

## Ruzong Fan, Ph.D

### Position:

July 31st 2011-present, Investigator  
Biostatistics and Bioinformatics Branch  
Division of Intramural Population Health Research (DIPHR)  
*Eunice Kennedy Shriver* National Institute of Child Health and Human Development (NICHD)  
National Institutes of Health (NIH)  
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### Education:

- 1998, Ph.D, Biostatistics, The University of Michigan, Ann Arbor, MI, Advisor: Dr. Kenneth Lange (currently at UCLA).
- 1996, M.S, Biostatistics, The University of Michigan, Ann Arbor, MI.
- 1988, Ph.D, Probability Theory, Institute of Applied Mathematics, Chinese Academy of Sciences, Beijing, China.
- 1985, M.S, Probability Theory, Yunnan University, Kunming, China.
- 1983, B.S, Mathematics, Yunnan University, Kunming, China.

### Research Interests:

- Statistical Genetics and Genomics;
- Stochastic Processes, Stochastic Modeling and Applications.

### Editorial Boards:

- Associate Editor, *Statistics and Its Interface*, 2014 - present.

### Guest Editor (2012–2014):

- A special issue of Statistical Research at the NIH in *Statistics and Its Interface*, 2014.

### **Previous Academic Appointments:**

- 2006–2011, Associate Professor (tenured), Department of Statistics, Texas A&M University; Department of Epidemiology and Biostatistics, School of Rural Public Health, TAMU Health Science Center.
- 2008—2009, Visiting Associate Professor, Department of Epidemiology, MD Anderson Cancer Center, University of Texas, Houston, TX 77030.
- 2001–2006, Assistant Professor, Department of Statistics, Texas A&M University; Department of Epidemiology and Biostatistics, School of Rural Public Health, TAMU Health Science Center.
- 1999–2001, Assistant Professor, Department of Health Evaluation Sciences, College of Medicine, Pennsylvania State University.
- 1998–1999, Research Associate, Center for Biostatistics in AIDS Research, Harvard School of Public Health.
- 1994, Research Scientist, Institute of Applied Mathematics, University of Bonn, Germany.
- 1992–1993, Research Scientist, Department of Mathematics, Ruhr-University Bochum, Germany.
- 1991–1992, Visiting Scholar, Department of Mathematics, Humboldt-University Berlin, Germany.
- 1988–1991, Lecturer, Department of Probability and Statistics, Peking University, Beijing, China.

### **Other Working Experience:**

- Summer 2010, Visiting Scholar, National Cancer Institute, NIH.
- Summer 2006, Humboldt Research Fellow, Institute of Applied Mathematics, University of Bonn, supported by The Alexander von Humboldt Foundation, Germany.
- Summer 2004, Humboldt Research Fellow, Institute of Medical Biometry, Informatics and Epidemiology, University of Bonn, supported by The Alexander von Humboldt Foundation, Germany.
- Summer 2002, Humboldt Research Fellow, Institute of Medical Biometry, Informatics and Epidemiology, University of Bonn, supported by The Alexander von Humboldt Foundation, Germany.

- 1995–1998, Research Assistant, Department of Biostatistics, University of Michigan.
- 1994–1995, Teaching Assistant, Department of Biostatistics, University of Michigan.
- 1986–1988, Research Assistant, Institute of Applied Mathematics, Chinese Academy of Sciences, Beijing, China.
- 1985–1986, Teaching Assistant, Department of Mathematics, Yunnan University, Kunming, China.
- 1984–1985, Research Assistant, Institute of Applied Mathematics, Chinese Academy of Sciences, Beijing, China.
- 1983–1984, Research Assistant, Department of Mathematics, Yunnan University, Kunming, China.

### **Academic and Professional Awards:**

- 2001, Research Fellowship, The Alexander von Humboldt Foundation, Germany.
- 1982, Excellent Student Award, Yunnan University.

### **Teaching Experience:**

- 2001-2011, Texas A&M University:
  1. Stat 211, Principles of Statistics I (undergraduate students).
  2. Stat 651, Statistics in Research I (Master students).
  3. Stat 652, Statistics in Research II (Master students).
  4. Stat 661, Statistical Genetics (Master students).
  5. Stat 662, Advanced Statistical Genetics (Ph.D students).
- 1999-2001, Pennsylvania State University:
  1. Statistical Genetics.
- 1988–1991, Peking University:
  1. Ergodic Theory.
  2. Martingale Limit Theory.
  3. Applied Stochastic Processes.
  4. Stochastic Differential Equations and Diffusion Processes.

## Publications:

### Refereed Research Monograph:

1. <sup>1</sup>Albeverio S, **Fan RZ**, and Herzberg F (2011) Hyperfinite Dirichlet Forms and Stochastic Processes. The Lecture Notes of the Unione Matematica Italiana (UMI LN), Springer-Verlag, Volume 10.

### Refereed Manuscripts (Methodological):

2. Lin N, Zhu Y, *Fan RZ* and Xiong MM (2016) A quadratically regularized functional canonical correlation analysis for identifying the global structure of pleiotropy with NGS data.
3. Jiang YD, Chiu CY, Yan Q, Chen W, Gorin MB, Conley YP, Lakhal-Chaieb ML, Cook RJ, Amos CI, Wilson AF, Bailey-Wilson JE, Xiong MM, Weeks DE, and **Fan RZ**<sup>2</sup> (2016) Gene-based association testing of dichotomous traits with generalized linear mixed models for family data. Under review.
4. Chiu CY, Jung JS, Chen W, Weeks DE, Ren H, Boehnke M, Amos CI, Liu AY, Mills JL, Lee MLT, Xiong MM and **Fan RZ**<sup>3</sup> (2016) Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. *European Journal of Human Genetics*, in press.
5. Chiu CY, Jung JS, Wang YF, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Mills JL, Boehnke M, Xiong MM, and **Fan RZ**<sup>4</sup> (2016) A comparison study of multivariate fixed models and gene association with multiple traits (GAMuT) for next-generation sequencing. *Genetic Epidemiology*, in press.
6. **Fan RZ**, Chiu CY, Jung JS, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Chen Z, Mills JL, and Xiong MM (2016) A comparison study of fixed and mixed effect models for gene level association studies of complex traits. *Genetic Epidemiology*, in press.
7. **Fan RZ**, Wang YF, Chiu CY, Chen W, Ren HB, Li Y, Boehnke M, Amos CI, Moore J, and Xiong MM (2016) Meta-analysis of complex diseases at gene level with generalized functional linear models. *Genetics* **202** (2):457-470.
8. **Fan RZ**, Wang YF, Qi Y, Ding Y, Weeks DE, Lu ZH, Ren HB, Cook RJ, Xiong MM, and Chen W (2016) Gene-based association analysis for censored traits via functional regressions. *Genetic Epidemiology* **40** (2):133-143.
9. **Fan RZ**, Wang YF, Boehnke M, Chen W, Li Y, Ren HB, Lobach I, and Xiong MM (2015) Gene level meta-analysis of quantitative traits by functional linear models. *Genetics* **200** (4):1089-1104.

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<sup>1</sup>Authorship is in alphabetical order of the last name. Dr. Fan contributed the first 4 chapters out of 6 as the main contributor.

<sup>2</sup>Corresponding author as mentor of post-doctoral fellow, Dr. Chiu CY

<sup>3</sup>Corresponding author as mentor of post-doctoral fellow, Dr. Chiu CY

<sup>4</sup>Corresponding author as mentor of post-doctoral fellow, Dr. Chiu CY

10. Wang YF, Liu AY, Mills JL, Boehnke M, Wilson AF, Bailey-Wilson JE, Xiong MM, Wu CO, and **Fan RZ**<sup>5</sup> (2015) Pleiotropy analysis of quantitative traits at gene level by multivariate functional linear models. *Genetic Epidemiology* **39** (4):259-275.
11. **Fan RZ**, Chen V, Xie YL, Yin LL, Kim SD, Albert P, and Simons-Morton B (2015) A functional data analysis approach to analyze circadian rhythm patterns in activity counts for teenage girls. *Journal of Circadian Rhythms* **13**(3):1-13,  
DOI: <http://dx.doi.org/10.5334/jcr.ac>
12. **Fan RZ**, Zhu B, and Wang Y (2014) Stochastic dynamic models and Chebyshev splines. *The Canadian Journal of Statistics* **42** (4):610-634.
13. **Fan RZ**, Wang YF, Mills JL, Carter TC, Lobach I, Wilson AF, Bailey-Wilson JE, Weeks DE, and Xiong MM (2014) Generalized functional linear models for case-control association studies. *Genetic Epidemiology* **38** (7):622-637.
14. Lobach I, **Fan RZ**, and Manga P (2014) Genotype-Based association models of complex diseases to detect gene-gene and gene-environment interactions. *Statistics and Its Interface* **7**:51-60.
15. **Fan RZ**, Wang YF, Mills JL, Wilson AF, Bailey-Wilson JE, and Xiong MM (2013) Functional linear models for association analysis of quantitative traits. *Genetic Epidemiology* **37** (7):726-742.
16. **Fan RZ**, Lee A, Liu AY, Troendle J, and Mills JL (2013) Association analysis of complex diseases using triads, parent-child dyads and singleton monads. *BMC Genetics* 14:78. DOI: 10.1186/10.1186/1471-2156-14-78. URL: <http://www.biomedcentral.com/1471-2156/14/78>.
17. **Fan RZ**, Zhang YW, Albert PS, Liu AY, Wang YJ, and Xiong MM (2012) Longitudinal association analysis of quantitative traits. *Genetic Epidemiology* **36**:856-869.
18. Lobach I, **Fan RZ** (2012) Genotype-based Bayesian analysis of gene-environment interactions with multiple genetic markers and misclassification in environmental factors. *Journal of Probability and Statistics*, Volume 2012, Article ID 151259, 15 pages, doi:10.1155/2012/151259.
19. Mechanic LE, Chen HS, Amos CI, Chatterjee N, Cox NJ, Divi RL, **Fan RZ**, Harris EL, et al. (2012) Next generation analytic tools for large scale genetic epidemiology studies of complex diseases. *Genetic Epidemiology* **36**:22-35.
20. **Fan RZ**, Zhong M, Wang SF, Zhang YW, Andrew A, Karagas M, Chen H, Amos CI, Xiong M, and Moore J (2011) Entropy-based information gain approaches to detect and to characterize gene-gene and gene-environment interactions/correlations of complex diseases. *Genetic Epidemiology* **35**:706-721.
21. Zhong M, Zhang YW, Lange K, and **Fan RZ**<sup>6</sup> (2011) A cross-population extended haplotype-based homozygosity score test to detect positive selection in genome-wide scans. *Statistics and Its Interface* **4**:51-63.

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<sup>5</sup>Corresponding author as mentor of post-doctoral fellow, Dr. Wang YF.

<sup>6</sup>Corresponding author as mentor of Ph.D student, Dr. Zhong M.

22. Lobach I, **Fan RZ**<sup>7</sup>, and Carroll RJ (2010) Genotype-based association mapping of complex diseases: a case-control approach of gene-environmental interactions with multiple markers and measurement errors in environmental exposures. *Genetic Epidemiology* **34**:792-802.
23. Zhong M, Lange K, Papp JC, and **Fan RZ**<sup>8</sup> (2010) Extended homozygosity score tests to detect positive selection in genome-wide scans. *European Journal of Human Genetics* **18**:1148-1159.
24. Chen LF, Zhong M, Chen WV, Amos C, and **Fan RZ**<sup>9</sup> (2009) A genome-wide association scan for rheumatoid arthritis data by Hotelling's  $T^2$  tests. *BMC Proceedings 3 (Suppl 7):S6*.
25. Jung JS, Zhong M, Liu L, and **Fan RZ**<sup>10</sup> (2008) Bi-variate combined linkage and association mapping of quantitative trait loci. *Genetic Epidemiology* **32**:396-412.
26. **Fan RZ**, Liu L, Jung J, and Zhong M (2008) Combined linkage and association mapping of quantitative trait loci with missing completely at random genotype data. *Behavior Genetics* **38**:316-336.
27. Yang Q, Biernacka JM, Chen MH, Houwing-Duistermaat JJ, Bergemann TL, Basu S, **Fan R**, Liu L, Bourgey M, Clerget-Darpoux F, Lin WY, Dupuis J, Elston RC, and Cupples LA (2007) Group 4: using linkage and association to identify and model genetic effects. *Genetic Epidemiology* **31 (Supplement 1)**:s34-s42.
28. **Fan RZ**, Jung JS, and Jin L (2006) High resolution association mapping of quantitative trait loci, a population based approach. *Genetics* **172**:663-686.
29. **Fan RZ** and Knapp M (2005) Sib-ship  $T^2$  association tests of complex diseases for tightly linked markers. *Human Genomics* **2**:90-112.
30. Jung JS, **Fan RZ**, and Jin L (2005) Combined linkage and association mapping of quantitative trait loci by multiple markers. *Genetics* **170**:881-898.
31. **Fan RZ**, Knapp M, Wjst M, Zhao CX, and Xiong MM (2005) High resolution  $T^2$  association tests of complex diseases based on family data. *Annals of Human Genetics* **69**:187-208.
32. **Fan RZ**, Spinka C, Jin L, and Jung JS (2005) Pedigree linkage disequilibrium mapping of quantitative trait loci. *European Journal of Human Genetics* **13**:216-231.
33. **Fan RZ** and Jung SJ (2004) High resolution joint linkage disequilibrium and linkage mapping of quantitative trait loci based on sibship data. *Human Heredity* **56**:166-187.
34. **Fan RZ** and Knapp M (2003) Genome association studies of complex diseases by case-control designs. *American Journal of Human Genetics* **72**:850-868.

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<sup>7</sup>Corresponding author. Fan RZ contributed the main idea and did most of the theoretical justification and was responsible to write the paper.

<sup>8</sup>Corresponding author as mentor of Ph.D student, Dr. Zhong M.

<sup>9</sup>Corresponding author as mentor of master student, Mr. Chen LF.

<sup>10</sup>Corresponding author as mentor of Ph.D student, Dr. Jung JS.

35. **Fan RZ** and Xiong MM (2003) Combined high resolution linkage and association mapping of quantitative trait loci. *European Journal of Human Genetics* **11**:125-137.
36. **Fan RZ** and Xiong MM (2003) Linkage and association studies of QTL for nuclear families by mixed models. *Biostatistics* **4**:75-95.
37. **Fan RZ** and Jung SJ (2003) Association studies of QTL for multi-allele markers by mixed models. *Human Heredity* **54**:132-150.
38. **Fan RZ** and Xiong MM (2002) High resolution mapping of quantitative trait loci by linkage disequilibrium analysis. *European Journal of Human Genetics* **10**:607-615.
39. Xiong MM, **Fan RZ**, and Jin L (2002) Linkage disequilibrium mapping of quantitative trait loci under truncation selection. *Human Heredity* **53**:158-172.
40. **Fan RZ**, Floros J, and Xiong MM (2002) Models and tests of linkage and association studies of QTL for multi-allele marker loci. *Human Heredity* **53**:130-145.
41. **Fan RZ**, Floros J, and Xiong MM (2001) Linkage transmission disequilibrium test of two unlinked disease loci; application to respiratory distress syndrome. *Advances and Applications in Statistics* **1**:277-308.
42. **Fan RZ** and Lange K (2000) Asymptotic properties of the maximal subinterval of a Poisson process. *Stochastic Processes, Physics and Geometry: New Interplays. II: A Volume in Honor of Sergio Albeverio*; Conference Proceedings, Canadian Mathematical Society, Volume 29; edited by Gesztesy F, Holden H, Jost J, Paycha S, Röckner M, and Scarlatti S; pp 175-187.
43. **Fan RZ** and Lange K (1999) Diffusion process calculations for mutant genes in nonstationary populations. *Statistics in Molecular Biology and Genetics*, Institute of Mathematical Statistics, Lecture Notes-Monograph Series, Volume 33, Published by the Institute of Mathematical Statistics and the American Mathematical Society; Ed. Seillier-Moisewitsch F, pp 38-55.
44. **Fan RZ**, Lange K, and Pena E (1999) Applications of a formula for the variance function of a stochastic process. *Statistics & Probability Letters* **43-2**:123-130.
45. **Fan RZ** and Lange K (1998) Models for haplotype evolution in a nonstationary population. *Theoretical Population Biology* **53**:184-198.
46. Lange K and **Fan RZ** (1997) Branching process models for mutant genes in nonstationary populations. *Theoretical Population Biology* **51**:118-133; Erratum, *Theoretical Population Biology* **52**:165.
47. **Fan RZ** (1996) Potential theory of hyperfinite Dirichlet forms. *Potential Analysis*, Netherlands **5**:417-462.

48. Albeverio S, **Fan RZ**, Röckner M, and Stannat W (1995) A remark on coercive forms and associated semigroups. *Partial Differential Equations and Mathematical Physics (Series: Operator Theory: Advances and Applications, Vol. 78, Birkhäuser Verlag, Basel/Switzerland)*, Eds. Demuth M and Schulze B, pp 1–8.
49. Albeverio S and **Fan RZ** (1995) Representation of martingale additive functionals and absolute continuity of infinite dimensional symmetric diffusions. *Dirichlet Forms and Stochastic Processes*, Proceedings of the International Conference in Beijing, Eds. Ma ZM, Röckner M, and Yan J, pp 25–45.
50. **Fan RZ** (1995) Nonstandard construction of symmetric strong Markov processes associated with Dirichlet forms. *Stochastic Processes, Physics and Geometry II*, Proceeding of the International Conference in Locarno, Switzerland, Eds Albeverio S, Cattaneo U, and Merlini D, pp 247–277.
51. **Fan RZ** (1992) Some diffusion processes on the half-space and their associated Dirichlet forms (in Chinese). *Acta Mathematica Sinica* **35**:418–430.
52. **Fan RZ** (1992) Decomposition of a class of functionals and the predictable representation theorem on Banach spaces. *Acta Mathematicae Applicatae Sinica, English Series* **8**:153–167.
53. **Fan RZ** (1992) Beurling-Deny formulae on Banach spaces. *Acta Mathematica Scientia* **12**:79–84.
54. **Fan RZ** (1991) Decomposition of a class of functionals. *Acta Mathematica Sinica, New Series* **7**:224–240.
55. **Fan RZ** (1991) Closabilities of certain symmetric forms on Banach spaces (in Chinese). *Chinese Annals of Mathematics* **12A**:202–209.
56. **Fan RZ** (1990) Representation of martingale additive functionals on Banach spaces. *Acta Mathematicae Applicatae Sinica, English Series* **6**:74–80.
57. **Fan RZ** (1989) An extension of Dynkin formula and probabilistic solutions of some second-order partial differential equations (in Chinese). *Journal of Yunnan University, Natural Science Edition* **11**:10–14.
58. **Fan RZ** (1987) A class of stochastic differential equations with local time and the skew Brownian motion with two barriers (in Chinese). *Chinese Journal of Applied Probability and Statistics* **3**:130–136.

**Refereed Manuscripts (Collaborative):**

59. Iannotti RJ, Li KG, Pratt CA, Lipsky L, D’Elio MA, Olson S, **Fan RZ**, and Simons-Morton B (2016) Body weight status as a moderator of associations among cardiometabolic risks and physical activity in U.S. adolescents. Under review.

60. Dimopoulos A, Sicko RJ, Kay DM, Rigler SL, Druschel CM, Caggana M, Browne ML, **Fan RZ**, Romitti PA, Brody LC, Mills JL (2016) Rare copy number variants in a population based investigation of hypoplastic right heart syndrome. Under review.
61. Dimopoulos A, Sicko RJ, Kay DM, Boghossian NS, Rigler SL, Hagen EM, M Ali, Druschel CM, Romitti PA, Browne ML, **Fan RZ**, Brody LC, Mills JL (2016) Rare copy number variants involving the sonic hedgehog signaling pathway: a population-based investigation of isolated tracheoesophageal fistula and esophageal atresia. Under review.
62. Sicko RJ, Browne ML, Rigler SL, Druschel CM, Liu G, **Fan RZ**, Romitti PA, Caggana M, Kay DM, Brody LC, Mills JL (2016) Rare copy number variants in isolated Ebstein anomaly implicate myocardial development pathways. PLOS ONE, revision submitted.
63. Hagen EM, Sicko RJ, Kay DM, Rigler SL, Dimopoulos A, Warmerdam B, Ahmad S, Doleman MH, **Fan RZ**, Romitti PA, Browne ML, Caggana M, Brody LC, Shaw GM, Jelliffe-Pawlowski LL, Mills JL (2016) Copy-number variant analysis of classic heterotaxy highlights the importance of body patterning pathways. Human Genetics, in press.
64. Deac O, Mills JL, Gardiner CM, Shane B, Quinn L, Midttun O, McCann A, Klaus Meyer K, Ueland PM, **Fan RZ**, Lu ZH, Brody LC, Molloy AM (2016) Serum inflammation bio-markers are strongly related to tryptophan metabolism in young healthy adults. *The Journal of Nutrition*, in press.
65. Dimopoulos A, Sicko RJ, Kay DM, Rigler SL, **Fan RZ**, Romitti PA, Browne ML, Druschel CM, Caganna M, Brody LC, Mills JL (2016) Copy number variants in population based investigation of Klippel Trenaunay Weber syndrome. *American Journal of Medical Genetics*, in press.
66. Boghossian NS, Sicko RJ, Kay DM, Rigler SL, Caggana M, Tsai M, Yeung EH, Pankratz N, Cole BR, Druschel CM, Romitti PA, Browne ML, **Fan RZ**, Liu AY, Brody LC, Mills JL (2016) Rare copy number variants implicated in posterior Urethral valves. *American Journal of Medical Genetics Part A* **170(3)**:622-633.
67. Ozaki M, Molloy AM, Mills JL, Pangilinan F, **Fan RZ**, Wang Y, Gibney E, Shane B, Brody LC, Parle-McDermott A (2015) The dihydrofolate reductase 19bp polymorphism is not associated with biomarkers of folate status in healthy young adults, irrespective of folic acid intake. *The Journal of Nutrition* **145 (10)**:2207-2211.
68. Bailey RL, Looker AC, Lu ZH, **Fan RZ**, Eicher-Miller HA, Fakhouri TH, Gahche JJ, Weaver CM, Mills JL (2015) B-vitamins and bone mineral density and risk of lumbar osteoporosis in older females in the U.S. *The American Journal of Clinical Nutrition* **102 (3)**:687-694.
69. Carter TC, Pangilinan F, Molloy AM, **Fan RZ**, Wang YF, Shane B, Gibney ER, Midttun O, Ueland PM, Cropp CD, Kim Y, Wilson AF, Bailey-Wilson JE, Brody LC, Mills JL (2015) Common variants at putative regulatory sites nonspecific alkaline phosphatase gene influence circulating pyridoxal 5-phosphate concentration in healthy adults. *The Journal of Nutrition* **145**:1386-1393.

70. Rigler SL, Kay DM, Sicko RJ, **Fan RZ**, Liu AY, Caggana M, Browne ML, Druschel CM, Romitti PA, Brody LC, Mills JL (2015) Novel copy-number variants in a population-based investigation of classic heterotaxy. *Genetics in Medicine* **17(5)**:348-357.
71. Deac O, Mills JL, Shane B, Midttun O, Ueland PM, Brosnan JT, Brosnan ME, Laird E, Gibney ER, **Fan RZ**, Wang YF, Brody LC, Molloy AM (2015) Tryptophan catabolism and vitamin B6 status are affected by gender and lifestyle factors in healthy young adults. *The Journal of Nutrition* **145 (4)**:701-707.
72. Zhang CL, Hu FB, Olsen SF, Vaag A, Gore-Langton R, Chavarro J, Bao W, Edwina Y, Bowers K, Grunnet LG, Sherman S, Kiely M, Strom M, Hansen S, Liu A, Mills JL, and **Fan R** (2014) Rationale, design, and method of the diabetes & Womens Health Study -a study of long-term health implications of glucose intolerance in pregnancy and their determinants. *Acta Obstetricia et Gynecologica Scandinavica (www.aogs-online.com)* **93**:1123-1130.
73. Mills JL, **Fan RZ**, Brody LC, Aiyi Liu A, Ueland P, Wang YF, Kirke PN, Shane B, AM Molloy (2014) Maternal choline concentrations during pregnancy and choline-related genetic variants as risk factors for neural tube defects. *The American Journal of Clinical Nutrition* **100(4)**:1069-1074.
74. Molloy AM, Einri CN, Jain D, Laird E, **Fan RZ**, Wang YF, Scott JM, Shane B, Brody LC, Kirke PN, Mills JL (2014) Is low iron status a risk factor for neural tube defects? *Birth Defects Research Part A: Clinical and Molecular Teratology* **100 (2)**:100106.
75. Feenstra B, Geller F, Carstensen L, Romitti PA, Körberg IB, Bedell B, Krogh C, **Fan RZ**, Svenningsson A, Caggana M, Nordenskjöld A, Mills JL, Murray JC, Melbye M (2013) Plasma lipids, genetic variants near APOA1, and the risk of infantile hypertrophic pyloric stenosis. *The Journal of American Medical Association* **310(7)**:714-721.
76. Massett MP, **Fan RZ**, and Berk BC (2009) Quantitative trait loci for exercise training responses in FVB/NJ and C57BL/6J mice. *Physiological Genomics* **40**:15-22.
77. Thomas NJ, DiAngelo S, Hess JC, **Fan RZ**, Ball MW, Geskey JM, Willson DF, and Floros J (2009) Transmission of surfactant protein variants and haplotypes in children hospitalized with respiratory syncytial virus. *Pediatric Research* **66**:70-73.
78. Thomas NJ, **Fan RZ**, DiAngelo S, Hess JC, and Floros Y (2007) Haplotypes of the surfactant protein genes A and D as susceptibility factors for the development of respiratory distress syndrome. *Acta Paediatrica* **96**:985-989.
79. Pavlovic J, Papagaroufalis C, Xanthou M, Liu W, **Fan RZ**, Thomas NJ, Apostolidou I, Papathoma E, Megaloyianni E, DiAngelo S, and Floros J (2006) Genetic variants of surfactant proteins A, B, C, and D in Bronchopulmonary Dysplasia. *Disease Markers* **22**:277-291.
80. Floros J, Thomas N, Liu W, Papagaroufalis C, Xanthou M, Pereira S, **Fan RZ**, Guo X, DiAngelo S, and Pavlovic J (2006) Family-based association tests suggest linkage between SP-B (and flanking region) and RDS; SP-B haplotypes and alleles from SP-B-linked loci are risk factors for RDS. *Pediatric Research* **59**:616-621.

81. Floros J, **Fan RZ**, Diangelo S, Guo XX, Wert J, and Luo JM (2001) SP-B associations and interactions with SP-A in RDS in whites and blacks. *Pediatric International* **43**:567-576.
82. Floros J, **Fan RZ**, Matthews A, DiAngelo S, Luo JM, Nielsen H, Dunn M, Gewolb I, Koppe J, vanSonderen L, Farri-Kostopoulos L, Rämetsä M, Merrill J, and Robbins (2001) Family based transmission disequilibrium test (TDT) and case-control association studies reveal surfactant protein A (SP-A) susceptibility alleles for respiratory distress syndrome (RDS) and possible race differences. *Clinical Genetics* **60**:178-187.
83. Floros Y and **Fan RZ** (2001) Surfactant protein (SP) B associations and interactions with SP-A in whites and black subjects with respiratory distress syndrome. *Pediatric International* **43**:567-576. *Biology of the Neonate* **80 (Suppl 1)**:22-25.

### Invited Commentaries

84. **Fan RZ**, Albert PS, and Schisterman EF (2012) A discussion of longitudinal genetic analysis as well as gene-gene and gene-environment interactions of complex traits. *Statistics in Medicine* **31**:2565-2568.

### Invited Book Reviews:

85. **Fan RZ** (2013) The Fundamentals of Modern Statistical Genetics, by Nan M. Laird and Christoph Lange. *Journal of the American Statistical Association* **108**:355.
86. **Fan RZ** (2012) Statistics in Human Genetics and Molecular Biology, by Cavan Reilly. *The American Statistician* **66**:71-72.

### Software Development: Refer to

<http://www.nichd.nih.gov/about/org/diphhr/bbb/software/fan/Pages/default.aspx>

1. R codes for gene level meta-analysis of quantitative pleiotropic traits with multivariate functional linear models.
2. R codes for gene-based association analysis for censored traits via functional regressions.
3. R codes for gene level meta-analysis of dichotomous traits by generalized functional linear models.
4. R codes for gene level meta-analysis of quantitative traits by functional linear models.
5. R codes for pleiotropy analysis of quantitative traits at gene level by multivariate functional linear models.
6. R codes for generalized functional linear models for association analysis of dichotomous traits.

7. R codes for functional linear models for association analysis of quantitative traits.
8. R codes for longitudinal association analysis of quantitative traits.
9. R codes for association analysis of complex diseases using triads, parent-child dyads and singleton monads.
10. R codes for entropy-based information gain approaches to detect gene-gene and gene-environment interactions/correlations of complex diseases.
11. SAS Macros for qualitative traits (joint work with Dr. Knapp at University of Bonn, Germany):
  - Hotelling  $T^2$  tests based on population case control data.
  - Hotelling  $T^2$  tests based on nuclear trio family data.
  - Hotelling  $T^2$  tests based on sib-ship data.
12. C++ software to detect positive selection in the human genome (joint work with Dr. Ming Zhong):
  - Extended homozygosity score test (EHHST).
  - A cross-population extended haplotype-based homozygosity score test (xp-EHHST).

### Research Grants:

- 2015-2018, Genetic Factors in Birth Defects-Genomic Testing, Dr. Mills (PI) in the Epidemiology Branch, Dr. Fan (co-PI), DIPHR, NICHD, pending.
- 2016-2018, Offspring Genome Wide DNA Methylation Patterns at Birth and the Intrauterine Environment in the EAGeR Trial, Dr. Yeung (PI) in the Epidemiology Branch, Dr. Fan (co-PI), DIPHR, NICHD.
- 2016-2017, Role of Ldb1 Complexes in T Cell Acute Lymphoblastic Leukemia, Dr. Love (PI) in Division of Intramural Research (DIR), Dr. Fan (co-PI), DIPHR, NICHD.
- 2011-2017, Irish Collaborative Study, Dr. Mills (PI) in the Epidemiology Branch, Dr. Fan (co-PI), DIPHR, NICHD.
- 2011-2017, New York Collaborative Study - Genetic Factors in Birth Defects, Dr. Mills (PI) in the Epidemiology Branch, Dr. Fan (co-PI), DIPHR, NICHD.
- 2014-2016, Genetic Factors in Cushings Disease: Whole Exome Sequencing, Dr. Mills (PIs), Dr. Fan (co-PI), DIPHR, NICHD.
- 2014-2016, Pregnancy Eating Attributes Study (PEAS), Dr. Nansel (PI) in Health Behavior Branch (HBB), Dr. Fan (co-PI), DIPHR, NICHD.

- 2014-2017, AMD Genetics: Methods and Analysis for Progression, Prediction, and Association, R01EY024226, Total Cost: \$904,000, Dr. Wei Chen at University of Pittsburgh (PI), Dr. Ruzong Fan (Co-PI, unpaid collaborator), and Dr. Daniel Weeks at University of Pittsburgh (Co-PI).
- 2014-2015, Investigating the Role of Ldb1 Transcription Complexes in T Cell Acute Lymphoblastic Leukemia and in Normal T Cell Development, Dr. Love (PI) in Division of Intramural Research (DIR), Dr. Fan (co-PI), DIPHR, NICHD.
- 2013-2016, Statistical Methods for Association Analysis of Complex Traits, ZIA HD008918-04, Dr. Fan (PI), NICHD, NIH.
- 2011-2013, Longitudinal Genetic Analysis of Complex Traits, ZIA HD008918-02, ZIA HD008918-03, Dr. Fan (PI), NICHD, NIH.
- 2011-2013, NEXT Generation Longitudinal Health Study, Dr. Simons-Morton and Dr. Iannotti (PIs) in Health Behavior Branch (HBB), Dr. Fan (co-PI), DIPHR, NICHD.
- 2010, Research and Travel Support from the Intergovernmental Personnel Act (IPA), National Cancer Institute, NIH, 25% effort and travel support for Dr. Fan.
- 2007-2011, Genetic Basis for Exercise Training Responses, NIH/NHLBI 1R01 HL085918-01, Dr. Massett (PI), Dr. Fan (5% effort, Biostatistician).
- 2005-2007, Haplotype Linkage and Association Mapping of Quantitative Trait Loci, DMS-0505025, The National Science Foundation, Dr. Fan (PI), \$61,147.
- 2004, International Research Travel Assistance Grant, International Center, Texas A&M University, Dr. Fan (PI), \$1,100.
- 2002, International Research Travel Assistance Grant, International Center, Texas A&M University, Dr. Fan (PI), \$2,000.
- 2001-2002, Statistical Analysis in Complex Disease Gene Mapping, Pilot Project Program, Center for Environmental and Rural Health (CERH), Texas A&M University, Dr. Fan (PI), \$20,000.
- 2001, Surfactant Proteins and Respiratory Distress Syndrome, NIH 4 R37 HL34788-15, Dr. Floros (PI), Dr. Fan (Collaborator as a Statistical Geneticist).
- 1999-2000, Pediatric Asthma Network Data Coordinating Center, NIH/NHLBI grant 1 U10 HL64313-01, Dr. Chinchilli (PI), Dr. Fan (Co-PI as a Statistical Geneticist).
- 1990–1992, Research Grant of Probability Theory and Stochastic Analysis, National Natural Science Foundation of China, Dr. Fan (PI).

## Grant Reviews:

- 2013, Health Behavior Branch, Division of Intramural Population Health Research, NICHD/NIH.
- 2012, Epidemiology Branch, Division of Epidemiology, Statistics, and Prevention, NICHD/NIH.
- 2011, Prevention Research Branch, Division of Epidemiology, Statistics, and Prevention, NICHD/NIH.
- 2002, The Wellcome Trust, London, UK

### **Membership:**

- 1998–present, The American Society of Human Genetics.
- 1999–present, The International Biometric Society.
- 2000–present, The International Genetic Epidemiology Society.

### **Mentoring at NIH:**

- **Post-doctoral Fellow:**

1. 2015 - present, Chi-yang Chiu, mainly works with Dr. Fan on statistical methods of methylation data.
2. 2012 - 2014, Yifan Wang, mainly works with Dr. Fan on functional regression models of gene level association studies of complex traits. After finishing the post-doctoral training, Yifan has worked:
  - (a) 2014 - present, Mathematical Statistician at Center for Drug Evaluation and Research, Food and Drug Administration (FDA), Silver Spring, MD.

- **Summer Interns:**

1. 2014, Victoria Chen, University of Connecticut.
2. 2012, Annie Lee, Division of Biostatistics, Columbia University; received a training grant of “TL1 Personalized Medicine Training Program” conducted at Columbia, funded by Clinical and Translational Science Awards (CTSA), NIH, May 2014.

### **Mentoring at Texas A&M:**

- **Visiting Scholar:**

1. 2010-2011, Dr. Shunfang Wang, School of Information Science and Engineering, Yunnan University, Kunming 650091, China.

- **Ph.D students (advisor):**

1. 2006-2010, Ming Zhong, Thesis: Extended Homozygosity Score Tests to Detect Positive Selection in Genome-wide Scans. After finishing the Ph.D study, Ming has worked:
  - (a) 2012 - present, Senior Applied Statistician, Baker Hughes Inc., Houston, TX.
  - (b) 2011 - 2012, Principal Statistician, Capital One, Dallas, TX.
  - (c) 2010 - 2011, Research Statistician, Abbott Lab, Chicago, IL.
2. 2001-2004, Jeesun Jung, Thesis: High Resolution Linkage and Association of Quantitative Trait Loci. After finishing the Ph.D study, Jeesun has worked:
  - (a) 2011 - present, Staff Scientist, Laboratory of Epidemiology and Biometry, National Institute on Alcohol Abuse and Alcoholism, National Institutes of Health, Bethesda, MD.
  - (b) 2006 - 2011, Assistant Professor, Department of Medical and Molecular, Genetics, Indiana University, School of Medicine, Indianapolis, IN.
  - (c) 2004 - 2006, Post-doctoral Fellow of Dr. Weeks, Departments of Biostatistics and Human Genetics, The University of Pittsburgh, PA.

- **Master Students (advisor):**

1. 2009-2011, Jianxu Lu.
2. 2009-2010, Manxi Gu.
3. 2008-2011, Qing Chang.
4. 2008-2010, Yiwei Zhang.
5. 2007-2008, Lianfu Chen.
6. 2005-2007, Ming Zhong.
7. 2003-2005, Lijun Ren.
8. 2003-2004, Minghua Mei.

- **Committee Member of Graduate Students in Statistics:**

1. 2009-2011, Rupa Sridevi Kanchi (Ph.D).
2. 2006-2008, Lian Liu (Ph.D).
3. 2005-2007, Sanghan Lee (Ph.D).
4. 2004-2006, Iryna Lobach (Ph.D).
5. 2004-2006, Ilsung Chang (Ph.D).
6. 2002-2005, Dan Gaile (Ph.D).
7. 2002-2004, Li-yu Liu (Ph.D).
8. 2001-2002, Shaokun Chuai (M.S).

• **Committee Member of Graduate Students Outside Statistics:**

1. 2009-2011, Igor Vilchez-Ramirez (Ph.D).
2. 2008-2009, Hui Zhi (M.S).
3. 2007-2009, Xiaohong Zhu (M.S.).
4. 2007-2009, Adam Ray Jarrett (M.S).
5. 2006-2010, Yunhua Liu (Ph.D).
6. 2006-2010, Tomasz E Koralews (Ph.D).
7. 2006-2008, Yen-hsuan Wu (M.S).
8. 2006-2008, Le Jing (M.S).
9. 2006-2008, Ning Xu (M.S).
10. 2005-2010, Xiaoyan Zhao (Ph.D).
11. 2005-2009, Hao Xiong (Ph.D).
12. 2005-2008, Haiwen Liu (Ph.D).
13. 2005-2007, Shridhar Yamijala (M.S).
14. 2005-2007, Reeta Krishna (M.S).
15. 2002-2004, Wenbo Chen (M.S).

**Steering Committee of Workshops:**

- Next generation analytic tools for large scale genetic epidemiology studies of complex diseases, National Cancer Institute, NIH, 2010.

**Organizer of Statistical Meeting Sessions:**

- 2016, Session 35, Recent Research of Omics Data by Young Investigators, The International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Atlanta, GA.
- 2016, Session 33, Survival Analysis and Genetics, Eastern North American Region/International Biometric Society, Austin, TX.
- 2014, Session 43, Functional Data Analysis and its Applications in Genetics, Eastern North American Region/International Biometric Society, Baltimore, MD.
- 2013, Session 27, Statistical Methods in Dissecting Complex Traits, The Joint Conference by the International Chinese Statistical Association (ICSA) and the International Society for Biopharmaceutical Statistics (ISBS), Washington, DC.

**Chair of Statistical Meeting Sessions:**

- 2016, Session 18, New Statistical Computing using R, The International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Atlanta, GA.
- 2013, Session 107 Chair: Multivariate Methods, Eastern North American Region/International Biometric Society, Orlando, FL.
- 2004, Eastern North American Region/International Biometric Society.
- August 2001, Section of Innovative Approaches for Teaching Statistical Topics, Joint Statistical meeting, Atlanta.

### **Referee for Scientific Papers:**

- September 2016, Bioinformatics.
- July 2016, Genetics.
- July 2016, Briefings in Bioinformatics.
- May 2016, Human Genetics.
- May 2016, Bioinformatics.
- April 2016, Genetics.
- April 2016, American Journal of Human Genetics.
- April 2016, PeerJ
- March 2016, BMC Bioinformatics.
- March 2016, Genetic Epidemiology.
- March 2016, Journal of the American Statistical Association.
- February 2016, Scientific Reports.
- February 2016, Journal of the American Statistical Association.
- January 2016, Statistics in Medicine.
- January 2016, Genetics.
- December 2015, Scientific Reports.
- November 2015, Nucleic Acids Research
- October 2015, Genetic Epidemiology.
- October 2015, BMC Bioinformatics.

- August 2015, Genetics.
- May 2015, Heredity.
- March 2015, Biostatistics.
- January 2015, Statistics and Its Interface.
- January 2015, Statistics in Medicine.
- January 2015, Entropy.
- January 2015, Genetic Epidemiology.
- November 2014, Plos One.
- November 2014, Genetic Epidemiology.
- October 2014, Bioinformatics.
- August 2014, Cancer Informatics.
- July 2014, Human Genetics.
- June 2014, Statistics and Its Interface.
- May 2014, Plos One.
- April and May 2014, Genetic Epidemiology.
- March 2014, International Chinese Statistical Association, Applied Statistics Symposium, 2013.
- February 2014, Human Genetics.
- January 2014, Statistics in Medicine.
- December 2013, Journal of Plant Interactions.
- November 2013, Biometrics.
- October 2013, Statistical Applications in Genetics and Molecular Biology.
- October 2013, Statistics in Medicine.
- February, March, April, May, and August 2013, Genetic Epidemiology.
- November 2012, Genetic Epidemiology.
- February 2012, Bioinformatics.
- January 2012, research paper for “Analysis of Mixed Data”, CRC/Chapman & Hall.

- 2011, Annals of Applied Statistics, Statistics in Medicine, Biomedcentral Bioinformatics, Bioinformatics, Statistical Applications in Genetics and Molecular Biology.
- 2010, Book review for CRC/Chapman & Hall, Annals of Human Genetics, Bioinformatics, Journal of Heredity, Genetic Epidemiology.
- 2009, Annals of Human Genetics, Genome Research, Applications and Applied Mathematics (AAM): an International Journal, BMC-series journals, Statistical Applications in Genetics and Molecular Biology.
- 2008, PLoS Genetics, Genetics, American Journal of Human Genetics, Biometrics, Advances in Bioinformatics, Genetic Epidemiology, Computational Statistics & Data Analysis.
- 2007, American Journal of Human Genetics, Statistical Applications in Genetics and Molecular Biology, Genetic Epidemiology.
- 2006, Biomedcentral Bioinformatics, Biometrics, Genetics, Current Progress in Bioinformatics, Biomedcentral Genetics.
- 2005, Genetics, Biomedcentral Genetics, Human Heredity, American Journal of Human Genetics, Federation of European Biomedical Societies Letters.
- 2004, American Journal of Human Genetics, Genetic Epidemiology, Biometrics, Proceedings of National Academy of Sciences USA.
- 2003, American Journal of Human Genetics, Nature Reviews Genetics, Human Heredity, Biometrics, Proceedings of National Academy of Sciences.
- 2002, Genetic Epidemiology, American Journal of Human Genetics, Bioinformatics.
- 2001, Human Heredity, American Journal of Human Genetics, Proceedings of the Short Course on Mathematical Biology, edited by Dr. Sneyd J, American Mathematical Society.
- 1999, Proceedings of National Academy of Sciences USA, Biometrics, Applied Mathematics Letters.
- 1998, Theoretical Population Biology.

### Posters and Abstracts:

1. **Fan RZ<sup>11</sup>**, Chiu CY, Wang Y, Jung JS, Jiang YD, Chen W, Weeks DE, Ren H, Amos CI, Bailey-Wilson JE, Wilson AF, Xiong M (2015) Functional Regression Models for Gene-based Association Studies of Complex Traits. The American Society of Human Genetics 65th Annual Meeting, Baltimore, MD.

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<sup>11</sup>top 10% of poster abstracts as determined by the reviewers score.

2. Wang Y<sup>12</sup>, Chen W, Weeks DE, Ren H, Li Y, Lobach I, Amos CI, Moore JH, Boehnke M, Xiong M, and **Fan RZ** (2015) Meta-analysis of complex diseases at gene level by functional regression. The American Society of Human Genetics 65th Annual Meeting, Baltimore, MD.
3. Chiu CY, Jung JS, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Xiong M, **Fan RZ** (2015) A comparison study of fixed and mixed effect models for gene level association studies of complex traits. The American Society of Human Genetics 65th Annual Meeting and 24th International Genetic Epidemiology Society Annual Meeting, Baltimore, MD.
4. **Fan RZ**, Wang Y, Chen W, Ren H, Li Y, Boehnke M, Amos CI, Moore JH, and Xiong M (2015) Meta-analysis of complex diseases at gene level by generalized functional linear models. International Biometric Society, East North American Region Meeting, Miami, FL.
5. Wang Y, **Fan RZ**, Boehnke M, Chen W, Li Y, Ren H, I Lobach I, and Xiong M (2015) Gene level meta-analysis of quantitative traits by functional linear models. International Biometric Society, East North American Region Meeting, Miami, FL.
6. Hagen E, Sicko R, Kay D, Rigler S, Dimopoulos A, Warmerdam B, Ahmad S, Doleman M, **Fan RZ**, Romitti P, Browne M, Caggana M, Brody L, Shaw G, Jelliiffe-Pawlowski L, Mills J (2015) Copy-number variant analysis of classic heterotaxy highlights the importance of body patterning pathways. Teratology Society Annual Meeting.
7. Ronald IJ, Pratt C Li KG, DElio M, Olson S, **Fan RZ**, and Simons-Morton B (2013) The role of weight status in associations of adolescent physical activity and sedentary behavior with cardiovascular risk indicators. The International Society for Behavioral Nutrition and Physical Activity.
8. Pratt CA, Iannotti RJ, Li KG, D’Elio M, Olson S, Lipsky L, **Fan RZ**, and Simons-Morton B (2012) Associations among body mass index, waist circumference, dietary factors and cardiometabolic risks in 10th grade students: The NEXT Generation Health Study. The Experimental Biology.
9. **Fan RZ**, Zhong M, Wang SF, Zhang YW, Andrew A, Karagas M, Moore J, Chen H, Amos CI, and Xiong M (2011) Entropy-based approaches to detect gene-gene and gene-environment interactions of complex diseases. The 12th International Congress of Human Genetics and The American Society of Human Genetics 61st Annual Meeting, 725W.
10. **Fan RZ**, Zhong M, and Lange K (2009) A powerful extended homozygosity score test to detect positive selection in genome-wide scans. The American Society of Human Genetics 59th Annual Meeting.
11. **Fan RZ**, Liu L, Jung J, and Zhong M (2008) Multivariate combined linkage and association mapping of quantitative trait loci. The 18th International Genetic Epidemiology Society Annual Meeting.

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<sup>12</sup>top 10% of poster abstracts as determined by the reviewers score.

12. **Fan RZ** and Knapp M (2004) High resolution  $T^2$  association tests of complex diseases using normal sibs as controls. The American Society of Human Genetics 54th Annual Meeting, abstract 1989/F3, page 365.
13. **Fan RZ**, Knapp M, Zhao C, Xiong M (2004) High resolution  $T^2$  association tests of complex diseases using parents as controls. *The American Journal of Human Genetics* **73 (Supplementary)**:609; The American Society of Human Genetics 53rd Annual Meeting, abstract 2588.
14. **Fan RZ** and Xiong MM (2002) Haplotype linkage disequilibrium mapping of quantitative trait loci. *The American Journal of Human Genetics* **71 (Supplementary)**:572; The American Society of Human Genetics 52nd Annual Meeting, abstract 2360.
15. **Fan RZ** and Xiong MM (2001) Combined linkage and association interval mapping of quantitative trait loci. *The American Journal of Human Genetics* **69 (Supplementary)**:396; The American Society of Human Genetics 51st Annual Meeting, abstract 1252.
16. Floros J, **Fan RZ**, Guo X, Matthews A, Luo J (2000) Family based transmission disequilibrium test reveals linkage between an SP-B-linked locus and RDS; SP-B linked alleles are susceptibility or protection factors for RDS. *The American Journal of Human Genetics* **67 (Supplementary 2)**:357; The American Society of Human Genetics 50th Annual Meeting, abstract 1996.
17. **Fan RZ**, Jin L, and Xiong MM (2000) Haplotype linkage disequilibrium mapping of quantitative trait loci under truncation selection. *The American Journal of Human Genetics* **67 (Supplementary 2)**:319; The American Society of Human Genetics 50th Annual Meeting, abstract 1767.

### Invited Talks and Seminars

1. 2016, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Statistics and Actuarial Science, Faculty of Mathematics, University of Waterloo, Canada.
2. 2016, A Comparison Study of Fixed and Mixed Effects Models for Gene Level Association Studies of Complex Traits, The International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Atlanta, GA.
3. 2016, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University.
4. 2016, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Mathematics and Statistics, University of Houston-Downtown.
5. 2016, Gene-based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions, International Biometric Society, East North American Region Meeting, Austin, TX.

6. 2016, Functional Regression Models for Gene-based Association Studies of Complex Traits, Laboratory of Genetics, National Institute on Aging, NIH, Baltimore, MD.
7. 2015, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Biostatistics, Florida University, Gainesville, FL.
8. 2015, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Biostatistics and Department of Medical and Molecular Genetics, Indiana University, Indianapolis, IN.
9. 2015, Functional Regression Models for Gene-based Association Studies of Complex Traits, Hollings Cancer Center and Department of Public Health Sciences, Medical University of South Carolina, Charleston, SC.
10. 2015, Gene-based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions, Joint Statistical Meeting, Seattle, WA.
11. 2015, Functional Regression Models for Gene-based Association Studies of Complex Traits, Washington Statistical Society/NCI Division of Cancer Prevention Colloquia Series.
12. September 2014, Functional Regression Models for Gene-based Association Studies of Complex Traits, Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA.
13. August 2014, Gene Level Meta-analysis of Quantitative Traits by Functional Linear Models, Joint Statistical Meeting, Boston, MA.
14. March 2014, Pleiotropy Analysis of Quantitative Traits at Gene Level by Multivariate Functional Linear Models, International Biometric Society, East North American Region Meeting, Baltimore, MD.
15. June 2013, Generalized Functional Linear Models for Case-Control Association Studies, The Joint Conference by the International Chinese Statistical Association (ICSA) and the International Society for Biopharmaceutical Statistics (ISBS), Washington, DC.
16. May 2013, Functional Linear Models for Association Analysis of Quantitative Traits, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD.
17. September 2012, Statistical Analysis of Complex Traits, Washington Statistical Society/ NCI Division of Cancer Prevention Colloquia Series.
18. June 2012, Stochastic Dynamic Models and Chebyshev Splines, The 21st Applied Statistics Symposium, International Chinese Statistical Association, Boston, MA.
19. June 2011, Extended Homozygosity Score Tests to Detect Positive Selection in Genome-wide Scans. School of Statistics and Mathematics, Yunnan University of Finance and Economics, Kunming, China.

20. June 2011, Entropy-based Information Gain Approaches to Detect Gene-gene and Gene-environment Interactions/correlations of Complex Diseases. Department of Statistics, Yunnan University, Kunming, China.
21. February 2011, Entropy-based Information Gain Approaches to Detect Gene-gene and Gene-environment Interactions/correlations of Complex Diseases. *Eunice Kennedy Shriver* National Institute of Child Health and Human Development, NIH.
22. October 2010, National Cancer Institute, NIH.
23. June 2010, Division of Intramural Research Programs, National Institute of Mental Health, NIH.
24. May 2010, Child Psychiatry Branch, National Institute of Mental Health, NIH.
25. October 2009, National Cancer Institute, NIH.
26. October 2008, Division of Biostatistics, University of Minnesota, MN.
27. September 2008, MD Anderson Cancer Center, The University of Texas, Houston.
28. December 2007, Mount Sinai Medical School, New York, NY.
29. December 2007, Columbia University, New York, NY.
30. February 2007, UCLA, CA.
31. August 2006, Bonn University, Germany
32. May 2006, University of Alabama at Birmingham, AL.
33. March 2006, Stanford University, CA.
34. September 2005, Case Western Reserve University, OH.
35. July 2004, University of Bonn, Germany.
36. June 2002, Hawaii International Conferences on Statistics, HI.
37. March 2000, Department of Statistics, Penn State University, College Park, PA.
38. May 1999, Department of Health Evaluation Sciences, Penn State University, Hershey, PA.
39. May 1999, Department of Biostatistics, University of Iowa, Iowa City, IA.
40. April 1999, Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA.
41. March 1999, Department of Biostatistics, University of North Carolina, Chapel Hill, NC.
42. March 1999, Department of Statistics, University of Georgia, Athens, GA.
43. March 1999, Anderson Cancer Center, University of Texas, Houston, TX.

44. June 1998, Department of Environmental Health, Harvard School of Public Health, Boston, MA.
45. April 1998, Department of Biostatistics, Washington University, St. Louis, MO.
46. April 1998, Department of Mathematics, University of South California, Los Angeles, CA.
47. March 1998, Department of Statistics, Iowa State University, Ames, IA.
48. March 1998, Comprehensive Cancer Center, University of Alabama, Birmingham, AL.
49. March 1998, Department of Statistics and Department of Biostatistics, University of Wisconsin, Madison, WI.
50. December 1997, School of Public Health, Columbia University, New York, NY.
51. September 1993, Department of Mathematics, University of Oslo, Norway.
52. August 1993, Oberwolfach Conference on Nonstandard Analysis, Germany.
53. July 1992, International Conference of Nonstandard Analysis, Blaubeuren, Germany.
54. November 1992, Department of Mathematics, University of Strasburg, France.
55. September 1991, Department of Mathematics, Humboldt University of Berlin, Germany.
56. June 1991, International Conference of Stochastic Processes, Physics and Geometry II, Locarno, Switzerland.

### **Contributed Talks**

1. March 2013, Association Analysis of Complex Diseases Using Triads, Parent-child Dyads and Singleton Monads, International Biometric Society, East North American Region Meeting, Orlando, FL.
2. August 2012, Joint Statistical Meeting, San Diego, CA.
3. April 2012, International Biometric Society, East North American Region Meeting, Washington DC.
4. March 2005, International Biometric Society, East North American Region Meeting, Austin, TX
5. March 2004, International Biometric Society, East North American Region Meeting, Pittsburgh, PA.
6. March 2003, International Biometric Society, East North American Region Meeting, Tampa, Florida.
7. March 2002, International Biometric Society, East North American Region Meeting, Washington, DC.

8. August 2001, Joint Statistical Meeting, Atlanta, GA.
9. March 2001, International Biometric Society, East North American Region Meeting, Charlotte, North Carolina.