

Contact Information

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Department of Mathematical Sciences
Michigan Technological University
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Education

- May 2005 **Ph.D.**, Applied Statistics
Department of Mathematical Sciences, Michigan Technological University
Dissertation Title: Multi-locus Association Tests for Detection Complex
Disease Genes
Advisor: Dr. Jianping Dong
- July 1998 **M.S.**, Mathematics
Department of Mathematics, Heilongjiang University, Harbin, China
- July 1985 **B.S.**, Mathematics
Department of Mathematics, Heilongjiang University, Harbin, China

Professional Experience

- Aug 2016 – present Professor, Department of Mathematical Sciences,
Michigan Technological University
- Aug 2011 – July 2016 Associate Professor, Department of Mathematical Sciences,
Michigan Technological University
- Aug 2007 – present Affiliated Faculty Member, Biotech Research Center,
Michigan Technological University
- Aug 2005 – July 2011 Assistant Professor, Department of Mathematical Sciences,
Michigan Technological University
- Aug 1997 – Dec 1999 Associate Professor, Department of Mathematics,
Heilongjiang University, China
- Aug 1990 – July 1997 Assistant Professor, Department of Mathematics,
Heilongjiang University, China
- Aug 1988 – July 1990 Lecturer, Department of Mathematical Sciences,
Heilongjiang University, China

Research Interests: Statistical Genetics

- Develop statistical methods and computational tools to identify complex disease genes based on family data or population data.
- Develop statistical methods used in microarray data analysis.

Honors and Awards

- Outstanding Faculty Research Award (senior level), Department of Mathematical Sciences, Michigan Technological University, 2016.
- Outstanding Teaching Award (senior level), Department of Mathematical Sciences, Michigan Technological University, 2014.
- Outstanding Faculty Research Award (senior level), Department of Mathematical Sciences, Michigan Technological University, 2014.
- Outstanding Teaching Award (junior level), Department of Mathematical Sciences, Michigan Technological University, 2011.
- 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 (graduate student level), Department of Mathematical Sciences, Michigan Technological University, April, 2002.
- Outstanding Academic Achievement Awards in the following graduate courses (for top 2 students): Mathematical Statistics I, II, Experimental Design, Regression Analysis, Categorical Data Analysis, Mathematical Modeling, 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++, SAS, R, and Mathematica.

Professional Memberships

The American Society of Human Genetics member

The International Genetic Epidemiology Society member

Peer-reviewed Publications (* denotes corresponding author)

1. Yang X, Wang S, Zhang S, **Sha Q*** (2017) Detecting association of rare and common variants based on cross-validation prediction error. *Genetic Epidemiol*, 41:233–242. PMID:28176359 DOI:10.1002/gepi.22034
2. **Sha Q**, Zhang K, Zhang S (2016) A nonparametric regression approach to control for population stratification in rare variant association studies. *Sci. Rep.* **6**, 37444; doi: 10.1038/srep37444.
3. Liang X, **Sha Q**, Zhang S (2016) An adaptive Fisher's combination method for joint analysis of multiple phenotypes in association studies. *Sci. Rep.* **6**, 34323; doi: 10.1038/srep34323.
4. Zhu H, Zhang S, **Sha Q*** (2015) A comparison of methods for joint association analysis of multiple traits. *Human Heredity*, 80:144-152 (DOI: 10.1159/000446239).

5. Zhu H, Wang Z, Wang X, **Sha Q*** (2016) A novel statistical method for rare variants association studies in general pedigrees. *BMC Proc*, 10 (Suppl 7): 22 DOI 10.1186/s12919-016-0029-6
6. Wang Z, Wang X, **Sha Q**, Zhang S (2016) Joint analysis of multiple traits in rare variant association studies. *Ann Hum Genet*, 80: 162-171. DOI: 10.1111/ahg.12149.
7. Fang S, Zhang S, **Sha Q*** (2016) Literature reviews on methods for rare variant association studies. *Human Genet Embryol* 6:133. doi:10.4172/2161-0436.1000133.
8. Wang Z, **Sha Q**, Zhang S (2016) Joint analysis of multiple traits using optimal maximum heritability test. *PLOS ONE* 11(3): e0150975. doi:10.1371/journal.pone.0150975.
9. Wang X, Zhang S, Li Y, Li M, **Sha Q*** (2015) A powerful approach to test an optimally weighted combination of rare variants in admixed populations. *Genetic Epidemiol*, 39: 294-305.
10. **Sha Q**, Zhang S (2015) Test of rare variant association based on affected sib-pairs. *Eur J Hum Genet*, 23: 229-237.
11. **Sha Q**, Zhang S (2014) A rare variant association test based on combinations of single-variant tests. *Genetic Epidemiol*, 38: 494-501.
12. Zhao X, **Sha Q**, Zhang S, Wang X (2014) Testing optimally weighted combination of variants for hypertension. *BMC Proc*, 8(Suppl 1): S59.
13. Wang S, Fang S, **Sha Q**, Zhang S (2014) Detecting association of rare and common variants by testing an optimally weighted combination of variants with longitudinal data. *BMC Proc*, 8(Suppl 1): S91.
14. **Sha Q**, Zhang S (2014) A novel test for testing the optimally weighted combination of rare and common variants based on data of parents and affected children. *Genetic Epidemiol*, 38: 135–143.
15. Fang S, Zhang S, **Sha Q*** (2013) Detecting association of rare variants by testing an optimally weighted combination of variants for quantitative traits in general families. *Ann Hum Genet*, 77(6): 524-534
16. **Sha Q**, Wang S, Zhang S (2013) Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. *Eur J Hum Genet*, 21(3): 332-7.
17. **Sha Q**, Wang X, Wang X, Zhang S (2012) Detecting association of both rare and common variants by testing an optimally weighted combination of variants. *Genetic Epidemiol*, 36: 561-571.
18. Fang S, **Sha Q**, Zhang S (2012) Two adaptive weighting methods to test for rare variant associations in family-based designs. *Genetic Epidemiol*, 36: 499–507.
19. Zhang Z, **Sha Q**, Wang X, Zhang S (2011) Two strategies of extreme values and iterative regression and their hybrid approach for rare variants in association studies. *BMC Proc*, 5(Suppl): S112.
20. Fang S, Ma W, Zhang S, **Sha Q*** (2011) A two-stage approach to detect gene-gene and gene-environment interaction: application to GAW17 dataset, *Journal of Natural Science of Heilongjiang University*, 28(6):767-770.
21. Niu A, Zhang S, **Sha Q*** (2011) A novel method to detect gene-gene interactions in structured populations: MDR-SP. *Ann Hum Genet*, 75: 742-754.
22. **Sha Q**, Zhang S (2011) A test of Hardy Weinberg equilibrium in structured populations. *Genetic Epi*, 35: 671-678.
23. **Sha Q**, Zhang Z, Zhang S (2011) Joint analysis for genome-wide association studies in family-based designs. *PLoS ONE* 6(7): e21957. doi:10.1371/journal.pone.0021957.

24. **Sha Q**, Zhang Z, Zhang S (2011) An improved score test for multi-marker association. *Genetic Epidemiol*, 35: 350-359.
25. Zhang Z, Niu A, **Sha Q*** (2010) Identify interaction genes in genome-wide association studies using a model-based two-stage approach. *Ann Hum Genet*, 74(5):406-415.
26. Qin H, Feng T, Zhang S, **Sha Q*** (2010) A data-driven weighting scheme for family-based genome-wide association studies. *Eur J Hum Genet*, 18:596-603.
27. **Sha Q**, Zhang Z, Schymick JC, Traynor BJ, Zhang S (2009) Genome-wide association reveals three SNPs associated with sporadic amyotrophic lateral sclerosis through their interactions. *BMC Med Genet*, 10:86.
28. Tang R, Tao F, **Sha Q**, Zhang S (2009) A new sliding-window test via principal component analysis. *Ann Hum Genet*, 73: 631–637.
29. **Sha Q**, Tang R, Zhang S (2009) Detect susceptibility genes for Rheumatoid Arthritis based on a novel sliding-window method. *BMC Proc*, 3:S14.
30. Niu A, Zhang Z, **Sha Q*** (2009) Application of seventeen two-locus models in genome-wide association studies by two-stage strategy. *BMC Proc*, 3:S26.
31. Wang X, Qin H, **Sha Q*** (2009) Incorporating multiple-marker information to detect risk loci for rheumatoid arthritis. *BMC Proc*, 3:S28.
32. Cui X, **Sha Q**, Zhang S, Chen H-S (2009) A combinatorial approach for detecting gene-gene interaction using multiple traits of Genetic Analysis Workshop 16 rheumatoid arthritis data. *BMC Proc*, 3:S43.
33. Wang X, Zhang S, **Sha Q*** (2009) A new association test to test multiple-marker association. *Genetic Epidemiol*, 33:164-171.
34. Zhang Z, Zhang S, Wong MY, Wareham NJ, **Sha Q*** (2008) Ensemble learning approach jointly modeling main and interaction effects in genome-wide association studies. *Genetic Epidemiol*, 32:285-300.
35. Zhang Z, Zhang S, **Sha Q*** (2007) A multi-marker test based on family data in genome-wide association study. *BMC Genet*, 8:65.
36. Feng T, Zhang S, **Sha Q*** (2007) Two-stage association tests for genome-wide association studies based on family data with arbitrary family structure. *Eur J Hum Genet*, 15:1169–1175.
37. **Sha Q***, Chen H, Zhang S (2007) New association tests based on haplotype similarity. *Genetic Epidemiol*, 31(6):577-93.
38. Feng T, Zhang S, **Sha Q*** (2007) A method dealing with a large number of correlated traits in a linkage genome scan. *BMC Proc*, 1:S84.
39. Tang R, Wang F, **Sha Q**, Zhang S, Chen HS (2007) Genome-wide association tests by using block information in family data. *BMC Proc*, 1:S149.
40. 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 Proc*, 1:S140.
41. **Sha Q**, Zhang X, Zhu X, Zhang S (2006). Analytical correction for multiple testing in admixture mapping. *Human Hered*, 62:55-63.
42. **Sha Q**, Zhu X, Cooper R, Zhang S (2006). A combinatorial searching method for detecting a set of interacting loci associated with complex traits. *Ann Hum Genet*, 70(5):677-692.
43. **Sha Q**, Dong J, Jiang R, Zhang S (2005). Tests of association between quantitative traits and haplotypes in a reduced-dimensional space. *Ann Hum Genet*, 69:715-732.

44. **Sha Q**, Dong J, Jiang R, Chen HS, Zhang S (2005). Haplotype sharing transmission/disequilibrium test that allows for genotyping error. *Genetic Epidemiol*, 28(4): 341-351.
45. Jiang H, Deng Y, Chen HS, Tao L, **Sha Q**, Chen J, Tsai CJ, Zhang S (2004). Joint analysis of multiple microarray gene-expression data sets to select lung adenocarcinoma marker genes. *BMC Bioinformatics* 5(1):81.
46. 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.
47. 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.
48. Zhang S, **Sha Q**, Zhou W (2001). Uniformly most powerful invariant test and its application. *Northeast Math*, 17(1):13-20.
49. Zhang S, **Sha Q**, Cheng M (2000). The strong consistency of nonlinear wavelet regression estimation. *Chinese J Appl Prob Statist*, 15(4):375-380.
50. 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.
51. **Sha Q**, Xiao C, (1999). Strong consistency of wavelet estimators of regression functions. *J. of Natural Science of Heilongjiang University*, 16(1):9-13.
52. 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.
53. **Sha Q** (1996). The relations of three topologies in the space of set-value mappings. *J Harbin Univ Sci & Tech*, 20(2):115-116.
54. **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.
55. **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.
56. 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.
57. 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.
58. **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.
59. **Sha Q** (1991). Two types of weak continuity of set-valued mappings. *Heilongjiang Daxue Ziran Kexue Xuebao*, 8(1):30-34.

Book Chapters

1. Zhang S, **Sha Q** (2007) Association tests for complex disease genes while controlling population stratification. In “Current Topics in Human Genetics: Studies in Complex Diseases” (H.W. Deng, H. Shen, Y.J. Liu, and H. Hu, eds), pp. 255-283. World Scientific Publishing Company, Singapore. Imperial College Press. ISBN 978-981-270-472-6.

Proceedings

1. Fang S, **Sha Q***. “Two-locus analysis for genome-wide association studies”, Joint Statistical Meetings, Section on Clinical Trials, Biopharmaceutical Section, 2010.

Papers Submitted for Publication

1. Liang X, **Sha Q**, Zhang S. Joint analysis of multiple phenotypes in association studies using allele-based K-means clustering approach for non-normal distributions. Submitted to *Ann Hum Genet*.

Papers in Progress

1. Zhu H, Zhang S, **Sha Q**. A novel method to detect associations between multiple phenotypes and genetic markers.
2. Wang Z, **Sha Q**, Zhang K, Zhang S. A novel test by testing an optimally weighted combination of common and rare variants with multiple traits.
3. Yang X, Zhang S, **Sha Q**. Joint analysis of multiple phenotypes in association studies based on cross-validation prediction error.

Conference Presentations

1. Wang Z, **Sha Q**, Zhang K, Zhang S. A novel test by testing an optimally weighted combination of common and rare variants with multiple traits (Poster). 2017 ENAR Spring Meeting. Washington, DC.
2. Yang X, Zhang S, **Sha Q**. Joint analysis of multiple phenotypes in association studies based on cross-validation prediction error. 2017 ENAR Spring Meeting. Washington, DC.
3. Zhu H, Zhang S, **Sha Q**. A novel method to detect associations between multiple phenotypes and genetic markers (Poster). Dahshu Data Science Symposium: Computational Precision Health 2017. San Francisco Bay Area.
4. Wang Z, **Sha Q**, Zhang K, Zhang S. A novel test by testing an optimally weighted combination of common and rare variants with multiple traits (Poster). Dahshu Data Science Symposium: Computational Precision Health 2017. San Francisco Bay Area, February 20-22nd, 2017.
5. Zhu H, Zhang S, **Sha Q**. A novel method to detect associations between multiple phenotypes and genetic markers (Poster). The 25th Annual Meeting of the International Genetic Epidemiology Society, Toronto, 2016.
6. Liang X, **Sha Q**, Zhang S. Joint analysis of multiple phenotypes in association studies using K-means clustering approach (Poster). *The 25th Annual Meeting of the International Genetic Epidemiology Society*, Toronto, 2016.
7. Wang Z, **Sha Q**, Zhang S. Joint analysis of multiple traits in rare variant association studies (Poster). *The 24th Annual Meeting of the International Genetic Epidemiology Society*, in Baltimore, Maryland, 2015.
8. Zhu H, Zhang S, **Sha Q**. A comparison of methods for joint association analysis of multiple traits (Poster). *The 24th Annual Meeting of the International Genetic Epidemiology Society*, in Baltimore, Maryland, 2015.

9. Liang X, **Sha Q**, Zhang S. A new method for joint analysis of multiple traits in association studies (Poster). *The 24th Annual Meeting of the International Genetic Epidemiology Society*, in Baltimore, Maryland, 2015.
10. Yang X, Zhang S, **Sha Q**. Detecting association of rare and common variants based on cross-validation prediction error (Poster). *The 24th Annual Meeting of the International Genetic Epidemiology Society*, in Baltimore, Maryland, 2015.
11. Wang Z, Wang X, **Sha Q**, Zhang S. Joint analysis of multiple traits using optimal principal components of heritability (Poster). *The 65th Annual Meeting of the American Society of Human Genetics*, in Baltimore, Maryland, 2015.
12. Zhu H, Wang Z, Wang X, **Sha Q**. A novel statistical method for rare variants association studies in general pedigrees (Talk). *The 19th Genetic Analysis Workshop*, in Vienna, Austria. 2014.
13. **Sha Q**, Zhang S. Test of rare variant association based on affected sib-pairs (Poster). *The 22th Annual Meeting of the International Genetic Epidemiology Society*, in Chicago, Illinois, 2013.
14. **Sha Q**, Fang S, Zhang S. Detecting association of rare variants by testing an optimally weighted combination of variants in family-based designs (Poster). *The 62th Annual Meeting of the American Society of Human Genetics*, in San Francisco, CA, 2012.
15. Wang S, Fang S, **Sha Q**, Zhang S. Detecting association of rare and common variants by testing an optimally weighted combination of variants with longitudinal data (Talk). *The 18th Genetic Analysis Workshop*, in Stevenson, WA. 2012.
16. Wang X, **Sha Q**, Zhang SL, Zhao X. Testing optimally weighted combination of variants for hypertension (Talk). *The 18th Genetic Analysis Workshop*, in Stevenson, WA. 2012.
17. Fang S, Zhang Z, Feng Q, Zhang S, **Sha Q**. Using both mean and variance to identify quantitative trait interaction effects (Talk). *The 17th Genetic Analysis Workshop*, in Boston, MA, 2010.
18. Zhang Z, **Sha Q**, Wang X, Zhang S, Shuanglin Zhang. Two strategies of extreme values and iterative regression and their hybrid approach for rare variants in association studies (Talk). *The 17th Genetic Analysis Workshop*, in Boston, MA, 2010.
19. Zhang Z, Qin H, Zhang S, **Sha Q**. A method to impute genotypes at untyped SNPs (Poster). *The 59th Annual Meeting of the American Society of Human Genetics*, Honolulu, Hawaii, 2009.
20. Fang S, **Sha Q**. Two-locus analysis for genome-wide association studies (Poster). *The 59th Annual Meeting of the American Society of Human Genetics*, Honolulu, Hawaii, 2009.
21. Zhang Z, Niu A, **Sha Q**. Identify interaction genes in genome-wide association studies using a model-based two-stage approach (Poster). *The 18th Annual Meeting of the International Genetic Epidemiology Society*, Kahuku, HI, 2009.
22. **Sha Q**, Tang R, Zhang S. Detect susceptibility genes for Rheumatoid Arthritis based on a novel sliding-window method (Talk). *The 16th Genetic Analysis Workshop*, St. Louis, MO, 2008.
23. Niu A, Zhang Z, Zhang S, **Sha Q**. Application of seventeen two-locus models in genome-wide association studies by two-stage strategy (Talk). *The 16th Genetic Analysis Workshop*, St. Louis, MO, 2008.
24. Qin H, Ye Z, Fang S, Zhang S, **Sha Q**. Incorporating multiple traits in genome-wide scans to find novel risk loci for rheumatoid arthritis (Talk). *The 16th Genetic Analysis Workshop*, St. Louis, MO, 2008.

25. Wang X, Qin H, Zhang S, **Sha Q**. Incorporating multiple-marker information to detect risk loci for rheumatoid arthritis (Talk). *The 16th Genetic Analysis Workshop*, St. Louis, MO, 2008.
26. Cui X, **Sha Q**, Zhang S, Chen H-S. Detecting gene-gene interaction using multiple traits in the genome-wide association study for rheumatoid arthritis data (Talk). *The 16th Genetic Analysis Workshop*, St. Louis, MO, 2008.
27. Zhang Z, **Sha Q**, Zhang S. A two-stage multi-marker test using the same data set in genome-wide association study based on family data (Poster). *The 15th Annual Meeting of the International Genetic Epidemiology Society*, Tampa Bay, FLA, 2006.
28. Chen H-S, **Sha Q**, Zhang S. Multi-marker association test while correcting population stratification (Poster). *The 15th Annual Meeting of the International Genetic Epidemiology Society*, Tampa Bay, FLA, 2006.
29. Wang X, Zhang Z, **Sha Q**, Zhang S. Genome-wide association tests by two-stage approaches with unified analysis of families and unrelated individuals (Talk). *The 15th Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
30. Tang R, Wang F, **Sha Qm**, Zhang S, Chen H-S. Genome-wide association tests by using block information in family data (Talk). *The 15th Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
31. Feng T, **Sha Q**, Zhang S. A method dealing with a large number of correlated traits in a linkage genome scan (Talk). *The 15th Genetic Analysis Workshop*, Tampa Bay, FLA, 2006.
32. Jiang R, Dong J, **Sha Q**, Zhang S. A multiple test procedure controlling Type I error for genome scan association studies using HapMap data (Talk). *Joint Statistical Meetings, Section on Statistics in Epidemiology, Biometrics*, ENAR, 2006.
33. **Sha Q**, Chen H-S, Zhang S. New association tests based on haplotype similarity (Poster). *The 14th Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
34. Chen H-S, **Sha Q**, Zhang S. A sequential association test in family-based analysis with parental phenotypes (Poster). *The 14th Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
35. Zhang S, **Sha Q**, Zhu X. Analytical correction for multiple testing in admixture mapping, including genome-scan (Poster). *The 14th Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
36. Jiang R, Dong J, Zhang S, **Sha Q**. A multilocus association analysis method based on projection pursuit discriminant analysis (Poster). *The 14th Annual Meeting of the International Genetic Epidemiology Society*. Salt Lake City, UT, 2005.
37. Zhang S, **Sha Q**, Zhu X. Disease gene location estimation using admixture population (Poster). *The 55th Annual Meeting of the American Society of Human Genetics*. Salt Lake City, UT, 2005.

Funded Grant Applications

- Identify gene-gene interactions in genome-wide association studies, REF (RS), MTU, 07/01/2009-08/30/2011, \$8661, PI.
- Statistical methods for family-based association studies, NIH, R03, 05/17/2012-3/31/2014, \$156,000, PI.
- Statistical methods for rare variant association studies, NIH, R15, 05/16/16 - 04/30/19, \$436,873, PI.

Pending Grant Applications

- Statistical methods for joint analysis of multiple traits, NIH, R15, 05/01/18 - 04/30/21, \$434,876, Co-PI (PI: Shuanglin Zhang). Submitted on Feb, 2017.

Teaching Activities

Course taught

Spring 2017	MA5741: Multivariate statistics. 13 graduate students
Fall 2016	MA4790/MA5790: Predictive Modeling. 8 under/4 graduate students MA5761: Computational Statistics. 8 graduate students
Spring 2016	MA5750: Statistical Genetics. 6 graduate students MA5712: Mathematical Statistics II. 2 graduate students
Fall 2015	MA4790: Predictive Modeling. 7 under/4 graduate students MA5761: Computational Statistics. 8 graduate students
Spring 2015	MA3710: Engineering Statistics. 54 students MA4780/MA5781: Time Series Analysis. 10/1 students
Fall 2014	MA4790: Predictive Modeling. 9 under/1 graduate student MA5761: Computational Statistics. 8 graduate students
Spring 2014	MA5750: Statistical Genetics. 9 graduate students MA4780: Time Series Analysis. 7 students
Fall 2013	MA5761: Computational Statistics. 10 graduate students
Spring 2013	Sabbatical
Fall 2012	MA5761: Computational Statistics. 5 graduate students
Spring 2012	MA3710: Engineering Statistics. 54 students MA3710: Engineering Statistics. 54 students
Fall 2011	MA5750: Statistical Genetics. 7 graduate students MA3710: Engineering Statistics. 54 students
Spring 2011	MA5712: Mathematical Statistics II. 9 graduate students
Fall 2010	MA5711: Mathematical Statistics I. 10 graduate students MA1032: Pre-calculus. 23 students. 4 hours/week
Spring 2010	MA4770: Mathematical Statistics II. 5 students
Fall 2009	MA5750: Statistical Genetics. 6 graduate students MA4760: Mathematical Statistics I. 32 students
Spring 2009	MA4770: Mathematical Statistics II. 6 students
Fall 2008	MA5750: Statistical Genetics. 6 graduate students

Spring 2008	MA4760: Mathematical Statistics I, 12 students
Fall 2007	MA3710: Engineering Statistics. 37 students
Spring 2007	MA3710: Engineering Statistics. 41 students
Fall 2006	MA4710: Regression Analysis. 20 students
Fall 2006	MA4760: Mathematical Statistics I. 9 students
Fall 2005	MA3710: Engineering Statistics. 61 students
Fall 2005	MA4760: Mathematical Statistics I. 12 students
Fall 2005	MA1032: Pre-Calculus. 31 students

Mentoring Activities

Jan 2017 – present:	Advisor of Sachithra Perera, PhD in Statistical Genetics, MTU
Jan 2016 – present:	Advisor of Fadhila Yosof, PhD in Statistical Genetics, MTU
Sep 2013 – present:	Advisor of Xinlan (Fiona) Yang, PhD in Statistical Genetics, MTU
Sep 2013 – present:	Advisor of Huanhuan (Sophi) Zhu, PhD in Statistical Genetics, MTU
Sep 2014 – present:	Advisor of Xueling Li, MS in Statistical Genetics, MTU
Jan 2016 – April 2017:	Advisor of Jack Tuomikoski, MS in Statistics, MTU
Sep 2013 – May 2014:	Advisor of Jeremy Syrjanen, MS in Statistics, (Mayo Clinic, MN , Statistical Programmer Analyst)
July 2008 – April 2013:	Advisor of Shurong Fang, PhD in Statistical Genetics, MTU (Southfield University, CT , Assistant Professor)
Jan 2011 – May 2012:	Advisor of Min (Sammi) Shu, MS in Statistical Genetic, MTU (SUNY , PhD program in Statistics)
Jan 2009 – May 2011:	Advisor of Meifang Zheng, MS in Statistical Genetics, MTU
May 2009 – Dec 2010:	Advisor of Heng Guo, MS in Statistical Genetics, MTU (AA Networks, Newark, California , Technician Associate)
July 2004 – Dec 2010:	Advisor of Adan Niu, PhD in Statistical Genetics, MTU (Hangzhou Dianzi University, Hangzhou, China . Assistant Professor)

Ph.D and MS Dissertation Committee Member

Binita Hona, PhD student in Physics
Chad Brisbois, PhD student in Physics
Wenping Deng, PhD student in Forestry
Priscilla Addison, PhD student in Geological Engineering
Zhenchuan Wang, PhD student in the Department of Mathematical Sciences
Xiaoyu Liang, PhD student in the Department of Mathematical Sciences
Chathura Gunasekara, PhD student in Computational Science and Engineering PhD program
Yadong Dong, PhD student in Civil Engineering (Dec 2016)
Henriette Groenvik, MS student in the Department of Mathematical Sciences (May 2016)
Wentao Wang, MS student in the Department of Mathematical Sciences (May 2015)
Brent Halonen, MS student in the Department of Mathematical Sciences (August, 2015)
Trevor Fisher, MS student in the Department of Computer Science (Aug, 2013)
Erin Thomas, MS student in the Department of Mathematical Sciences (May 2013)
Shuaicheng Wang, MS student in the Department of Mathematical Sciences (May 2013)
Zhitong Zhao, MS student in the Department of Mathematical Sciences (May 2012)

Sirry Bjarnadottir, PhD student in Civil Engineering (May, 2012)
Xiaoqi Cui, PhD student in the Department of Mathematical Sciences (April, 2010)
Sirry Bjarnadottir, MS student in Civil Engineering (March, 2010)
Kang Xie, PhD student in Mechanical Engineering (Dec. 2009)
Xuexia Wang, PhD student in the Department of Mathematical Sciences (Dec. 2008)
Rui Tang, PhD student in the Department of Mathematical Sciences (Dec. 2008)
Clara Anton, PhD student in the Forest Science (Oct. 2008)
Zhan Ye, PhD student in the Department of Mathematical Sciences (Aug. 2008)
Jiping Tang, PhD student in the Mechanical Engineering (Dec, 2007)
Gongyi Feng, MS student in the Department of Mathematical Sciences (August, 2007)
Mohit Bansal, MS student in the Mechanical Engineering-Engineering Mechanics (May, 2007)
Rui Tang, MS student in the Department of Mathematical Sciences (May, 2007)
Xuexia Wang, MS student in the Department of Mathematical Sciences (May, 2007)
Eric Kamischke, MS student in the Department of Mathematical Sciences (April, 2007)
Kumari, Sapna, MS student in the Department of Mathematical Sciences (April, 2007)
Zhan Ye, MS student in the Department of Mathematical Sciences (April, 2006)
Jiang Zheng, PhD student in Mechanical Engineering (EME) (Dec, 2006)
Li Li, MS student in the Department of Mathematical Sciences (May, 2006)

Service Activities

Departmental Service

Advisor for undergraduate students majoring in statistics (Fall 2013-present)
 Chair Recruitment Committee (2016-2017)
 Chair Recruitment Committee (2014-2015)
 Member Recruitment Committee (2013-2014)
 Member Recruitment Committee (2012-2013)
 Member Recruitment Committee (2011-2012)
 Wrote and graded the Qualifying Exam in Statistics for graduate students (July 2008, Sep 2010, Sep 2011, Sep 2012, Jan 2014)
 Wrote and graded Comprehensive Exam for graduate students in Linear Models (Sep 2013)
 Wrote and graded Comprehensive Exam for graduate students in Mathematical Statistics (Jan 2009, August 2009, Jan 2010, Jan 2016, Sep 2016)
 Member Graduate Committee (2010-2011)
 Participated in the Graduate Student Orientation Program: met with mentee and observed student presentations (Fall 2010)
 Mentored one graduate student in teaching: CJ Samarasinghe (Fall 2010)
 Member Statistics Recruitment Committee (2009-2010)
 Member Statistics Recruitment Committee (2008-2009)
 Member Advisory Committee (2007-2008)
 Mentored one graduate student in teaching: Chao Zhong (Fall 2005)
 Participated in the Graduate Student Orientation Program: met with mentee and observed student presentations (Fall 2005)

College and University Service

Review one SURF proposal (Feb 2017)

Served as a judge for LSTI Research forum (Sep 2016)

Served as an internal advocate for an ECM Committee: Zheyang Wang (Sep 2016-May 2017).

Task force member of H-STEM: Health Science, Technology, Engineering and Mathematics (2014-2015 academic year).

Executive Committee of Data Science (2014-2015 academic year)

Member of the Senate Committee on Research Policy (2010-2012 academic years)

Evaluated one candidate for the Strategic Faculty Hiring Initiative (SFHI) position in Energy and Health (Fall 2010)

Evaluated one candidate for the Strategic Faculty Hiring Initiative (SFHI) positions (Spring 2010)

Evaluated three candidates for the Strategic Faculty Hiring Initiative (SFHI) Computational Discovery and Innovation (Spring 2009)

Professional Service

Refereed manuscripts for the following journals:

Bioinformatics; Statistical Applications in Genetics and Molecular Biology; Genetic Epidemiology; Annals of Human Genetics; BMC Medical Genetics; BMC Genetics; IEEE/ACM Transactions on Computational Biology and Bioinformatics; PNAS; Frontiers in Genetics, section Statistical Genetics and Methodology; Journal of Heredity; Genetics Research; Genetics; Heredity; PLOS ONE; Scientific Reports; Genetica; Annals of Applied Statistics; BMC Bioinformatics.

Refereeing Grant Proposals

Served on NIH review panels for PAR-16-234: Accelerating the Pace of Drug Abuse Research Using Existing Data (R01), ZRG1 PSE-P (55) R. March 2017

Served on NIH R15 review panels for ZRG1 GGG R 80 S (Genes, Genomes and Genetics review group). Nov. 2014.

Ralph E. Powe Junior Faculty Enhancement Awards Program, Oak Ridge Associated Universities, Feb. 2008

Serving as Review Editor

Frontiers in Statistical Genetics and Methodology (since Dec. 2010)