Fei Zou

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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 2007 ~
Department of Biostatistics, University of North Carolina, Chapel Hill
Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill

Assistant Professor 2001 ~ 2007
Department of Biostatistics, University of North Carolina, Chapel Hill
Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill

Assistant Professor 1993~ 1995
Department of Mathematics, Changsha Railway University, China.

Honors

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

EDITORIAL ACTIVITIES

1. Associate Editor: Genetics

Publications

Peer reviewed

1. **Zou, F**., Huang, H., Lee, S. and Hoeschele, I. (2009). Nonparametric Bayesian variable selection with applications to multiple quantitative trait loci mapping with epistasis and gene-environment interaction. *Genetics* (tentatively accepted)
2. TEAM: Efficient two-Locus epistasis tests in human genome-wide association study, by Zhang, X., Huang, S., **Zou, F.,** and Wang, W. (2010) *Proceedings of the*

18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), accepted

3. Huang, H., Zhou, H., Cheng, F., Hoeschele, I., and **Zou, F.** (2010). Gaussian process based Bayesian semiparametric quantitative trait loci interval mapping. *Biometrics*. 66: 222-232. (.http://www3.interscience.wiley.com/user/accessdenied?ID=122384323&Act=2138&Code=4717&Page=/cgi-bin/fulltext/122384323/PDFSTART)
4. Chang, Y. L, Wright, F. A. and **Zou., F**. (2009) An Approximate Bayesian Approach for Quantitative Trait Loci Estimation. *Computational Statistics and Data Analysis*. In press.
5. **Zou, F**., Huang, H., Ibrahim, J. G. (2009) A Semiparametric Bayesian Approach for Estimating the Gene Expression Distribution. Journal of Biopharmaceutical Statistics. accepted.
6. Sun, W, Ibrahim, J. G., and **Zou, F** (2009) Variable Selection by Bayesian Adaptive Lasso and Iterative Adaptive Lasso, with Application for Genome-wide Multiple Loci Mapping, Genetics, accepted.
7. Liu, F., Dunson, D. and **Zou, F** (2009) High-Dimensional Variable Selection in Meta Analysis for Censored Data. Biometrics, accepted.
8. Lee, S., **Zou, F**. and Wright, F.A. (2009). Convergence and prediction of principal component scores in high dimesional settings. Annals of Statistics, accepted.
9. **Zou, F.,** Lee, S. Knowles, M., and Wright, F.A. (2009). Control of population stratification using correlated SNPs by shrinkage principal components. Human Heredity, accepted.
10. 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.
11. Zhang, X, **Zou, F.** and Wang, W. (2009). FastChi: an efficient algorithm for analyzing gene-gene interactions**.** *Pacific Symposium on Biocomputing*: 528-39.
12. 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.
13. 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. *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, pp. 253-269, 2009. Also to appear in *Journal of Computational Biology (JCB).*
14. **Zou, F.**, Nie, L., Wright, F.A., and Sen, P.K. (2009). A robust QTL mapping procedure. Journal of Statistical Planning and Inference. 139:978-989.

15. 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.
16. 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).*
17. 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.
18. 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.
19. Huang, C., Qin, J. and **Zou, F**. (2007). Empirical likelihood-based inference for genetic mixture models. *The Canadian Journal of Statistics*, 35: 563-574.
20. Gelfond, J., Ibrahim, J. G. and **Zou, F.** (2007). Proximity model for expression trait loci detection. *Biometrics*, 63: **1108–1116.**
21. 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.
22. 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.
23. 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.
24. 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.
25. **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.
26. Hu, J., Wright, F.A. and **Zou, F.** (2006). Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101: 41-50.
27. **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.
28. 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.

29. 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.
30. 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.
31. Hu, J., **Zou, F.**, and Wright FA (2005). Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21: 3264-3272.
32. **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.
33. 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.
34. Lin, D., and **Zou, F.** (2004). Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27: 202-214.
35. Diao, G., Lin, D., and **Zou, F**. (2004). Mapping quantitative trait loci with censored observations. *Genetics*, 168: 1689-1698.
36. Churchill, G. A. *et al*. (2004). The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics*, 36:1133-1137.
37. **Zou, F.**, Yandell, B.S., and Fine, J.P. (2003). Rank based statistical methodologies for QTL mapping. *Genetics*, 165: 1599-1605.
38. Flaherty, L. *et al.* (2003). The nature and identification of quantitative trait loci: a community's view. *Nature Genetics Review*, 4: 911-916.
39. 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
40. 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.
41. 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.
42. **Zou, F.**, and Fine, J.P. (2002). Note on a partial empirical likelihood. *Biometrika*, 89: 958-961.
43. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002). On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89: 61-75.
44. 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.
45. **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 and Book Review

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.
4. **Zou, F. (2010)** JASA book review of "The statistics of gene mapping" by David Siegmund and Benjamin Yakir. Springer 2006.

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, 2004~2010

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, Dept. of Bios., joint with Dr. Fred Wright. (graduated in 2009).
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".*
3. Joe Rigdon

Service on Doctoral Committee

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

Others

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

Contracts & Grants

Ongoing Research Support

1. 1 R01 GM074175-01 (PI: **Zou**) 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. Plant and Animal Genome XVII Conference. San Diego 2009.
2. Statistical Genomics workshop, Institute for Mathematical Sciences. Singapore. 2009.
3. Department of Statistics, Duke University, 2008.
4. Departments of Statistics and Biostatistics, University of Wisconsin at Madison 2008.
5. Bioinformatics Center, MD Anderson. 2007.
6. International Chinese Statistical Association (ICSA) meeting. 2007.
7. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007.
8. Department of Mathematics and Statistics. Wuhan University, China, 2007.
9. Department of Mathematics and Statistics. York University, Canada, 2006.

10. Bioinformatics Research Center, NC State University 2003
11. WNAR invited section I: Mixture Models and Statistical Genetics, Los Angeles, CA. 2002
12. Special invited session at AMS Sectional Meeting, Orlando, FL. 2002
13. National Genomic Symposium: The Analysis of Human Biology - Genes, Genomes and Molecules, Madison, Wisconsin. 2001
14. National Cancer Institute Satellite: Statistical Genetics Section, Madison, Wisconsin. 2001
15. Department of Statistics, University of California – Berkeley. 2001
16. Department of Statistics, Texas A&M University. 2001
17. Department of Biostatistics, School of Public Health, University of Washington. 2001
18. Department of Statistics, Ohio State University. 2001
19. Department of Statistics, Virginia Polytechnic Institute and State University. 2001
20. Department of Statistics and Probability, Michigan State University. 2001
21. Department of Biostatistics and Medical Informatics, University of Wisconsin – Madison. 2001
22. Statistical Genomics workshop, June 1-28, 2009. Institute for Mathematical Sciences.
23. Plant and Animal Genome XVII Conference, 2009.
24. Royal Netherlands Academy of Sciences and Arts (KNAW): Genomics of gene expression. 2010

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