

March 2012

## CURRICULUM VITAE

### **Gang Zheng, Ph.D.**

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**Citizenship** US Citizen

#### **Education**

09/1996 - 05/2000: PhD in Statistics, Dept of Statistics, George Washington University, Washington DC.

Thesis title: "Fisher information in order statistics and ordered randomly censored data".  
Directed by Prof. Joseph Gastwirth.

09/1994 - 05/1996: MS in Mathematics, Dept of Mathematical Science, Michigan Tech University, Houghton, MI.

09/1983 - 07/1987: BS in Applied Mathematics, Dept of Mathematics, Fudan University, Shanghai, China.

#### **Work Experience**

##### **Non-teaching**

06/2000 - date: Mathematical Statistician, Office of Biostatistics Research, National Heart, Lung and Blood Institute, Bethesda, MD.

05/1997 - 08/1999: Biostatistics COOP, Statistics Collaborative Inc., Washington, DC.

10/1996 - 01/1997: Statistics Intern, Department of Cardiology, Washington Hospital Center, Washington, DC.

01/1993 - 07/1994: Consultant, Shanghai Run-Fong Commodity Futures Co., Shanghai, China.

##### **Teaching**

09/1996 - 05/2000: Teaching Assistant, Dept of Statistics, George Washington University.

09/1994 - 05/1996: Teaching Assistant, Dept of Mathematical Science, Michigan Tech University.

09/1987 - 05/1994: Teaching Assistant, Dept of Applied Mathematics, Shanghai Second Polytechnic University, Shanghai, China.

**Co-directing PhD students in statistics and biostatistics:**

1. Terrence Hui: “Bootstrap and likelihood based inference for ranked set sampling”. PhD in statistics, 2005, Department of Statistics, George Washington University (with Prof. Reza Modarres)
2. Lihan Yan: “Group sequential robust designs in genetic studies”. PhD in biostatistics, 2009, Department of Statistics, George Washington University (with Prof. Zhaohai Li)
3. Min Yuan: “Statistical methods to detect genetic associations: robust tests and genetic model selection”. PhD in statistics, 2009, Department of Statistics and Finance, University of Science and Technology of China (with Prof. Zhiliang Ying)
4. Zang Yong: “Robust tests under genetic model uncertainty in case-control association studies”. PhD in statistics, 2011, Department of Statistics and Actuarial Science, University of Hong Kong (with Prof. Wing Kam Fung)
5. Linglu Wang: “Bayesian analysis of case-control genetic association studies in the presence of population stratification or genetic model uncertainty”. PhD in biostatistics, 2011, Department of Statistics, George Washington University (with Prof. Zhaohai Li)

**NIH Mentoring**

- Mark Meyer: Summer Intern, 2007, Department of Mathematics and Statistics, American University.
- Mark Meyer: Post-Baccalaureate Fellow, Summer, 2008 - Summer, 2009.

**NHLBI Workshop**

- Member of organizing committee: “Clinical Trials: Its Past, Present and Future” Sept 13-14, 2010, Bethesda, MD.
- Member of organizing committee: “Computational Models for Analyzing Genotype-Phenotype Associations in Rare Diseases” July 24-25, 2008, Bethesda, MD.
- Member of organizing committee: “Trans-NIH Workshop: Genome-wide Association: Analyze This! The Genes, Environment, and Health Initiative”, Aug 4-5, 2008, Bethesda, MD.
- Member of NHLBI Data Access Committee (DAC): Jan., 2010 - June, 2012.

**Honors and Awards**

1. Elected member of International Statistical Institute (ISI), 2005.
2. Received NSF-CBMS funding for attending the lecture-series on Statistical Inference from Genetic Data on Pedigrees, MTU, Houghton, 1999.
3. Outstanding Graduate Student, Washington Statistical Society, 1998.
4. Passed Ph.D. Comprehensive Examinations with Distinction, 1997.

## Professional Membership and Activities

- American Statistical Association, including Washington Statistical Society
- Institute of Mathematical Statistics
- International Chinese Statistical Association
- The Royal Statistical Society, UK
- International Indian Statistical Association
- International Statistical Institute (Elected, 2005)

### Guest Editorship for Journals

- “Statistical Methods for Genome-Wide Association Studies”. *Statistical Science* (Eds. Gang Zheng, Jonathan Marchini, and Nancy Geller): November issue of 2009.
- Festschrift for Professor Joseph Gastwirth for his Forty-Five Years of Statistical Activity. *Statistics and Its Interface* (Eds. Efstathia Bura, Mitchell Gail, Zhaohai Li, and Gang Zheng): 2009 (website: <http://www.intlpress.com/SII/SII-vol-2.php#SII-2-1>)

### Committee membership

- Associate Editor, *Statistics and Its Interface*, since 2010.
- Member, Program Committee, 2011 ICSA Applied Statistics Symposium, New York, NY, June 26-29, 2011.
- Member, Scientific Committee for 2011 IMS-China International Conference on Statistics and probability, Xian, China, July 8-11, 2011
- Member, Noether Award Committee, ASA 2011-2013
- Member, Program Committee for conference in honor of Prof. Joseph Gastwirth August 1, 2009
- Member, Award Committee of International Chinese Statistical Association (2005 - 2007)
- Member, Board of Directors of International Chinese Statistical Association (2008 - 2010)
- Member, Organizing Committee of 2005 ICSA Applied Statistics Symposium, Washington, DC
- Member, Program Committee for 39th Symposium on the Interface, Philadelphia, PA, May, 2007
- Member, Scientific Committee for International Conference on Ordered Statistical Data and Inequalities, Jordan, June, 2007

### Invited sessions organized at professional meetings

- 2012 IBC, Kobe, Japan: Statistical challenges in the analysis of rare genetic variants in association studies (joint with Taesung Park)

- 2011 IMS-China, Xian, China: Statistical methods for GWAS
- 2011 IMS-China, Xian, China: Statistical genetics
- 2011 ICSA, NYC, NY: Statistics and Law.
- 2011 ICSA, NYC, NY: Statistical challenges arising from design and analysis of NIH studies (with Colin Wu).
- 2010 IBC, Florianopolis-SC, Brazil: Challenges of multiple gene-based analysis in GWAS (joint with Taesung Park).
- 2010 ENAR, New Orleans, LA: Opportunities for biostatisticians inside (research) and outside (funding) of NIH.
- 2009 JSM, Washington, DC: After the 100th Anniversary of Hardy-Weinberg Equilibrium
- 2009 ICSA Applied Statistics Symposium, San Francisco, CA: Statistical research and collaboration at NIH and FDA
- 2008 ICSA Applied Statistics Symposium, Piscataway, NJ: Methods for detecting multiple loci that influence complex diseases
- 2008 IBC, Dublin, Ireland: Statistical methods for genome-wide association studies (organized with Peter Donnelly)
- 2007 39th Symposium on the Interface, Philadelphia, PA: Statistical methods for genetic association studies
- 2007 ICSA Applied Statistics Symposium, Raleigh, NC: Statistical analysis of genetic data
- 2005 JSM, Minneapolis, MN: Statistical methods for gene-environmental interaction studies (organized with Colin Wu)
- 2005 ICSA Applied Statistics Symposium, Washington, DC: Industrial statistics I

**Served as a referee for the following journals**

*American Statistician; American Journal of Human Genetics; Annals of Applied Statistics; Annals of Human Genetics; Annals of the Institute of Statistical Mathematics; Applied Mathematics Letters; Bioinformatics; Biometrical Journal; Biometrics; Biometrika; Biostatistics; BMC Genetics; BMC Genomics; Briefings in Bioinformatics; Cancer Epidemiology, Biomarkers and Prevention; Circulation: Cardiovascular Genetics; Communications in Statistics; Computational Statistics and Data Analysis; Genetic Epidemiology; Human Genetics; Human Heredity; Information Sciences; International Journal of Biostatistics; Journal of American Statistical Association; Journal of Applied Statistics; Journal of Clinical Epidemiology; Journal of Nonparametric Statistics; Journal of Statistical Computation and Simulation; Journal of Statistical Planning and Inference; Mathematical and Computer Modelling; Metrika; PLOS Genetics; PLOS One; Statistics; Statistical Methodology; Statistics and Probability Letters; Statistics in Medicine; Statistical Papers; Statistica Sinica; Statistical Science; Test; Wiley Encyclopedia of Clinical Trials.*

## INVITED Talks and seminars

### 2011

“Joint analysis of binary and quantitative traits with data sharing and outcome dependent sampling”, Seminar, Department of Biostatistics, Virginia Commonwealth University, November 11, 2011.

“Efficiency robust tests for case-control genetic association studies”, Seminar, Academy of Mathematics and Systems Science, Beijing, July 13, 2011.

“Bayes factor based on a maximum statistic for case-control genetic association studies”, The 3rd IMS-China Statistics and Probability Conference, Xian, China, July 10, 2011.

“Joint analysis of binary and quantitative traits with missing data”, ICSA Applied Statistics Symposium, New York, NY, June 27, 2011.

### 2010

“Analysis of Genetic Associations with Deviation from Hardy-Weinberg Equilibrium”, Symposium for Celebrating the 75th Anniversary of the Department of Statistics, George Washington University, September 25, 2010.

“Robust Transmission Disequilibrium Test for Family Trio Design” (topic contributed), 2010 JSM, Vancouver, Canada, July 21-August 5, 2010.

“Bayesian genetic model averaging and selection for case-control association studies”, Fudan University School of Public Health, April 9, 2010.

“Bayesian model averaging for case-control genetic association studies”, Penn State Hershey Cancer Institute Symposium on “Frontiers in the Interface between Statistics and Genetics”, Penn State Hershey Cancer Institute, Feb 25, 2010.

“Bayesian model averaging for case-control genetic association studies”, Statistics Seminar at Department of Mathematics and Statistics, University of Maryland at Baltimore County, Feb 19, 2010.

“Robust genome-wide scans under incomplete linkage disequilibrium”, Seminar at Division of Biostatistics, Department of Epidemiology and Preventive Medicine, University of Maryland at Baltimore, Feb 2, 2010.

### 2009

“Approximate Bayes factors for case-control genetic association studies”, Seminar at Department of Biostatistics, Columbia University, Dec 3, 2009.

“Robust tests for genome-wide scan under two-locus models”, International Conference of Biostatistics, University of Science and Technology of China, July 4, 2009.

“Robust tests for genome-wide scan under two-locus models”, Conference celebrating 75 years of statistics at Iowa State. Department of Statistics and Statistical Laboratory, Iowa State University. June 3-5, 2009.

“On robust tests for case-control genetic association studies” Statistics Seminar at Department of Statistics, George Mason University. Feb 27, 2009.

**2008**

- “On robust tests for case-control genetic association studies” Biostatistics Seminar at Office of Biostatistics Research, National Heart, Lung and Blood Institute. Dec 12, 2008.
- “On robust tests for case-control genetic association studies” Statistics Seminar at Department of Statistics, Columbia University. Dec 1, 2008.
- “On robust tests for case-control genetic association studies” Statistics Seminar at Department of Mathematics, University of Maryland, College Park, MD. Nov 20, 2008.
- “Applying ranked set sampling to genetic studies” JSM (topic contributed), Denver, CO, August, 2008.
- “Two-phase analysis: with applications to case-control genetic association studies”. ICSA Applied Statistics Symposium, NJ, June, 2008.
- “Statistical issues and challenges arising from analysis of genome-wide association studies”. Biostatistics Seminar Series, Division of Biostatistics, University of Pennsylvania, Feb 26, 2008.

**2007**

- “Statistical issues and challenges arising from analysis of genome-wide association studies”. Seminar Series, Washington Statistical Society, Oct 25, 2007.
- “Analysis of case-control association with genetic model selections” Weekly Seminar, Department of Statistics, Ohio State University, Columbus, OH, Oct 18, 2007.
- “Multi-stage sampling for genetic studies” Seminar, Department of Statistics, George Washington University, Sept 28, 2007.
- “Statistical issues and challenges arising from analysis of genome-wide association studies”. Joint Statistical Meeting, Salt Lake City, UT, July 29, 2007.
- “Two-stage analysis of case-control genetic associations” 39th Symposium on the Interface: Computing Science and Statistics (Theme: System Biology). Philadelphia, PA, May 24, 2007.
- “Population structure and genetic case-control association studies” Biostatistics Branch Seminar, National Cancer Institute, April 27, 2007.

**2006**

- “Two-stage analysis for genome-wide association studies” Seminar, Department of Health Evaluation Sciences, Division of Biostatistics, Penn State College of Medicine, Hershey, PA, June 9, 2006.
- “Two-stage analysis for genome-wide association studies” Weekly Seminar, Department of Statistical Science, Southern Methodist University, Dallas, TX, April 2006.
- “Combining trend tests for genome-wide association studies: a double trend test” Seminar Series, Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University, Washington DC, January 2006.

**2005**

- “A statistical method adjusting for covariates in linkage analysis using sib-pairs” 2005 Joint Statistical Meeting, Minneapolis, MN, August 2005.

“Time saving in censored life testing” International Chinese Statistical Association (ICSA), Applied Statistics Symposium, Washington DC, June 2005.

“Fisher information in ordered data” Conference on Ordered Data and Applications, Department of Mathematics and Statistics, Bowling Green State University, Bowling Green, OH. May 2005.

“Robust tests and two robust criteria using Kullback-Leibler information: with applications to genetic linkage and association studies” Statistics Seminar at Department of Mathematics, University of Maryland, College Park, MD. March 2005.

“Genomic Control for association studies using case-control data” NHLBI PROGENI Workshop, New Orleans, LA. January 2005.

“Robust tests for genetic linkage and association studies” ASA Nonparametric Statistics Section Workshop, College Station, Texas A&M University. January 2005.

#### **2004**

“Robust tests for genetic linkage and association studies” Division of Epidemiology, Statistics and Prevention Research, National Institute of Child Health and Human Development. December 2004.

“Another look at life testing” Fifth Biennial International Conference on Statistics, Probability and Related Areas. University of Georgia, Athens, GA. May 2004.

#### **2001**

“Modified maximum likelihood estimators using ranked set samples”, Dept of Statistics, George Washington University, DC. November 9 2001.

“Fisher information in order statistics with applications”, Dept of Mathematics and Statistics, University of Maryland, Baltimore County. March 30 2001.

#### **1999**

“Fisher information in ordered data with applications”, Division of Biostatistics, Indiana University School of Medicine. December 6 1999.

## **Current Research Interests and Publications**

Statistical genetics; Robust methods and inference with nuisance parameters; Biostatistics methods and applications; Bayesian data analysis

### **Books**

1. Zheng G, Yang Y, Zhu X, and Elston RC. (2012) *Analysis of Genetic Association Studies*. Springer (over 400 pages).

## I. Refereed Journal articles (statistical methodology and applications; \* corresponding author)

### Manuscripts under revision, revised and to appear

1. Wang L, Li Q, Li Z and **Zheng G\***. Bayes factor based on a maximum statistic for case-control genetic association studies (revised).
2. Xu J, Yuan A and **Zheng G\***. Bayes factor based on the trend test incorporating Hardy-Weinberg disequilibrium: More powerful to detect genetic association (revised).
3. Wu CO, **Zheng G** and Kwak M. A joint regression analysis for genetic association studies with outcome stratified samples (revised).
4. Xu J, **Zheng G** and Yuan A. Case-control genome-wide joint association study using semiparametric empirical model and approximate Bayes factor. *Journal of Statistical Computation and simulation* (in press).
5. **Zheng G\***, Wu CO, Kwak M, Jiang W, Joo J and Lima JAC. Joint analysis of binary and quantitative trait with data sharing and outcome-dependent sampling. *Genetic Epidemiology* (in press).
6. Yuan A, Xu J, Yue Q and **Zheng G**. Detecting case-control expression quantitative trait loci using locally most powerful or maximin robust rank tests. *Statistics in Medicine* (in press).

### 2012

7. Yuan A, Xu J and **Zheng G**. Root-n estimability of some missing data models. *Journal of Multivariate Analysis* **106**, 147-166.

### 2011

8. Yan LK, Liu A, Li Z and **Zheng G**. Optimal two-stage sequential robust design for genetic intervention studies. *Statistics and Its Interface* **4**, 431-441.
9. Li Q, **Zheng G** and Tiwari RC. Analysis of ordered categorical data with score averaging: With applications to case-control genetic associations. *Journal of Applied Statistics* **38**, 1833-1843.
10. Jiang R, Dong J, Joo J, Geller N and **Zheng G\***. Simple strategies for haplotype analysis of the X chromosome with application to age-related macular degeneration. *European Journal of Human Genetics* **19**, 801-806.
11. **Zheng G\***, Yuan A and Jeffries N. Hybrid Bayes factors for genome-wide association studies when a robust test is used. *Computational Statistics and Data Analysis* **55**, 2698-2711.

12. Wang L, Li Q, Li Z and **Zheng G\***. Bayes factors in the presence of population stratification. *Statistics and Probability Letters* **81**, 836-841.
13. Yuan M, Xu J, Yang Y and **Zheng G\***. A robust test for  $2 \times J$  contingency table. *Statistics and Its Interface* **4**, 1-10.

#### 2010

14. Li Q, **Zheng G**, Liu A, Li Z and Yu K. (2010). Approximating probabilities of correlated events. *Science China Series A: Mathematics* **53**, 2937-2948.
15. **Zheng G\***, Li Z, Gail MH and Gastwirth JL (2010). Impact of population sub-structure on trend tests for genetic case-control association studies. *Biometrics* **66**, 196-204.
16. Joo J, Kwak M and **Zheng G** (2010). Improving power for testing genetic association in case-control studies by reducing alternative space. *Biometrics* **66**, 266-276.
17. Zang Y, Fung WK and **Zheng G** (2010). Simple algorithms to calculate asymptotic null distributions for robust tests in case-control genetic association studies in R. *Journal of Statistical Software* **33**, issue 8.
18. Li Q, **Zheng G**, Liu A, Xiong S, Li Z and Yu K. (2010). The limiting bound of Efron's W-formula for hypothesis testing when a nuisance parameter is present only under the alternative. *Journal of Statistical Planning and Inference* **140**, 1610-1617.
19. Joo J, Kwak M, Chen Z and **Zheng G\*** (2010). Efficiency robust statistics for genetic linkage and association studies under genetic model uncertainty. *Statistics in Medicine* **29**, 158-180.
20. Zang Y, Fung WK and **Zheng G** (2010). Asymptotic powers for matched trend tests and robust matched trend tests in case-control genetic association studies. *Computational Statistics and Data Analysis* **54**, 65-77.

#### 2009

21. **Zheng G\***, Joo J, Zaykin D, Wu CO and Geller NL (2009). Robust tests in genome-wide scans under incomplete linkage disequilibrium. *Statistical Science* **24**, 503-516.
22. Joo J, Kwak M, Ahn K and **Zheng G\*** (2009). A robust genome-wide scan statistic of the Wellcome Trust Case-Control Consortium. *Biometrics* **65**, 1115-1122.
23. Kwak M, Joo J and **Zheng G\*** (2009). A robust test for two-stage design in genome-wide association studies. *Biometrics* **65**, 1288-1295.
24. Hui TP, Modarres R and **Zheng G** (2009\*). Pseudo-maximum likelihood estimates using ranked set samples with applications to estimating correlation. *Test: Journal of Spanish Statistical Society* **18**, 365-380.

25. Yuan M, Yang Y and **Zheng G\*** (2009). Two-stage genome-wide association studies with DNA pooling and genetic model selection. *Statistica Sinica* **19**, 1769-1786.
26. Yuan M, Tian X, **Zheng G** and Yang Y (2009). Adaptive transmission disequilibrium test for family trio design. *Statistical Applications in Genetics and Molecular Biology* **8**: Issue 1, Article 30. DOI: 10.2202/1544-6115.1451.
27. **Zheng G\***, Joo J, Tian X, Wu CO, Lin J-P, Stylianou M, Waclawiw MA and Geller NL (2009). Robust genome-wide scans with genetic model selection using case-control design. *Statistics and Its Interface* (Festschrift for Prof. Joseph Gastwirth) **2**, 145-151.
28. Li Q, **Zheng G**, Liang X and Yu K (2009). Power of the robust single-marker tests for case-control association studies. *Annals of Human Genetics* **73**, 245-252.
29. **Zheng G\***, Joo J and Yang Y (2009). Pearson's test, trend test, and MAX are all trend tests with different types of scores. *Annals of Human Genetics* **73**, 133-140.
30. Zang Y, Fung WK and **Zheng G\*** (2009). Tail strength to combine two p-values: Their correlation cannot be ignored. *American Journal of Human Genetics* **84**, 291-295 (letter).
31. Li Z, Zhang H, **Zheng G**, Gastwirth JL and Gail MH (2009). Excess false positive rate caused by population stratification and disease rate heterogeneity in case-control association studies. *Computational Statistics and Data Analysis* **53**, 1767-1781.
32. **Zheng G\***, Balakrishnan N and Park S (2009). Fisher information in ordered data: A review. *Statistics and Its Interface* **2**, 101-113.

## 2008

33. **Zheng G\*** (2008). Can the allelic test be retired from analysis of case-control association studies? *Annals of Human Genetics* **72**, 848-851.
34. **Zheng G\***, Meyer M, Li W and Yang Y (2008). Comparison of two-phase analyses for case-control genetic association studies. *Statistics in Medicine* **27**, 5054-5075.
35. Li Q, Yu K, Li Z and **Zheng G\*** (2008). MAX-Rank: A simple and robust genome-wide scan for case-control association studies. *Human Genetics* **123**, 617-623.
36. Yan LK, **Zheng G** and Li Z (2008). Two-stage group sequential robust tests in family-based association studies: Controlling Type I error. *Annals of Human Genetics* **72**, 557-565.
37. **Zheng G** and Ng HKT (2008). Genetic model selection in two-phase analysis for case-control association studies. *Biostatistics* **9**, 391-399.
38. Li Q, **Zheng G**, Li Z and Yu K (2008). Efficient approximation of p-value of maximum of correlated tests, with applications to genome-wide association studies. *An-*

*nals of Human Genetics* **72**, 397-406.

39. **Zheng G\*** (2008). Analysis of ordered categorical data: Two score-independent approaches. *Biometrics* **64**, 1276-1279.
40. Ng HKT, Filardo G and **Zheng G** (2008). On confidence interval estimating procedures for standardized incidence rates. *Computational Statistics and Data Analysis* **52**, 3501-3516.
41. Park S, Balakrishnan N and **Zheng G** (2008). Fisher information in hybrid censored data. *Statistics and Probability Letters* **78**, 2781-2786.

#### 2007

42. **Zheng G\***, Joo J, Zhang C and Geller NL (2007). Testing association for markers on the X chromosome. *Genetic Epidemiology* **31**, 834-843.
43. Zang Y, Zhang H, Yang Y and **Zheng G\*** (2007). Robust genomic control and robust delta-centralization for case-control association studies. *Human Heredity* **63**, 187-195.
44. **Zheng G\***, Song K and Elston RC (2007). Adaptive two-stage analysis of genetic association for case-control designs. *Human Heredity* **63**, 175-186.
45. Zhang H, Zhang H, Li Z and **Zheng G** (2007). Statistical methods for haplotype inference based on matched case-control design. *Genetic Epidemiology* **31**, 316-326.
46. Elston RC, Lin DY and **Zheng G** (2007). Multi-stage sampling for genetic studies. *Annual Reviews of Genomics and Human Genetics* **8**, 327-342.

#### 2006

47. **Zheng G\***, Ghosh K, Chen Z and Li Z (2006). Extreme rank selection for linkage analysis of quantitative trait loci using selected sib-pairs. *Annals of Human Genetics* **70**, 857-866.
48. Zhang H, **Zheng G** and Li Z (2006). Statistical Analysis for haplotype-based matched case-control studies. *Biometrics* **62**, 1124-1131.
49. **Zheng G\***, Freidlin B and Gastwirth JL (2006). Robust genomic control for association studies. *American Journal of Human Genetics* **78**, 350-356.
50. **Zheng G\*** and Gastwirth JL (2006). On estimation of the variance in Cochran-Armitage trend tests for genetic association using case-control studies. *Statistics in Medicine* **25**, 3150-3159.
51. **Zheng G\*** and Tian X, for ACCESS Research Group (2006). Robust trend tests for genetic association using matched case-control design. *Statistics in Medicine* **25**, 3160-3173.

52. Modarres R, Hui TP and **Zheng G** (2006). Resampling method for ranked set sampling. *Computational Statistics and Data Analysis* **51**, 1039-1050.
53. **Zheng G\*** and Modarres R (2006). A robust estimate of correlation coefficient of bivariate normal distribution using ranked set samples. *Journal of Statistical Planning and Inference* **136**, 298-309.

#### 2005

54. Chen Z and **Zheng G\*** (2005). Exact robust tests for detecting candidate-gene association in case-control trio design. *Journal of Data Science* **3**, 19-33.
55. **Zheng G\***, Freidlin B, Li Z and Gastwirth JL (2005). Genomic control for association studies under various genetic models. *Biometrics* **61**, 186-192.
56. **Zheng G\*** and Tian X (2005). The impact of diagnosis error on testing genetic association in case-control studies. *Statistics in Medicine* **24**, 869-882.
57. **Zheng G\***, Joo J, Ganesh S, Nabel E and Geller NL (2005). On averaging power for genetic association and linkage studies. *Human Heredity* **59**, 14-20.
58. Chen Z, **Zheng G**, Ghosh K and Li Z (2005). Linkage disequilibrium mapping for quantitative trait loci by selective genotyping. *American Journal of Human Genetics* **77**, 661-669.
59. **Zheng G\*** and Chen Z (2005). Comparison of maximum statistics for hypothesis testing when a nuisance parameter is only present under the alternative. *Biometrics* **61**, 254-258.
60. Hui TP, Modarres R and **Zheng G\*** (2005). Bootstrap confidence interval estimation of the regression mean with ranked set sampling. *Journal of Statistical Computation and Simulation* **75**, 543-553.
61. **Zheng G\*** and Park S (2005). Another look at life testing. *Journal of Statistical Planning and Inference* **127**, 103-117.
62. **Zheng G\*** and Gastwirth JL (2005). Fisher information in random sampled sib pairs and extremely discordant sib pairs in genetic linkage analysis for a quantitative trait locus. *Journal of Statistical Planning and Inference* **130**, 299-315 (Herman Chernoff: Eightieth Birthday Felicitation Volume).

#### 2004

63. **Zheng G\*** and Chen Z (2004). Maximal robust tests for candidate-gene association using case-parents trios with a multi-allelic marker. *Biometrical Journal* **46**, 606-611.
64. **Zheng G\*** (2004). Maximizing a family of optimal statistics over a nuisance parameter with applications to genetic data analysis. *Journal of Applied Statistics* **31**,

661-671.

65. **Zheng G\***, Freidlin B, and Gastwirth JL (2004). On the Kullback-Leibler information when the data-generating model is unknown with applications to genetic testing problems. *Statistica Sinica* **14**, 1021-1036.
66. Modarres R and **Zheng G\*** (2004). Maximum likelihood estimate for dependence using ranked set samples. *Statistics and Probability Letters* **68**, 315-323.
67. **Zheng G\*** (2004). Some remarks on the Fisher information in a ranked set sample. *Communications in Statistics: Theory and Methods* **33**, 1511- 1525.
68. **Zheng G\*** and Park S (2004). On the Fisher information in multiply censored and progressively censored data. *Communications in Statistics: Theory and Methods* **33**, 1821-1835.
69. Park S and **Zheng G** (2004). Equal Fisher information in order statistics. *Sankhya* **66**, 20-34.
70. **Zheng G\*** and Park S (2004). A note on time saving in censored life testing. *Journal of Statistical Planning and Inference* **124**, 289-300.

### 2003

71. **Zheng G\***, Freidlin B, Li Z and Gastwirth JL (2003). Choice of scores in trend tests for case-control studies of candidate-gene associations. *Biometrical Journal* **45**, 335-348.
72. **Zheng G\*** (2003). Use of max and min scores for trend tests for associations when the genetic model is unknown. *Statistics in Medicine* **22**, 2657-2666.
73. **Zheng G\***, Chen Z and Li Z (2003). Tests for candidate-gene association using case-parents design. *Annals of Human Genetics* **67**, 589-597.
74. **Zheng G\*** and Al-Saleh MF (2003). Improving best linear unbiased estimators for the scale parameter of symmetric distributions using the absolute value of ranked set samples. *Journal of Applied Statistics* **30**, 253-265.
75. Al-Saleh MF and **Zheng G\*** (2003). Controlled ranked set sampling. *Journal of Nonparametric Statistics* **15**, 505-516.
76. **Zheng G\*** and Gastwirth JL (2003). Fisher information in ordered randomly censored data with applications to characterization. *Statistica Sinica* **13**, 507-517.
77. Freidlin B, **Zheng G**, Li Z and Gastwirth JL (2003). Robust tests for mapping

quantitative trait loci using extremely discordant sib pairs. *Human Heredity* **55**, 117-124 (A Celebration of the 30th Anniversary of the Haseman-Elston Method).

78. Gastwirth JL, Miao WW and **Zheng G** (2003). Statistical issues arising in disparate impact cases and the use of the expectancy curve in assessing the validity of pre-employment tests. *International Statistical Review* **71**, 565-580.

## 2002

79. **Zheng G\***, Freidlin B, and Gastwirth JL (2002). Robust TDT-type candidate-gene association tests. *Annals of Human Genetics* **66**, 145-155.
80. Freidlin B, **Zheng G**, Li Z and Gastwirth JL (2002). Trend tests for case-control studies of genetic markers: Power, sample size and robustness. *Human Heredity* **53**, 146-152.
81. Al-Saleh MF and **Zheng G\*** (2002). Estimation of bivariate characteristics using ranked set sampling. *Australia and New Zealand Journal of Statistics* **44**, 221-232.
82. **Zheng G\*** and Al-Saleh MF (2002). Modified Maximum likelihood estimators based on ranked set samples. *Annals of the Institute of Statistical Mathematics* **54**, 641-658.
83. **Zheng G\*** (2002). On the Fisher information matrix in Type II censored data from the exponentiated exponential family. *Biometrical Journal* **44**, 353-357.
84. **Zheng G\*** and Gastwirth JL (2002). Do tails of symmetric distributions contain more Fisher information about the scale parameter? *Sankhya Series B* **64**, 289-300.

## 2001

85. **Zheng G\*** and Gastwirth JL (2001). On the Fisher information in randomly censored data. *Statistics and Probability Letters* **52**, 421-426.
86. **Zheng G\*** (2001). A characterization of the factorization of hazard function by the Fisher information under Type II censoring with application to Weibull distribution. *Statistics and Probability Letters* **52**, 249-253.

## 2000

87. **Zheng G\*** and Gastwirth JL (2000). Where is the Fisher information in an ordered sample? *Statistica Sinica* **10**, 1267-1280.

88. **Zheng G\*** (2000). On the rate of convergence of the Fisher information in multiple Type II censored data. *Journal of the Japan Statistical Society* **30**, 171-178.

## II. Refereed or Invited Contributions for Book Chapters, Encyclopedia and Proceedings (Statistical Methods, Applications and Comments)

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### III. Other Refereed Publications (Applications)

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### V. Non-refereed Publications

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