative quadratic estimator of variance components. (Chinese) *J. Sys. Sci. & Math. Sci.* 16(4): 361—366.
26. Zhang S, **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
27. **Sha Q** (1995). The topology of star point wise convergence and the topology of star uniform convergence in the space of S-continuous set-valued mappings. *Heilongjiang Daxue Ziran Kexue Xuebao* 12(3): 9-12.
28. **Sha Q** (1991). Two types of weak continuity of set-valued mappings. *Heilongjiang Daxue Ziran Kexue Xuebao* 8(1): 30--34.

### Papers submitted for publication:

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 Journal of Human Genetics*)
2. Z Zhang, H Qin, S Zhang, **Sha Q\***. 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, **Sha Q\***. Genome-wide Data-driven Weighted Association Testing Boosted by Founder Information (submitted to *European Journal of Human Genetics*)

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**Papers in preparation:**

1. H.S. Chen, **Q. Sha**, S. Zhang. Multi-marker association test while correcting population stratification.
2. T Feng, **Q Sha**, S Zhang. Using the mixture of multiple methods to reduce SNPs for genome-wise studied.
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.

**Conference presentation:**

1. Z. Zhang, **Q. Sha**, S. Zhang. A two-stage multi-marker test using the same data set in genome-wide association study based on family data. *15<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*, Tampa Bay, FLA, 2006.
2. H.S. Chen, **Q. Sha**, S. Zhang. Multi-marker association test while correcting population stratification. *15<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*, Tampa Bay, FLA, 2006.
3. X. Wang, Z. Zhang, **Q. Sha**, S. Zhang, Genome-wide association tests by two-stage approaches with unified analysis of families and unrelated individuals. *15<sup>th</sup> Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
4. R. Tang, F. Wang, **Q. Sha**, S. Zhang, H.S. Chen. Genome-wide association tests by using block information in family data. *15<sup>th</sup> Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
5. T. Feng, **Q. Sha**, S. Zhang, A method dealing with a large number of correlated traits in a linkage genome scan. *15<sup>th</sup> Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
6. R. Jiang, J. Dong, **Q. Sha**, S. Zhang. 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.
7. **Q. Sha**, H.S. Chen, S. Zhang. New association tests based on haplotype similarity. *14<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
8. H.S. Chen, **Q. Sha**, S. Zhang. A sequential association test in family-based analysis with parental phenotypes. *14<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
9. S. Zhang, **Q. Sha**, X. Zhu. Analytical correction for multiple testing in admixture mapping, including genome-scan. *14<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
10. R. Jiang, J. Dong, S. Zhang, **Q. Sha**. A multilocus association analysis method based on projection pursuit discriminant analysis. *14<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.

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11. S. Zhang, **Q. Sha** and X. Zhu. Disease gene location estimation using admixture population. *55<sup>th</sup> Annual Meeting of the American Society of Human Genetics*. Salt Lake City, UT, 2005.

### **Published Abstract:**

1. 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.
2. 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.
3. 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.
4. **Sha Q**, Chen HS, Zhang S. New association tests based on haplotype similarity. *GENETIC EPIDEMIOLOGY* 29 (3): 277-277 145 NOV 2005.
5. 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.
6. S. Zhang, **Q. Sha**, X. Zhu. Analytical correction for multiple testing in admixture mapping, including genome-scan. *GENETIC EPIDEMIOLOGY* 29 (3): 291-291 193 NOV 2005.
7. An Ensemble Learning Approach for Identifying a Set of Interacting Loci with Complex Traits. S. Zhang(1,2), Z. Zhang (1,2), **Q. Sha** (1), M.Y. Wong(3) *GENETIC EPIDEMIOLOGY* 31(5); 506-507 July 2007
8. A Two-stage Multi-marker Test using the Same Data Set in Genome-wide Association Study based on Family Data Zhaogong Zhang(1), **Qiuying Sha**(2), Shuanglin Zhang(3) *GENETIC EPIDEMIOLOGY* 31(5); 506 July 2007
9. Multi-marker association test while controlling population stratification H.S. Chen, **Q. Sha**, S. Zhang *GENETIC EPIDEMIOLOGY* 31(5); 466 July 2007

### **Courses taught in recent years:**

Spring 2008: Engineering Statistics  
 Fall 2007: Engineering Statistics  
 Spring 2007: Regression Analysis  
 Fall 2006: Mathematical Statistics, Engineering Statistics  
 Fall 2005: Mathematical Statistics, Pre-Calculus  
 Fall 2004: Pre-Calculus  
 Summer 2004: Pre-Calculus  
 Spring 2004: Pre-Calculus  
 Fall 2003: Pre-Calculus  
 Summer 2003: Calculus II  
 Spring 2003: Calculus I

### **Advisor of PhD student**

2004-present: Adan Niu (Statistical Genetics, MTU)

2008-present: Shurong Fang (Statistical Genetics, MTU)

**Committee member of the following graduate students:**

Jiping Tang (EME) PhD (Dec, 2007)

Clara Anton (Forest Science) PhD

Gongyi Feng (MA) MS (August, 2007)

Mohit Bansal (MEEM) MS (May, 2007)

Rui Tang (MA) MS (May, 2007)

Xuexia Wang (MA) PhD (May, 2007)

Eric Kamischke (MA) MS (April, 2007)

Kumari, Sapna (MA) MS (April, 2007)

Jiping Tang (EME) PhD (May, 2006)

Zhan Ye (MA) PhD (April, 2006)

Jiang Zheng (EME) PhD (Dec, 2006)

Li Li (MA) MS (May, 2006)

**As a reviewer for the following journal:**

*Bioinformatics; Statistical Applications in Genetics and Molecular Biology; Genetic Epidemiology*

**Committees Services:**

Advisory committee (2007)