CURRICULUM VITAE

Dabao Zhang

Associate Professor

Department of Statistics
Purdue University
150 N. University Street
West Lafayette, IN 47907

Office: MATH 534
Tel: (765)494-6046
Fax: (765)494-0558
Email: zhangdb@purdue.edu

EDUCATION

Ph.D., 2003	**Statistics** (with Minors in Biometry and Capital Management), Cornell University.
M.Sc., 2001	**Statistics**, Cornell University.
M.Sc., 1993	**Probability & Statistics**, Peking University, Beijing, China
B.Sc., 1990	**Mathematical Statistics**, Nankai University, Tianjin, China.

HONORS AND AWARDS

- Purdue University Seed for Success Award, 2011

  This award recognizes accomplishments of single investigators and teams of investigators for their efforts in obtaining $1 million dollars or more in research grant funding.
- National Science Foundation CAREER Award, 2009

  This prestigious award of NSF recognizes and supports junior faculty's development for a lifetime of leadership in integrating education and research.
- Purdue University College of Science Interdisciplinary Award, 2009

  This award recognizes an extraordinary and significant outcome as the result of a current or recent interdisciplinary collaboration with faculty and staff in the College of Science.
- Cornell University Liu Memorial Award, 2003

  This award is for doctoral students at Cornell who has an excellent progress in graduate program and high potential for a successful academic career.
- First Prize Winner of National PC-Software Competition, 1995

  This award is for the the best software developed in China, i.e., Founder FIT, for which Dr. Zhang is one of the five major developers.

RESEARCH INTEREST

- **Statistical Theory and Methodology**

  Analysis of Life Times; Bayesian Statistics; Construction of Large Systems of Structural Equations; Dimension Reduction; Exploratory Analysis of High-Dimensional Data; (Generalized) Linear (Mixed) Models; Graphical Models; Integrative Analysis of Big Data; Model Predictability Evaluation; Multivariate Extreme Values; Multivariate Statistics; High-Dimensional Variable Selection; Sparse Parameter Estimates; Supervised Dimension Reduction of Big Data; Visualization of Big Data.

- **Statistical Genetics and Bioinformatics**
  Analysis of Genetic Genomics Data; Analysis of Systems Biology Data; Construction of Genome-Wide Gene Regulatory Networks; Genomic Selection; Genetic Epidemiology; Genome-Wide/Sequencing-Based Association Study; Identification of Molecular Signatures; (Integrative) Analysis of Omics Data (e.g., Genetic, Genomic, Proteomic, and Metabolomic Data); Quantitative Trait Loci (QTL) Mapping.

PROFESSIONAL EXPERIENCE

- **Academic Positions**

  Associate Professor of Statistics, Purdue University, since 2010.

  Affiliated Member, Oncological Science Center, Purdue University, since 2006.

  Affiliated Member, Bindley Bioscience Center, Purdue University, since 2006.

  Assistant Professor of Statistics, Purdue University, 2005 - 2010.

  Assistant Professor of Biostatistics and Computational Biology, University of Rochester Medical Center, 2003 - 2005.

- **Managerial Experience**

  Associate Director: Statistical Consulting Service Center, Department of Statistics, Purdue University, Summer 2011.

  Assistant Director: Statistical Consulting Service Center, Department of Statistics, Purdue University, January 2006 - May 2010.

  Director: Division of Trans-Platform Text Processing, R & D Center, Peking University Founder Group Co., 1996-1998.

- **Statistical Consulting**

  The Nathan Shock Center for Aging and Developmental Biology, University of Rochester, Fall 2003 - Spring 2005.

  Purdue Statistical Consulting Service Center, Spring 2006 - Summer 2011.

- **Teaching Experience**

  Advanced Statistical Methodology, Purdue University.

  Applied Regression Analysis, Purdue University.

  Applied Survival Analysis, Purdue University.

  Current Topics in Bioinformatics, University of Rochester.

  Design of Experiments, Purdue University.

  Dimension Reduction, Purdue University.

  High Dimensional Data Analysis, Purdue University.

  Intermediate Statistical Methodology, Purdue University.

  Time Series and Application, Purdue University.

RESEARCH FUNDING

- *A proteomic platform to identify and validate biomarkers in metabolic syndrome and coronary artery disease* (PI: Andy Tao), NIH/NIGMS. Role: Co-PI, 09/15/2015 –

09/14/2018.

- *Targeting PRMT5 as a novel radiosensitization approach for primary and recurrent prostate cancer radiotherapy* (PI: Changdeng Hu), DoD. Role: Co-PI, 08/01/2012-07/30/2015. Total Award: $559,269.91.
- *CAREER: A new regularization framework for identifying composite signatures* (PI: Dabao Zhang), NSF. 6/1/2009-5/31/2014. Total Award: $433,291.
- *New Statistical Approaches to Enhance Genome-Wide Single Nucleotide Polymorphism Association Mapping to Identify Genetic Markers for Common Complex Human Diseases* (PI: Min Zhang), Purdue Discovery Park. Role: Co-PI, 04/2009 – 12/2010. Total Award: $39,442.
- *Cook Med Institute Grant from Cook Med Institute Incorporated* (PI: Dabao Zhang). 9/1/2006 – 04/30/2011. Total Award: $25,942/year (financial support of a student).
- *Use of External Cueing to Treat Hypophonia in Parkinson's Disease* (PI: Jessica E. Huber), NIH/NIDCD. Role: Key Personnel, 4/1/2008 – 3/31/2013. Total Award: $386,027 (year 1).
- *Warfighter Cancer Care Engineering* (PI: Pat Loehrer), US Army Medical Research and Material Command. Role: Co-Investigator. 09/1/2010 – 10/31/2012. Total Award: $2,152,805.
- *Warfighter Cancer Care Engineering* (PI: Pat Loehrer), US Army Medical Research and Material Command. Role: Co-Investigator. 7/1/2008 – 8/1/2011. Total Award: $2,400,000.
- *Empirical Bayes Variable Selection with $p \gg n$ Data.* Summer Faculty Grant from Purdue Research Foundation (PI: Dabao Zhang). Summer 2007; Total Award: $7,000.

PAPERS

1. C. Chen, M. Zhang and D. Zhang (2016) Two-stage penalized least squares method for constructing large systems of structural equations. *arXiv:1511.00370.*
2. D. Zhang (2016). A Coefficient of determination for generalized linear models. *The American Statistician*, tentatively accepted.
3. C. Shi, Z. Zheng, Q. Wang, C. Wang, D. Zhang, M. Zhang, P. Chan, and X. Wang (2016). Exploring the Effects of Genetic Variants on Clinical Profiles of Parkinson's Disease Assessed by the Unified Parkinson's Disease Rating Scale and the Hoehn-Yahr Stage. Accepted by *PLoS ONE.*
4. Guan L, Wang Q, Wang L, Wu B, Chen Y, Liu F, Ye F, Zhang T, Li K, Yan B, Lu C, Su L, Jin G, Wang H, Tian H, Wang L, Chen Z, Wang Y, Chen J, Yuan Y, Cong W, Zheng J, Wang J, Xu X, Liu H, Xiao W, Han C, Zhang Y, Jia F, Qiao X, Genetic REsearch on schizophreniA neTwork-China and Netherland (GREAT-CN), Zhang D, Zhang M, and Ma H (2016). Common Variants on 17q25 and Gene-Gene Interactions Conferring risk of Schizophrenia in Han Chinese Population and Regulating Gene Expressions in Human Brain. *Molecular Psychiatry*, 2016, 1-7.
5. V. Pungpapong, M. Zhang, and **D. Zhang** (2015) Selecting massive variables using an iterative conditional modes/medians algorithm. *The Electronic Journal of Statistics*, 9, 1243-1266.
6. Y. Lin, M. Zhang, **D. Zhang** (2015). Generalized orthogonal components regression for

high dimensional generalized linear models. *Computational Statistics & Data Analysis*, 88, 119-127.

7. C. Chen, L. Deng, S. Wei, G. A. N. Gowda, H. Gu, G. Chiorean, M. Zaid, M. Harrison, J. Pekny, P. Loehrer, **D. Zhang**, M. Zhang, D. Raftery. (2015). Exploring Metabolic Profile Differences between Colorectal Polyp Patients and Controls Using Seemingly Unrelated Regression. *Journal of Proteome Research*, 14: 2492-2499.
8. H. T. Zhang, **D. Zhang**, Z. G. Zha, C. D. Hu (2014). Transcriptional activation of PRMT5 by NF-Y is required for cell growth and negatively regulated by the PKC/c-Fos signaling in prostate cancer cells. *BBA - Gene Regulatory Mechanisms*, 1839, 1330-1340.
9. H. Li, Y. J. Wang, L. Hua, Y. T. Yang, M. Zhang, **D. Zhang**, C. Y. Wang, and Z. Q. Xu (2013). Lack of association between dendritic cell nuclear protein-1 gene and major depressive disorder in the Han Chinese population. *Progress in Neuro-Psychopharmacology & Biological Psychiatry*, 45, 7-10.
10. J. E. Huber, M. Darling, E. J. Francis, and **D. Zhang** (2012). Impact of typical aging and Parkinson's disease on the relationship among breath pausing, syntax, and punctuation. *American Journal of Speech-Language Pathology*, 21: 368-379.
11. V. Pungpapong, W. M. Muir, X. Li, **D. Zhang**, and M. Zhang (2012). A fast and efficient approach for genomic selection with high density markers. G3: Genes, Genomes, Genetics, 2: 1179-1184.
12. V. Pungpapong, L. Wang, Y. Lin, **D. Zhang**, and M. Zhang (2011). Genome-Wide Association Analysis of GAW17 Data Using Empirical Bayes Variable Selection. Accepted by *BMC Proceedings.*
13. L. Wang, V. Pungpapong, Y. Lin, M. Zhang, and **D. Zhang** (2011). Genome-Wide Case-Control Study in GAW17 Using Coalesced Rare Variants. Accepted by *BMC Proceedings.*
14. X. Li, C. Zhu, Z. Lin, Y. Wu, **D. Zhang**, G. Bai, W. Song, J. Ma, G.J. Muehlbauer, M.J. Scanlon, M. Zhang, and J. Yu (2011). Chromosome size in diploid eukaryotic species centers on the average length with a conserved boundary. *Molecular Biology and Evolution*, 28: 1901-1911.
15. M. T. Wells and **D. Zhang** (2011). Graphical models for clustered binary and continuous responses. In *Advances in Directional and Linear Statistics* (edited by M.T. Wells and A. SenGupta), 305-321, Springer-Verlag Berlin Heidelberg.
16. M. Zhang, **D. Zhang** and M.T. Wells (2010). Generalized thresholding estimators for high-dimensional location parameters. *Statistica Sinica*, 20: 911-926.
17. N.-H. Chan, L. Peng and **D. Zhang** (2007). Empirical likelihood based confidence intervals for conditional variance in heteroscedastic regression models. *Econometric Theory*, 27: 1-24.
18. M. Zhang, Y. Lin, L. Wang, V. Pungpapong, J. C. Fleet, and **D. Zhang** (2009). Case-control genome-wide association study of rheumatoid arthritis from Genetic Analysis Workshop 16 using penalized orthogonal-components regression-linear discriminant analysis. *BMC Proceedings*, 3 (Suppl 7): S17.

19. Y. Lin, M. Zhang, L. Wang, V. Pungpapong, J. C. Fleet, and **D. Zhang** (2009). Simultaneous genome-wide association studies of anti-cyclic citrullinated peptide in rheumatoid arthritis using penalized orthogonal-components regression. *BMC Proceedings*, 3 (Suppl 7): S20.

20. **D. Zhang**, Y. Lin and M. Zhang (2009). Penalized orthogonal-components regression for large p small n data. *The Electronic Journal of Statistics*, 3: 781-796.

21. N. Liu, **D. Zhang** and H. Zhao (2008). Detection of genotyping errors without replicates in samples from unrelated individuals. *Human Heredity*, 67: 154-162.

22. **D. Zhang**, X. Huang, F.E. Regnier and M. Zhang (2008). Two-dimensional correlation optimized warping algorithm for aligning GC×GC-MS data. *Analytical Chemistry*, 80: 2664-2671.

23. M. Zhang, **D. Zhang**, M. T., Wells (2008). Variable selection with large p small n regression models: mapping QTL with epistasis. *BMC Bioinformatics*, 9:251.

24. **D. Zhang**, M. T. Wells and L. Peng (2008). Nonparametric estimation of the dependence function for a multivariate extreme value distribution. *Journal of Multivariate Analysis*, 99: 577-588.

25. T.R. Mhyre, R. Loy, P.N. Tariot, L.A. Profenno, K.A. Maguire-Zeiss, **D. Zhang**, P.D. Coleman and H.J. Federoff (2008). Proteomic analysis of peripheral leukocytes in Alzheimer's disease patients treated with divalproex sodium. *Neurobiology of Aging*, 29: 1631-1643.

26. **D. Zhang** and M. Zhang (2007). Bayesian profiling of molecular signatures to predict event times. *Theoretical Biology & Medical Modelling*, 4:3, doi:10.1186/1742-4682-4-3.

27. **D. Zhang**, M. Zhang, M. T. Wells (2006). Multiplicative background correction for spotted microarrays to improve reproducibility. *Genetical Research*, 87: 195-206.

28. **D. Zhang**, M. T. Wells, B. W. Turnbull, D. Sparrow and P. A. Cassano (2005). Hierarchical Graphical Models: An Application to Pulmonary Function and Cholesterol Levels in the Normative Aging Study. *Journal of American Statistics Association*, 100: 719-727.

29. M. Zhang, K. L. Montooth, M. T. Wells, A. G. Clark and **D. Zhang** (2005). Mapping Multiple Quantitative Trait Loci by Bayesian Classification, *Genetics*, 169: 2305-2318.

30. **D. Zhang**, M. T. Wells, C. D. Smart and W. E. Fry (2005). Bayesian Normalization and Inference for Differential Gene Expression Data. *Journal of Computational Biology*, 12: 391-406.

31. S. W. Perry, J. P. Norman, A. Litzburg, **D. Zhang**, S. Dewhurst and H. A. Gelbard (2005). HIV-1 Tat Induces Mitochondrial Hyperpolarization and Synaptic Stress Leading to Apoptosis, *Journal of Immunology*, 174: 4333-4344.

32. Complex Traits Consortium (including **D. Zhang**). (2004). The Collaborative Cross: A Community Resource for the Genetic Analysis of Complex Traits. *Nature Genetics*, 36: 1133-1137.

33. M. Zhang, X. Wang, **D. Zhang**, G. Xu, H. Dong, Y. Yu and J. Han (2004). Orphanin FQ antagonizes the inhibition of Ca2+ currents induced by mu-opioid receptors. *Journal of Molecular Neuroscience*, 25: 21-27.

34. **D. Zhang**, S. He and Z. Xie (1993). Outlier Detection and Intervention for $ARIMA(p, d, 0)$. *Proceedings of First Asian Conference on Statistical Computation.*

PRESENTATIONS/INVITED TALKS

- *A New Method to Construct Large Gene Regulatory Networks Using Genetical Genomics Data*, Weldon School of Biomedical Engineering, Purdue University, October 21, 2015.
- *A New Method to Construct Large Gene Regulatory Networks Using Genetical Genomics Data*, The Gavriel Salvendy International Symposium on Information Engineering, September 29-30, 2015.
- *A New Method to Construct Large Gene Regulatory Networks Using Genetical Genomics Data*, The Chicago Chapter of the American Statistical Association, September 15, 2015.
- *Multilocus Methods for Family-Based Genome-Wide Association Studies*, 2015 Nankai Statistics Forum, Tianjin, China. July 6-9, 2015.
- *A fast construction of large gene regulatory network using genetical genomics data*, 2015 IMS-China International Conference on Statistics and Probability, Kunming, China. July 1-4, 2015.
- *Penalized Orthogonal-Components Regression for High-Dimensional Variable Selection*, School of Mathematics and Statistics, Wuhan University, Wuhan, China. May 9, 2014.
- *Experimental Design and Analysis*, Capital Medical University, Beijing, China. May 4-5, 2014.
- *Empirical Bayes variable selection using iterative conditional modes/medians*, The 59th ISI World Statistics Congress, Hong Kong, China. August 28, 2013.
- *Employing Bioinformatics to Find a Needle in Haystack*, The Third Graduates Forum, School of Biomedical Engineering, Capital Medical University, Beijing, China. November 9, 2012.
- *High Dimensional Data Analysis with Supervised Dimension Reduction*, Department of Mathematics, Hong Kong University of Science and Technology. October 26, 2012.
- *High Dimensional Data Analysis with Supervised Dimension Reduction.* International Symposium on Mapping the Genetic Regulation of Forest Ecosystems. Beijing Forestry University, Beijing, China. October 12, 2012.
- *Fundamentals of High-Dimensional Data Analysis*, Department of Statistics, Nankai University, Tianjin, China. June 27-29, 2012.
- *Penalized Orthogonal-Components Regression for Large p Small n Data*, Department of Statistics, Fudan University, Shanghai, China. June 4, 2012.
- *Generalized Thresholding Estimators for High Dimensional Location Parameters.* School of Biomedical Engineering, Capital Medical University, Beijing, China. March 23, 2012.
- *High Dimensional Data Analysis*, Department of Biomedical Informatics, Capital Medical University, Beijing, China. March 22, 2012.
- *How to Effectively Extract Information from Clinical and Experimental Data*, Capital Medical University, Beijing, China. March 15, 2012.

- *Penalized Orthogonal-Components Regression: Selecting Sparse Variables in High-Dimensional Data.* Department of Statistics, Northwestern University, October 27, 2010.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* International Chinese Statistical Association (ICSA) 2010 Applied Statistics Symposium, June 22, 2010.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* Northeast Normal University, Changchun, China, June 8, 2010.
- *POCRE: A Supervised Learning of Sparse Components.* Center for Research on Genomics and Global Health, National Institute of Health, November 24, 2009.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* Department of Mathematics, Statistics, and Computer Science, University of Illinois at Chicago, September 9, 2009.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* Department of Statistics, Purdue University, September 3, 2009.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* Department of Mathematics & Statistics, Georgia State University, August 28, 2009.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* School of Mathematics, Georgia Institute of Technology, August 27, 2009.
- *Two-Dimensional Correlation Optimized Warping Algorithm for Aligning GC×GC-MS Data.* The International Chinese Statistical Association (ICSA) Applied Statistics Symposium, San Francisco, CA, June 24, 2009.
- *Penalized Orthogonal-Components Regression for Large p Small n Data.* Yale Statistics Workshop, May 16, 2009.
- *Systems Biology and Genome-Wide Association Study.* Systems Biology Luncheon at Computational Research Institute, Purdue University, April 14, 2009.
- *Some Multivariate Statistical Methods for Genome-Wide Association Study.* StatDay, Purdue University, April 2, 2009.
- *Some Multivariate Statistical Methods for Genome-Wide Association Study.* Genetic Analysis Workshop 16, St. Louis, Missouri, September 19, 2008.
- *Nonparametric Estimation of the Dependence Function for a Multivariate Extreme Value Distribution.* Department of Bioinformatics and Biostatistics, School of Public Health, University of Louisville, November 7, 2008.
- *On Preprocessing and Analyzing GC×GC-MS Data.* Bioinformatics Seminar, Purdue University, West Lafayette, IN. September 9, 2008.
- *On Preprocessing and Analyzing GC×GC-MS Data.* The Monthly Cancer Career Engineering Meeting, Purdue University, West Lafayette, IN. May 22, 2008.
- *Generalized Shrinkage Estimators Adaptive to Sparsity and Asymmetry of High Dimensional Parameter Spaces.* Department of Statistics, University of Illinois at Urbanan-Champaign, September 20, 2007.
- *Generalized Shrinkage Estimators Adaptive to Sparsity and Asymmetry of High Dimensional Parameter Spaces.* Seminar on Bayesian Inference in Econometrics and Statistics, St. Louis, Missouri, May 4, 2007.
- *Background Correction and Normalization of Spotted Microarray.* Center for Computational Biology and Bioinformatics, Indiana University School of Medicine, October 27, 2006.

- *Nonparametric Estimation of the Dependence Function for a Multivariate Extreme Value Distribution.* VIGRE Seminar, Department of Statistics, Purdue University, West Lafayette, IN. September 13, 2006.
- *Nonparametric Estimation of the Dependence Function for a Multivariate Extreme Value Distribution.* Ninth Meeting of New Researchers in Statistics and Probability, Seattle, WA, August 2006.
- *Background Correction and Normalization of Spotted Microarray.* Department of Statistics, Iowa State Univeristy. April 26, 2006.
- *Identifying Molecular Signatures for Survival Outcommes and Hierarchical Graphical Models.* Presented to Genentech Visitors, Department of Statistics, Purdue University. March 20, 2006.
- *Bayes, Empirical Bayes and Adaptive Bayes.* VIGRE Seminar, Department of Statistics, Purdue University. October 5, 2005.
- *Double Shrinkage Estimator and Its Implementation.* JSM, Minneapolis, MN, 2005.
- *Multivariate Statistics with Application to Bioinformatics.* Division of Biostatistics, Department of Public Health Sciences, University of California, Davis, 2005.
- *Hierarchical Graphical Models: An Application to Pulmonary Function and Cholesterol Levels in the Normative Aging Study.* Center for Statistical Sciences, Brown University, 2005.
- *Multivariate Statistics with Applications.* Department of Statistics, Purdue University, 2005.
- *Multivariate Statistics with Application to Bioinformatics.* Department of Statistics and Probability, Michigan State University, 2005.
- *Bayesian Identification of Prognostic Molecular Signatures for Survival Phenotypes.* ENAR, Austin, TX, 2005.
- *Microarray, QTL Mapping and Identifying Molecular Markers/Signatures*, Center for Aging and Developmental Biology, University of Rochester Medical Center, 2005.
- *Double-Shrinkage Estimator and Its Implementation.* Department of Biostatistics and Computational Biology, University of Rochester Medical Center, 2004.
- *QTLBayes: Mapping Multiple Quantitative Trait Loci Using Bayesian Variable Selection.* The Third Annual Conference of Complex Trait Consortium, Bar Harbor, ME, 2004.
- *Bayesian Normalization and Identification for Differential Gene Expression Data.* International Conference on Analysis of Genomic Data, Boston, MA, 2004.
- *Bayesian Variable Selection to Identify Quantitative Trait Loci.* Poster at the Eighth Annual International Conference on Research in Computational Molecular Biology, San Diego, CA, 2004.
- *Inference for Nonrecursive Graphical Model Mixed with Discrete and Censored Continuous Clustered Responses.* JSM, San Francisco, CA, 2003.
- *Bayesian Normalization and Identification for Differential Gene Expression Data.* Department of Biostatistics and Computational Biology, University of Rochester Medical Center, 2003.
- *Bayesian Normalization and Identification for Differential Gene Expression Data.* The Computational and Applied Genomics Program, Duke University Medical Center, 2003.

- *Bayesian Normalization and Identification for Differential Gene Expression Data.* Department of Biostatistics, University of Minnesota, 2003.
- *Bayesian Normalization and Inference on Differential Gene Expression Data.* Biometrics Unit Discussion Series, Cornell University, 2002.

SOFTWARE DEVELOPED

- *rsq:* A R Package to Calculate Coefficients of Determination for Generalized Linear Models.
- *GOCRE:* Generalized Orthogonal-Components Regression for Fitting High-Dimensional Generalized Linear Models.
- *POCRE:* Penalized Orthogonal-Components Regression for Variable Selection with High-Dimensional Data.
- *2DCOW:* Two-Dimensional Correlation Optimized Warping Algorithm for Aligning GC×GC-MS Data.
- *QTLBayes:* Mapping Multiple QTL with Bayesian Classification.
- *MicroBayes:* Bayesian Normalization of cDNA Microarray Data.
- *SEMMIX:* Simultaneous Equation Models with Mixed Coefficients.

JOURNAL REFEREEING

American Statistician, Bernoulli Journal, Bioinformatics, Biometrical Journal, Biometrics, BMC Bioinformatics, BMC Genetics, Electronic Journal of Statistics, Entropy, Genetics, Human Molecular Genetics, Journal of Agricultural Biological and Environmental Statistics, Journal of American Statistical Association, Journal of Computational and Graphical Statistics, Journal of Machine Learning Research, Journal of Multivariate Analysis, Journal of Nonparametric Statistics, Journal of Statistical Planning and Inference, Neurobiology of Aging, PLoS Genetics, PLoS ONE, Statistical Applications in Genetics and Molecular Biology, Statistica Sinica, Statistics and Its Interface, Test, The Plant Cell.

OTHER PROFESSIONAL ACTIVITIES

- Organized and chaired the invitation session “Inference of Network Structures” in the Joint Statistical Meetings, 2016, July 30-August 4, 2016, Chicago.
- Served on Program Committee of the GLBIO/CCBC Great Lakes Bioinformatics and the Canadian Computational Biology Conference 2016.
- Served on the GLBIO (Great Lakes Bioinformatics) 2015 Conference Program Committee.
- Served in Special Emphasis Panel/Scientific Review Group for Aging Systems and Geriatrics Study Section of NIH (October 6-7, 2014).
- Dr. Zhang has served in the Editorial Board: The Scientific World Journal (Impact Factor: 1.73), 2013-2014.
- Dr. Zhang has reviewed grants for the following agencies: The Wellcome Trust (2012); Michael Smith Foundation for Health Research (2012).
- Organized and chaired the session “Computational Statistics in Modern Biology” in the International Society for Computational Biology – Asia / the ShenZhen Conference on Computational Genomics (ISCB-Asia/SCCG), 2012, Shenzhen, China.

- Organized and chaired the session “Bayesian/Empirical Bayes Inference on High-Dimensional Data Analysis” in 8th International Purdue Symposium on Statistics, 2012, West Lafayette, Indiana.
- Chaired the session “Topics in Bioinformatics” in the International Chinese Statistical Association (ICSA) Applied Statistics Symposium, 2009, San Francisco, California.
- Program committee of the 12th International Conference on Artificial Intelligence and Statistics, 2009.
- Statistical Expert of *The Plant Cell*.
- Member of the Editorial Board of *The Scientific World Journal*.

PROFESSIONAL AFFILIATIONS

American Statistical Association (ASA)

International Chinese Statistical Association (ICSA)

International Genetic Epidemiology Society (IGES)

Institute of Mathematical Statistics (IMS)