Fei Zou Phone: (919)843-4822 Email: fzou@bios.unc.edu

EDUCATION

Ph.D., Statistics, 2001: University of Wisconsin - Madison M.S., Statistics, 1993: Wuhan University (China) B.S., Mathematics, 1990: Wuhan University (China)

PROFESSIONAL EXPERIENCE

Associate Professor Department of Biostatistics, University of North Carolina, Chapel Hill.	2007 ~
Assistant Professor Department of Biostatistics, University of North Carolina, Chapel Hill.	2001 ~ 2007
Assistant Professor Department of Mathematics, Changsha Railway University, China.	1993~ 1995

<u>Honors</u>

- 1. David P. Byar Young Investigator Award (2001)
- 2. Gordon Research Fellowship (2001)

Membership

- 1. Member of American Statistical Association
- 2. Member of Institute of Mathematical Statistics
- 3. Member of the American Society of Human Genetics

PUBLICATIONS

Accepted and Published

- 1. Huang, H., Zhou, H., Cheng, F., Hoeschele, I., and **Zou, F.** (2009). Gaussian process based Bayesian semiparametric quantitative trait loci interval mapping. *Biometrics*. In press.
- Bartlett JR, Friedman KJ, Ling SC, Pace RG, Bell SC, Bourke B, Castaldo G, Castellani C, Cipolli M, Colombo C, Colombo JL, Debray D, Fernandez A, Lacaille F, Macek M Jr, Rowland M, Salvatore F, Taylor CJ, Wainwright C, Wilschanski M, Zemková D, Hannah WB, Phillips MJ, Corey M, Zielenski J, Dorfman R, Wang Y, **Zou, F**, Silverman LM, Drumm ML, Wright FA, Lange EM, Durie PR, Knowles MR (2009). Genetic Modifiers of Liver Disease in Cystic Fibrosis. *JAMA*, 302:1076-1083.

- 3. Zhang, X, **Zou, F.** and Wang, W. (2009). FastChi: an efficient algorithm for analyzing gene-gene interactions. *Pacific Symposium on Biocomputing*: **528-39**.
- Levy, H., Murphy, A., Zou, F., Gerard, C., Klanderman, B., Schuemann, B., Lazarus, R., García, K.C., Celedón, J.C., Drumm, M., Dahmer, M., Quasney, M., Schneck, K., Reske, M., Knowles, M.R., Pier, G.B., Lange, C., and Weiss, S.T. (2009). IL1B polymorphisms modulate cystic fibrosis lung disease. Pediatr Pulmonol, 44:580-93.
- 5. Zhang, X., Pan, F., Xie, Y., **Zou, F.** and Wang, W.(2009). A General approach for efficient genome-wide two-locus epispastic test in disease association study. *RECOMB*. In press.
- 6. **Zou, F.**, Nie, L., Wright, F.A., and Sen, P.K. (2009). A robust QTL mapping procedure. Journal of Statistical Planning and Inference. In press.
- 7. Ghosh, A., Zou, F., and Wright, F.A. (2008). Estimating odds ratios in genome scans: an approximate conditional likelihood approach. *The American Journal of Human Genetics* 82: 1064-1074.
- 8. Zhang, X, Wang, W., and **Zou, F.** (2008). FastANOVA: an efficient algorithm for genome-wide association study. *Proceedings of the 14th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (SIGKDD).*
- 9. Huang, C., Qin, J. and **Zou, F**. (2007). Empirical likelihood-based inference for genetic mixture models. *The Canadian Journal of Statistics*, 35: 563-574.
- Sullivan, P. F., Lin, DY., Tzeng, JY, van den Oord, E., Perkins, D., Stroup, T. S., Wagner, M., Lee, S., Wright, F. A., Zou, F., Liu, W., Downing, A. M., Lieberman, J., and Close, S. L. (2008). Genomewide association for Schizophrenia in the CATIE study. *Molecular Psychiatry*. 13(6):570-84.
- 11. Lee, S., Sullivan, P. F., **Zou, F.** and Wright F. A. (2008). Comment on a simple and improved correction for population stratification. *The American Journal of Human Genetics*, 82: 524-531.
- 12. Gelfond, J., Ibrahim, J. G. and **Zou, F.** (2007). Proximity model for expression trait loci detection. *Biometrics*, 63: 1108–1116.
- 13. Huang, H., **Zou, F.** and Wright, F. A. (2007). Bayesian analysis of loss of heterozygosity by modeling of frequency of allelic loss data. *JASA*, 102: 1245-1253.
- 14. Huang, H., Eversley, C. D., Threadgill, D. W. and **Zou, F.** (2007). Bayesian multiple quantitative trait loci mapping for complex traits using markers of the entire genome. *Genetics*, **176**, 2529-2540.
- Wright, F. A. Huang, H., Guan, X., Gamiel, K., Jeffries, C., Barry, W.T., Pardo-Manuel, F., Sullivan, P. F., Wilhelmsen, K. C. and **Zou, F**. (2007). Simulating association studies: a data-based resampling method for candidate regions or whole genome scans. *Bioinformatics*, 23(19):2581-2588.
- Nadler, J., Zou, F., Huang, H., Moy, S., Lauder, J., Crawley, J., Threadgill, D. W., Wright, F. A., and Magnuson T. (2006). Large scale gene expression differences among brain regions in ten inbred mouse strains and their correlation with behavioral phenotype. *Genetics*, 174, 1229-1236.
- 17. Zou, F., Xu, Z. L. and Vision, T. J. (2006). Assessing the significance of quantitative trait loci in replicated mapping populations. *Genetics* 174: 1063–1068.

- 18. Hu, J., Wright, F.A. and **Zou, F.** (2006). Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101: 41-50.
- Zou, F., Gelfond, J., Airey, D., Lu, L., Manly, K., Williams, W. and Threadgill, D. (2005). Quantitative trait locus analysis using recombinant inbred intercrosses (RIX): theoretical and empirical considerations. *Genetics*, 170: 1299-1311.
- Drumm, M.L., Konstan, M.W., Schluchter, M.D., Handler, A., Pace, R., Zou, F., Zariwala, M., Fargo, D., Xu, A., Dunn, J.M., Darrah, R.J., Dorfman, R., Sandford, A.J., Corey, M., Zielenski, J., Durie, P., Goddard, K., Yankaskas, J.R., Wright, F.A., and Knowles, M.R. (2005). Gene Modifier Study Group. Genetic modifiers of lung disease in cystic fibrosis. *N Engl J Med*, 353:1443-1453.
- 21. Xu, Z. L., **Zou, F**., and Vision, T. J. (2005). Improving QTL mapping resolution in experimental crosses by the use of genotypically selected samples. *Genetics*, 170: 401-408.
- 22. Hester, S. D., Barry, W. T., **Zou, F**., and Wolf, D. C. (2005). Transcriptomic analysis of F344 rat nasal epithelium suggests that the lack of carcinogenic response to glutaraldehyde is due to its greater toxicity compared to formaldehyde. *Toxicologic Pathology*, **33**: 415-424.
- 23. Hu, J., **Zou, F.**, and Wright FA (2005). Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21: 3264-3272.
- 24. **Zou, F**., Fine, J. P., Hu, J. and Lin, D. Y. (2004). An efficient resampling method for assessing genome-wide statistical significance in mapping quantitative trait loci. *Genetics* 168: 2307-2316.
- Fine, J. P., Zou, F., and Yandell, B. S. (2004). Nonparametric estimation of mixture models, with application to quantitative trait loci. *Biostatistics*, 5: 501-513.
- 26. Lin, D., and **Zou, F.** (2004). Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27: 202-214.
- 27. Diao, G., Lin, D., and **Zou, F**. (2004). Mapping quantitative trait loci with censored observations. *Genetics*, 168: 1689-1698.
- 28. Churchill, G. A. *et al.* (2004). The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics*, 36:1133-1137.
- 29. Zou, F., Yandell, B.S., and Fine, J.P. (2003). Rank based statistical methodologies for QTL mapping. *Genetics*, 165: 1599-1605.
- 30. Flaherty, L. *et al.* (2003). The nature and identification of quantitative trait loci: a community's view. *Nature Genetics Review*, 4: 911-916.
- Hester, S. D., Benavides, G. B., Yoon, L., Morgan, L. K., Zou, F., Barry, W., and Wolf, D. C. (2003). Formaldehyde-induced gene expression in F344 rat nasal respiratory epithelium. *Toxicology*, 187:13-24
- 32. Lukens, L., **Zou, F.**, Lydiate, D., Parkin, I., and Osborn, T. (2003). Comparison of a *Brassica Oleracea* genetic map with genome of *Arabidopsis Thallana*. *Genetics*, 164: 359-372.
- 33. Lan, H., Rabaglia, M.E., Stoehr, J.P., Nadler, S.T., Schueler, K.L., Zou, F., Yandell, B.S., and Attie, A.D. (2003). Gene expression profiles of nondiabetic and diabetic obese mice suggest a role of hepatic lipogenic capacity in diabetes susceptibility. *Diabetes*, 52: 688-700.

- 34. **Zou, F.**, and Fine, J.P. (2002). Note on a partial empirical likelihood. *Biometrika*, 89: 958-961.
- 35. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002). On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89: 61-75.
- 36. Dwinell, K.L., Bass, P., **Zou, F.,** and Oaks, J.A. (2002). Small intestinal transactions decrease the occurrence of tapeworm-induced myoelectric patterns in the rat. *Journal of Neurogastroenterology and Motility*, 14: 349-356.
- 37. Zou, F., Yandell, B.S., and Fine, J.P. (2001). Statistical issues in the analysis of quantitative traits in combined crosses. *Genetics*, 158: 1339-1346.

Book Chapter

- 1. **Zou, F.,** Yandell, B.S., Fine, J.P. (2007) Semiparametric and nonparametric gene mapping. In Advances in *Statistical Modeling and Inference: Essays in honor of Kjell A. Doksum.* Ed. by V Nair. World Scientific, pp. 387-404.
- 2. Threadgill, D. W., Hunter, K. W., **Zou, F.,** and Manly, K, F. (2003). Genetic modifiers in "*mouse models of cancer*" (Editor: Eric C. Holland). Wiley.
- 3. **Zou F.** (2009) QTL Mapping in Intercross and Backcross Populations. *Molecular Genetics (Editor:* Keith DiPetrillo). THE HUMANA PRESS INC.

TEACHING ACTIVITIES

Courses

Statistical Methods in Quantitative Genetics (Bios 783), Spring 2003, Spring 2004, Spring 2006, and Spring 2008 instructor

Basic Elements of Probability and Statistical Inference (Bios 550), Fall 2004, instructor

Biostatistics in Bioinformatics and Computational Biology (Gnet 215), Fall 2003, Fall 2004, Fall 2005 and Fall 2007, co-instructor

Statistical Methods in Human Genetics (Bios 781), Fall 2002 and Fall 2003, guest lecturer

Guidance of Post-Doctoral Research

1. Hanwen Huang, 2004~Current

Guidance of Doctoral Research

- 1. Jonathan Gelfond, PhD, Dept. of Bios., joint with Drs. Joe Ibrahim and Mayetri Gupta. "Bayesian Model-based Methods for the Analysis of DNA Microarrays with Survival, Genetic and Sequence Data" (graduated in 2007).
- 2. Yu-Ling Chang, PhD, Dept of Bios., joint with Dr. Fred Wright. "Fast Bayesian Methods for Genetic Mapping with Applications to eQTL Analysis" (graduated in 2008).
- 3. Seunggeun Lee, PhD candidate, Dept. of Bios., joint with Dr. Fred Wright.
- 4. Arpita Gosh, PhD candidate, Dept. of Bios., joint with Dr. Fred Wright.
- 5. Yi Gong, PhD candidate, Dept. of Bios.

Guidance of Master Research

- 1. Tania Robbins, 2004 "Combining Microarrays with QTL Analysis".
- 2. Niki Arya, 2002 "QTL Analysis of Body Weight Gain in Recombinant Inbred Intercross Mice".

Service on Doctoral Committee

- 1. Tsui-Shan (Eva) Lu, PhD, Department of Biostatistics
- 2. Chaeryon Kang, PhD, Department of Biostatistics
- 3. Shiliang Wang, PhD candidate, Department of Cell &
- 4. Rong Jiang, PhD candidate, Department of Environment Sciences & Engineer
- 5. Xiang Zhang, , PhD candidate, Department of Computer Science
- 6. Chevonne Eversley, PhD candidate, Department of Genetics
- 7. Guoqing Diao, PhD, Department of Biostatistics
- 8. Andrew Sterrett, PhD, Department of Biostatistics
- 9. Chaehyung Ahn, PhD, Department of Biostatistics
- 10. Jianhua Hu, PhD, Department of Biostatistics
- 11. Szu-Yun Leu, PhD, Department of Biostatistics
- 12. Kwanhye Jung, PhD Candidate, Department of Environmental Science and Engineering

Others

1. Evita Hollis (minority female student), 2002, the Summer Pre-Graduate Research Experience Program (SPGRE).

CONTRACTS & GRANTS

1. 1 R01 GM074175-01 (PI: **Zou**)

Ongoing Research Support

4/1/2006-3/31/2010

Natl Inst Gen Medical Sciences "Robust Methods for Complex Trait Association Mapping"

The objectives of this research are to address some statistical issues related to association mapping (or disequilibrium mapping) for complex traits.

2. Zou05P0 (PI: **Zou**) 12/1/2005-11/30/06

Cystic Fibrosis Foundation "Robust Methods for Complex Trait Association Mapping"

The objectives of this research are to address some statistical issues related to association mapping (or disequilibrium mapping) for complex traits.

3. 1 R03 MH070504-01 (PI: Zou)

4/1/2004-3/31/07

National Inst. of Health "**Statistical Analysis of RIX for Complex Traits**" The objectives of this research are the development of simple yet useful statistical methods for complex quantitative trait loci mapping using RIX.

4. 5 R01 DK066368-02 (PI: Knowles) 3/1/2004-2/28/09

Natl Institute of Diabetes & Dig & Kidney Disease "Genetic Modifiers of CF Liver Disease"

This project is designed to identify associations between non-CFTR genes and CFLD, and test the biological effect of selected alleles on hepatic fibrosis in transgenic murine models.

Role: co-investigator

6. 5 R01 CA082659-07 (PI: Lin) 4/1/2004-3/31/08 National Cancer Institute "Statistical Methods in Current Cancer Research"

The broad, long-term objectives of this research are the developments of statistical methods for the analysis of censored failure times and incomplete repeated measures from longitudinal cancer studies.

Role: co-investigator

7. 2 P30 ES10126-05 (PI: Swenberg) 4/1/2005-3/31/10 Natl Inst Envr Health Sciences "UNC-CH Center for Environmental Health & Susceptibility-Facility Core 2-Competing Renewal"

The UNC-CH Center on Environmental Health and Susceptibility brings population science, medical and biomedical researchers together to examine major issues in environmental health resulting from gene-environment interactions that affect an individual's susceptibility to disease.

Role: Biostatistician

8. RD-83272001 (PI: Wright) 10/1/2005-9/30/10 Environmental Protection Agency "Computational Toxicology: Environmental **Bioinformatics Research Center- Project 1"**

The Environmental Bioinformatics Research Center's goal is to enhance and advance the field of Computational Toxicology. The center works to develop analytic and computational methods, to create efficient user-friendly tools, to disseminate the methods to the wider community, and to apply the computational methods to data from molecular toxicology and other studies. Role: co-investigator

Pending grants (PI only)

1. "Nonparametric Bayesian Variable Selection with Applications to Genetics and Genomics". PI: Zou. NIH

SERVICE

Referee

- 1. American Journal of Epidemiology
- 2. Annals of the Institute of Statistical Mathematics
- 3. The Annals of Applied Statistics
- 4. Annals of Statistics

- 5. The Australian and New Zealand Journal of Statistics
- 6. Biometrics
- 7. Bioinformatics
- 8. BMC Genetics
- 9. Canadian Journal of Statistics
- 10. Genetic Epidemiology
- 11. Genetics
- 12. Genetic Selection Evolution
- 13. Computational Statistics and Data Analysis
- 14. Journal of Computational and Graphical Statistics
- 15. Journal of American Statistical Association
- 16. The international Journal of Biostatistics
- 17. Theoretical and Applied Genetics
- 18. Lifetime Data Analysis
- 19. Mammalian Genomics
- 20. Statistics in Medicine
- 21. Scientific Committee Member, 2002 International Conference on Critical Assessment of Microarray Data Analysis
- 22. the Australian and New Zealand Journal of Statistics
- 23. the International Journal of Biostatistics

Service to the University

- 1. Faculty of the UNC-CH Bioinformatics and Computational Biology Training Program.
- 2. Bioinformatics and Computational Biology (BCB) curriculum committee.

Service to the Department of Biostatistics

- 1. Graduate Admissions Committee 2003-present
- 2. Graduate Studies Committee 2001-2006
- 3. Faculty Search Committee 2002, 2003, 2005
- 4. Masters Examinations Committee 2006-present
- 5. Seminar Committee 2008-present

Invited Presentations

- 1. Department of Statistics, Duke University, Nov 2008.
- 2. Departments of Statistics and Biostatistics, University of Wisconsin at Madison 2008.
- 3. Bioinformatics Center, MD Anderson. 2007.
- 4. International Chinese Statistical Association (ICSA) meeting. 2007.
- 5. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007.
- 6. Department of Mathematics and Statistics. Wuhan University, China, 2007.
- 7. Department of Mathematics and Statistics. York University, Canada, 2006.
- 8. Bioinformatics Research Center, NC State University 2003

- 9. WNAR invited section I: Mixture Models and Statistical Genetics, Los Angeles, CA. 2002
- 10. Special invited session at AMS Sectional Meeting, Orlando, FL. 2002
- 11. National Genomic Symposium: The Analysis of Human Biology Genes, Genomes and Molecules, Madison, Wisconsin. 2001
- 12. National Cancer Institute Satellite: Statistical Genetics Section, Madison, Wisconsin. 2001
- 13. Department of Statistics, University of California Berkeley. 2001
- 14. Department of Statistics, Texas A&M University. 2001
- 15. Department of Biostatistics, School of Public Health, University of Washington. 2001
- 16. Department of Statistics, Ohio State University. 2001
- 17. Department of Statistics, Virginia Polytechnic Institute and State University. 2001
- 18. Department of Statistics and Probability, Michigan State University. 2001
- 19. Department of Biostatistics and Medical Informatics, University of Wisconsin Madison. 2001

Other Presentations

- 1. American Society of Human Genetics Meeting,, Nov 2009.
- 2. Complex Trait Consortium, 5th Annual Conference, 2006
- 3. Complex Trait Consortium, 3rd Annual Conference, 2004
- 4. Eastern North American Region, 2007, 2004
- 5. Joint Statistical Meetings, 2001
- 6. Gordon Research Conference on Quantitative Genetics and Genomics, 2001