Fei Zou

# 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**

Statistical and Applied Mathematical Sciences Institute (SAMSI) Fellow 2014-2015

Member of NIH study section GVE 2015 ~ current

Professor 2014 ~ present Department of Genetics, University of North Carolina, Chapel Hill

Professor 2012 ~ present Department of Biostatistics, University of North Carolina, Chapel Hill

Professor 2015- 2017 Department of Biostatistics, University of Florida

Associate Professor 2007 ~ 2012 Department of Biostatistics, University of North Carolina, Chapel Hill

Assistant Professor 2001 ~ 2007 Department of Biostatistics, University of North Carolina, Chapel Hill

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

## Honors

## David P. Byar Young Investigator Award (2001), ASA Biometrics Section

## Membership

1. Member of American Statistical Association
2. Member of Institute of Mathematical Statistics
3. Member of American Society of Human Genetics
4. Member of International Chinese Statistical Association
5. Member of Statistical Society of Canada
6. Member of Genetics Society of America

**Publications**

### Book Chapters

1. **Zou, F.** (2009) QTL Mapping in Intercross and Backcross Populations.   
   *Molecular Genetics (Editor:* Keith DiPetrillo). *The human press Inc.* 157-173.
2. **Zou, F.,** Yandell, B.S., and 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.
3. 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, pp. 263-291.

Peer reviewed papers

(\* student first author advised or co-advised)

1. Dong, M., Thennavan, A., Urrutia, E., Li, Y., Perou, C. M., **Zou, F**., & Jiang, Y. (2020). SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. Briefings in Bioinformatics, bbz166, <https://doi.org/10.1093/bib/bbz166>.
2. Kim, Y., Chi, Y. Y., & **Zou, F.** (2020). An efficient integrative resampling method for gene–trait association analysis. *Genetic Epidemiology*, *44*(2), 197-207.
3. Li, D., Avinash, K., Darville, T., **Zou, F.,** & Xiaojing, Z. (2020). Semi-CAM: A semi-supervised deconvolution method for bulk transcriptomic data with partial marker gene information. *Scientific Reports (Nature Publisher Group)*, *10*(1).
4. Yang, G. S., Mi, X., Jackson-Cook, C. K., Starkweather, A. R., Lynch Kelly, D., Archer, K. J., ..., **Zou, F.** & Lyon, D. E. (2020). Differential DNA methylation following chemotherapy for breast cancer is associated with lack of memory improvement at one year. *Epigenetics*, *15*(5), 499-510.
5. Tozay, S., Fischer, W. A., Wohl, D. A., Kilpatrick, K., **Zou, F**., Reeves, E., ... & Grant, D. (2019). Long-Term Complications of Ebola Virus Disease: Prevalence and Predictors of Major Symptoms and the Role of Inflammation. *Clinical Infectious Diseases*.
6. Zhang, T., Yang, F., Tang, W., Huang, W., Wang, Y., Alexander, M., ...**Zou, F.,…** & Yang, L. (2019). P018 Pay-it-forward gonorrhea and chlamydia testing among chinese men who have sex with men: a cluster randomized controlled trial.
7. Zhao Y, Zhu H, Lu Z, Knickmeyer RC, & **Zou F.** (2019) [Structured Genome-Wide Association Studies with Bayesian Hierarchical Variable Selection.](https://www.ncbi.nlm.nih.gov/pubmed/31010934) Genetics. Accepted
8. Jha SC, Xia K, Ahn M, Girault JB, Li G, Wang L, Shen D, **Zou F**, Zhu H, Styner M, Gilmore JH, Knickmeyer RC. (2019) [Environmental Influences on Infant Cortical Thickness and Surface Area.](https://www.ncbi.nlm.nih.gov/pubmed/29420697) Cereb Cortex. 29:1139-1149.
9. Zimmerman H, Yin Z, **Zou F,** Everett ET. (2019) [Interfrontal Bone Among Inbred Strains of Mice and QTL Mapping.](https://www.ncbi.nlm.nih.gov/pubmed/31001328)  10:291.
10. Mi X, **Zou F**, Zhu R. (2019) [Bagging and deep learning in optimal individualized treatment rules.](https://www.ncbi.nlm.nih.gov/pubmed/30365175) Biometrics. 75(2): 674-684.
11. Jha SC, Xia K, Schmitt JE, Ahn M, Girault JB, Murphy VA, Li G, Wang L, Shen D, **Zou F,** Zhu H, Styner M, Knickmeyer RC, Gilmore JH. (2018) [Genetic influences on neonatal cortical thickness and surface area.](https://www.ncbi.nlm.nih.gov/pubmed/30144223)

Hum Brain Mapp. 39:4998-5013.

1. Shah C, Bishnoi R, Wang Y, **Zou F**, Bejjanki H, Master S, Moreb JS. (2018) [Efficacy and safety of carfilzomib in relapsed and/or refractory multiple myeloma: systematic review and meta-analysis of 14 trials.](https://www.ncbi.nlm.nih.gov/pubmed/29805768) Oncotarget. 9(34):23704-23717.
2. Shah C, Bishnoi R, Jain A, Bejjanki H, Xiong S, Wang Y, **Zou F,** Moreb JS. (2018) [Cardiotoxicity associated with carfilzomib: systematic review and meta-analysis.](https://www.ncbi.nlm.nih.gov/pubmed/29465266) Leuk Lymphoma. 59:2557-2569.
3. Liu Y, Xiong S, Sun W, **Zou F**. (2018) J[oint Analysis of Strain and Parent-of-Origin Effects for Recombinant Inbred Intercrosses Generated from Multiparent Populations with the Collaborative Cross as an Example.](https://www.ncbi.nlm.nih.gov/pubmed/29255115) G3 8:599-605.
4. Farhadfar, N., Stan, M. N., Shah, P., Sonawane, V., Hefazi, M. T., Murthy, H. S., ... **Zou, F.,** Xiong S., & Hashmi, S. K. (2018). Thyroid dysfunction in adult hematopoietic cell transplant survivors: risks and outcomes. *Bone marrow transplantation*, *53*(8), 977-982.
5. Yang D, **Zou F**, Xiong S, Forde JJ, Wang Y, Draganov PV. (2018) [Endoscopic submucosal dissection for early Barrett's neoplasia: a meta-analysis.](https://www.ncbi.nlm.nih.gov/pubmed/28993137) Gastrointest Endosc. 87:1383-1393.
6. Polineni, D., Dang, H., Jones, L., Gallins, P., Pace, R., Stonebraker, J., Commander, L., Krenicky, J., Zhou, Y., Corvol, H., Cutting, G., Drumm, M., Strug, L., Boyle, M., Durie, P., Chmiel, J., **Zou, F.**, Wright, F., O'Neal, W., Knowles, M. (2018) Airway mucosal host defense is key to genomic regulation of cystic fibrosis lung disease severity. Am J Respir Crit Care Med. 197:79-93.
7. Moreb, J. S., Byrne, M., Shugarman,I., **Zou, F.,** Xiong, S., May, W. S., Norkin, M., Hiemenz, J., Brown, R., Cogle, C., . Wingard, J. R., Hsu, J. W. (2018) Poor peripheral blood stem cell mobilization affects long-term outcomes in multiple myeloma patients undergoing autologous stem cell transplantation. Journal of Clinical Apheresis. 33: 29-37.
8. Bishnoi R, Bajwa R, Franke AJ, Skelton WP 4th, Wang Y, Patel NM, Slayton WB, **Zou F**, Dang NH. (2017) [Post-transplant lymphoproliferative disorder (PTLD): single institutional experience of 141 patients.](https://www.ncbi.nlm.nih.gov/pubmed/29021921) Exp Hematol Oncol. 6:26.
9. Liao, M.; Zhou, J.; Wang, F.; Ali, Y.; Chan, K.; **Zou, F.;** Offermanns, S.; Jiang, Z. and Jiang, Z. (2017) An X-linked Myh11-CreER T2 mouse line resulting from Y to X chromosome-translocation of the Cre allele :  Genesis. [55.](https://www.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmed&retmode=ref&cmd=prlinks&id=28845554" \t "pmc_ext)
10. Zou, B.; Cai, J.; Gary, K., ; Zhou, H., and **Zou, F.** (2017) A Model-Based Conditional Power Assessment for Decision Making in Randomized Controlled Trial Studies. Statistics in Medicine. 36:4765-4776.
11. Xia, K., Zhang, J., Ahn, M., Jha, S., Crowley, J.J., Szatkiewicz, J., Li, T., **Zou**, **F.,** Zhu, H., Hibar, D., Thompson, P., ENIGMA Consortium, Sullivan, P.F., Styner, M., Gilmore, J.H., and Knickmeyer. R.C. (2017), Genome-Wide Association Analysis Identifies Common Variants Influencing Infants Brain Volumes. *Accepted to Translational Psychiatry*. 7:e1188. PMID: 28763065
12. Kang, G., Bi, W., Zhang, H., Pounds, S., Cheng, C., Shete, S., **Zou, F.,** Zhao, Y., Zhang, Y., Zhang, J., and Yue, W. (2017) [A Robust and Powerful Set-Valued Approach to Rare Variant Association Analyses of Secondary Traits in Case-Control Sequencing Studies.](https://www.pubfacts.com/detail/28040743/A-Robust-and-Powerful-Set-Valued-Approach-to-Rare-Variant-Association-Analyses-of-Secondary-Traits-i) Genetics 30:1049-1062.
13. Lee, S., Sun, W., Wright, F.A., **Zou, F.** (2017) An improved and explicit surrogate variable analysis procedure by coefficient adjustment, Biometrika, 104, 303-316.
14. Chaudhry, N.A., Riverso, M., Grajo, J.R., Moser, P.P., **Zou, F.,** Homsi, M., Punglia, D.R., and Zimmermann, E.M. (2017) [A Fixed Stricture on Routine Cross-sectional Imaging Predicts Disease-Related Complications and Adverse Outcomes in Patients with Crohn's Disease.](https://www.pubfacts.com/detail/28267043/A-Fixed-Stricture-on-Routine-Cross-sectional-Imaging-Predicts-Disease-Related-Complications-and-Adve) Inflamm Bowel Dis 23:641-649
15. Mazul, A., Siega-Riz, A. M., Weinberg, C. R., Engel, S. M.,  **Zou, F.,** Carrier, K. S., Basta, P. V., Vaksman, Z., Maris, J.M., Diskin, S. J., Maxen, C., A., and Olshan, A. F. (2016) A family-based study of gene variants and maternal folate and choline in neuroblastoma: a report from the Children’s Oncology Group. Cancer Causes and Control, 27: 1209–1218.
16. Zou, B., **Zou, F.,** Shuster, J.J. Tighe, P. J., Koch, G.G., and Zhou, H., (2016) On variance estimate for covariate adjustment by propensity score analysis. Statistics in Medicine 35: 3537-3548.
17. Schmit, J., Meyer, L.E., Duff, J.M., Dai, Y., **Zou, F.,** and Close, J. L. (2016) [Perspectives on death and dying: a study of resident comfort with End-of-life care.](https://www.pubfacts.com/detail/27871287/Perspectives-on-death-and-dying-a-study-of-resident-comfort-with-End-of-life-care) BMC Med Educ 21: 297
18. Knickmeyer, R.C., Xia, K., Lu, Z., Ahn, M., Jha, S.C., **Zou, F.,** Zhu, H., Styner, M., Gilmore, J. H. (2016) [Impact of Demographic and Obstetric Factors on Infant Brain Volumes: A Population Neuroscience Study.](https://www.pubfacts.com/detail/27797836/Impact-of-Demographic-and-Obstetric-Factors-on-Infant-Brain-Volumes-A-Population-Neuroscience-Study) Cereb Cortex: 1-10.
19. Lu, Z., Zhu, H., Knickmeyer, R. C., Sullivan, P. F., Williams S. N. and **Zou, F.** (2015) Multiple SNP-sets Analysis for Genome-wide Association Studies through Bayesian Latent Variable Selection. *Genetic Epidemiology*. 39: 664-677.
20. Yin, Z.\*, Xia, K., Chung, W., Sullivan, F.P., and **Zou, F.** (2015) Fast eQTL Analysis for Twin Studies. *Genetic Epidemiology*. 39: 357–365.
21. Sun, W., Liu, Y., Crowley, J.J., Chen, T.H., Zhou, H., Chu, H.T., Huang, S., Kuan, P.F., Li, Y., Miller, D., Shaw, G., Wu, Y.C., Zhabotynsky, V., McMillan, L., **Zou, F.,** Sullivan, P.F., Pardo-Manuel de Villena, F. (2015) [IsoDOT Detects Differential RNA-isoform Usage with respect to a Categorical or Continuous Covariate with High Sensitivity and Specificity](http://arxiv.org/abs/1402.0136). *JASA* 110: 975-986.
22. Jansen, R., Penninx, B., Madar, V., Xia, K., Milaneschi, Y., Hottenga, J.J., Hammerschlag, A.R., Beekman, A., van der Wee, N., Smit, J. H., Brooks, A.I., Tischfield, J., Posthuma, D., Schoevers, R., van Grootheest, G., Willemsen, G., de Geus, E. J., Boomsma, D.I., Wright, F.A., **Zou, F.,** Sun, W., Sullivan, P. F. (2015) Gene expression in major depressive disorder. Molecular Psychiatry,  *[10.1038/mp.2015.94](http://dx.doi.org/10.1038/mp.2015.94).*
23. Crowley, J.J., Zhabotynsky, V., Sun, W., Huang, S., Pakatci, I. K., Kim, Y., Wang, J. R., Morgan, A.P., Calaway, J. D., Aylor, D. L., Yun, Z., Bell, T. A., Buus, R. J., Calaway, M. E., Didion, J. P., Gooch, T. J., Hansen, S. D., Robinson, N. N., Shaw, G. D., Spence, J. S., Quackenbush, C. R., Barrick, C. J., Nonneman, R. J., Xie, Y., Valdar, W., Lenarcic, A. B., Wang, W., Welsh, C.E., Fu, C.P., Zhang, Z., Holt, J., Guo, Z., Threadgill, D. W., Tarantino, L. M., Miller, D. R., **Zou, F**.\*, McMillan, L.\*, Sullivan, P. F.\*, Pardo-Manuel de Villena, F.\* (2015) Pervasive Allelic Imbalance Revealed By Allele-Specific Gene Expression In Highly Divergent Mouse Crosses. *Nature Genetics*. 47:353-60 (\*: co-senior authors.)
24. Wiltshire, T., Ervin, R.B., Duan, H., Bogue, M.A., Zamboni, W.C., Cook, S., Chung, W., **Zou, F.,** and Tarantino, L.M . (2015) Initial locomotor sensitivity to cocaine varies widely among inbred mouse strains. Genes Brain Behav. 14:271-80.
25. Xia, K., Yu, Y., Ahn, M., Zhu, H., **Zou, F.,** Gilmore, J., and Knickmeyer, R. C. (2014) Environmental and genetic contributors to salivary testosterone levels in infants. *Frontiers in Endocrinology*. 5: 187.
26. Ghosh, A. \*, Nobel, A. B., Zou, F. and Wright, F. A. (2014) Variable Selection and Shrinkage via a Conditional Likelihood-based Penalty. *Journal of the Indian society of agricultural statistics.* 68: 227-236.
27. Yu, J., Zhou, H., Liu, X., **Zou, F.**,and Willke, R. J. (2014) Adjusting Complex Heterogeneity in Treatment Assignment in Observational Studies. *International Journal of Statistics in Medical Research,*3*:* 203-214.
28. Wright, F.A., Sullivan, P., Brooks, A., **Zou, F.,** Sun, W., Xia,K., Madar, V., Abdellaoui, A., Batista, S., Butler, C., Chen, G., Chen, T., Chung W., et al. (2014), Heritability and Genomics of Gene Expression In Peripheral Blood. *Nature Genetics*, 46: 430-437.
29. [**Zou, F**](http://www.ncbi.nlm.nih.gov/pubmed?term=Zou%20F%5BAuthor%5D&cauthor=true&cauthor_uid=24561482)**.**, [Sun, W](http://www.ncbi.nlm.nih.gov/pubmed?term=Sun%20W%5BAuthor%5D&cauthor=true&cauthor_uid=24561482)., [Crowley, J.J](http://www.ncbi.nlm.nih.gov/pubmed?term=Crowley%20JJ%5BAuthor%5D&cauthor=true&cauthor_uid=24561482)., [Zhabotynsky, V](http://www.ncbi.nlm.nih.gov/pubmed?term=Zhabotynsky%20V%5BAuthor%5D&cauthor=true&cauthor_uid=24561482)., [Sullivan, P.F](http://www.ncbi.nlm.nih.gov/pubmed?term=Sullivan%20PF%5BAuthor%5D&cauthor=true&cauthor_uid=24561482)., [Pardo-Manuel de Villena, F.F](http://www.ncbi.nlm.nih.gov/pubmed?term=Pardo-Manuel%20de%20Villena%20FF%5BAuthor%5D&cauthor=true&cauthor_uid=24561482). (2014) A Novel Statistical Approach for Jointly Analyzing RNA-seq Data from F1 Reciprocal Crosses and Inbred Lines. Genetics, 197:389-99..
30. Lee. S.\*, **Zou, F.**, and Wright, F.A.(2014) Convergence of sample eigenvalues, eigenvectors, and principal component scores for ultra-high dimensional data. *Biometrika*, 2014 101: 484-490.
31. Chung, W.\*, and **Zou, F.** (2014) Mixed effects models for GAW18 longitudinal blood pressure data. *BMC proceedings.* 8: S87.
32. Zhou, Y.H., Mayhew, G., Sun, Z., Xu, X., **Zou, F.** and Wright, F.A. (2013) [Space–time clustering and the permutation moments of quadratic forms](http://scholar.google.com/citations?view_op=view_citation&hl=en&user=fJ_WwMkAAAAJ&citation_for_view=fJ_WwMkAAAAJ:Zph67rFs4hoC)  
    Stat. 2: 292-302.
33. Ghosh, Arpita\*, **Zou, F.,** and Wright*,* F.A. (2013) Unified Analysis of Secondary Traits in Case-Control Association Studies. *JASA*. 108: 566-576.
34. Kang, C. Zhu, H., Wright, F.A., **Zou, F**., Kosorok MR (2012) The interactive decision committee for chemical toxicity analysis. Journal of Statistical Research, *46: 157-186.*
35. Gong, Y.\*, and **Zou, F**. (2012) Varying coefficient models for mapping quantitative trait loci using recombinant inbred intercrosses. *Genetics,* 190:475-486.
36. Xia, K, Shabalin, A.A., Huang, S., Madar, V., Zhou, Y.H., Wang, W., **Zou, F.,** Sun,W., Sullivan, P.F., and Wright, F.A. (2012) seeQTL: A searchable database for human eQTLs. *Bioinformatics*, 28: 451-452.
37. Sun, W., Zhabotynsky, V., **Zou, F.**, Wright, F.A., Crowley, J.J., Yun, Z., Buus, R., Miller, D., Wang, J., McMillan, L., Pardo-Manuel de Villena, F., and Sullivan P.F. (2012) Transcriptome atlases of mouse brain reveals differential expression across brain regions and genetic backgrounds. *G3*, 2:203-211.
38. Collaborative Cross Consortium (2012) The genome architecture of the Collaborative Cross mouse genetics reference population. *Genetics,* 190:389-402.
39. Li, W., Sun, L., Corey, M., **Zou, F.,** Lee, S., Cojocaru, A., Taylor, C., Blackman, S., Stephenson, A., Sandford, A., Dorfman, R., Drumm, M., Cutting, G., Knowles, M., Durie, P., Wright, F.A., and Strug, L. (2011) Under[standing the population structure of North American patients with cystic fibrosis.](http://www.ncbi.nlm.nih.gov/pubmed/20681990) *Clin Genet.,* 79:136-46. PMC2995003.
40. Lee, S.\*, Wright, F.A., and **Zou, F.** (2011) [Control of population stratification by correlation-selected principal components](http://www.bios.unc.edu/~slee/Paper/EigenCorr_Biometrics.pdf). *Biometrics,* 67: 967-974.
41. Liu, F., Dunson, D., and **Zou, F.** (2011) High-dimensional variable selection in meta analysis for censored data*. Biometrics,* 67:504–512.
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43. Everett, E.T., Yin, Z., Yan, D., and **Zou, F.** (2011) Fine mapping of dental fluorosis quantitative trait loci in mice. *European Journal of Oral Sciences*, 119(S1):8-12.
44. Zhang, X., Huang, S., **Zou, F**., and Wang, W. (2011) Tools for efficient epistasis detection in genome-wide association study. *Source Code for Biology and Medicine,* 6:1-3.
45. Yuan, Z., **Zou, F.,** and Liu, Y. (2011) Bayesian multiple quantitative trait loci mapping for recombinant inbred intercrosses*. Genetics,* 188:189-195.
46. Wright, F., Strug, L.J., Doshi, V., Commander, C., Blackman, S.L., Sun, S., Berthiaume, Y., Cojocaru, A., Collaco, M., Corey, M., Cutler, D., Dorfman, R., Goddard, K., Green, D., Kent, J., Lange, E., Lee, S., Li, W., Luo, J., Mayhew, G., Naughton, K., Pace,R., Paré, P., Rommens, J., Sandford, A., Stonebraker, J., Sun, W., Taylor, C, Vanscoy, L., **Zou, F.,** Blangero, J., Zielenski, J., O’Neal, W., Drumm, M., Durie, P., Knowles, M., and Cutting, G.R. (2011) Genome-wide association and linkage identify modifier loci of lung disease severity in cystic fibrosis at 11p13 and 20q13.2. *Nature Genetics,* 43:539–546.
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48. **Liu,**Q., **Zhang,** H., **Smeester,L., Zou, F., Kesic,** M., **Jaspers, I., Pi,** J. and **Fry, R.C. (2010)** The NRF2-mediated oxidative stress response pathway is associated with tumor cell resistance to arsenic trioxide across the NCI-60 panel. BMC Medical Genomics,**3:**37 (total 12 pages). PMC2939609
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51. 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.** PMC2875332
52. Chang, Y. L\*, Wright, F. A., and **Zou, F**. (2010) An approximate Bayesian approach for quantitative trait loci estimation. *Computational Statistics and Data Analysis*, 54:565-574.
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55. Lee, S\*., **Zou, F**., and Wright, F.A. (2010) Convergence and prediction of principal component scores in high dimensional settings. *Annals of Statistics*, 38: 3605-36.
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67. 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.
68. 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.
69. 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*, 23:2581-2588.
70. 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.
71. **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.
72. Hu, J., Wright, F.A., and **Zou, F.** (2006) Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101:41-50*.*
73. **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.
74. 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.
75. 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.
76. 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.
77. Hu, J., **Zou, F.**, and Wright, F.A.(2005) Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21:3264-3272.
78. **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.
79. 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.
80. Lin, D., and **Zou, F.** (2004) Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27:202-214.
81. Diao, G., Lin, D., and **Zou, F**. (2004) Mapping quantitative trait loci with censored observations. *Genetics,* 168:1689-1698.
82. Churchill, G. A. *et al*. (2004). The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics*, 36:1133-1137.
83. **Zou, F.**, Yandell, B.S., and Fine, J.P. (2003) Rank based statistical methodologies for QTL mapping. *Genetics,* 165:1599-1605.
84. Flaherty, L. *et al.* (2003). The nature and identification of quantitative trait loci: a community's view. *Nature Genetics Review*, 4:911-916.
85. 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
86. 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.
87. 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.
88. **Zou, F.**, and Fine, J.P. (2002) Note on a partial empirical likelihood. *Biometrika,* 89:958-961.
89. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002) On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89:61-75.
90. 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.
91. **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 Reviews

1. **Zou, F.** (2010) Review of “The statistics of gene mapping” by David Siegmund and Benjamin Yakir. *JASA,* 105: 1283.

Invited Presentations (2006-present)

1. Department of Statistics, University of Florida, 2015
2. NC-Tracs, University of North Carolina at Chapel Hill, 2015
3. IMS-China, Yunnan, China, 2015
4. Department of Biostatistics, [University of Pennsylvania](http://www.upenn.edu/), 2014
5. **Joint Applied Statistics Symposium of International Chinese Statistical Association & Korean International Statistical Society,** Portland, Oregon, 2014
6. Science at the Edge seminar, Michigan state university, 2013
7. Department of Biostatistics, University of Florida, 2013
8. Department of Genetics, University of North Carolina at Chapel Hill, 2013
9. Triangle Statistical Genetics Conference, RTP, 2012
10. The 34th Finnish Summer School on Probability Theory and Statistics, Finland, 2012
11. Second Joint Biostatistics Symposium, Beijing, China 2012
12. Centers of Excellent in Genomic Science (CEGS) 9th Annual meeting, 2011
13. Department of Mathematics and Statistics. Wuhan University, China, 2011
14. Department of Statistics, George Mason University, 2011
15. IMS China, Xi’an, China, 2011
16. Statistical Society of Canada meeting. Canada, 2011
17. ICSA 2011 APPLIED STATISTICS SYMPOSIUM, New York, 2011
18. Royal Netherlands Academy of Sciences and Arts (KNAW): Genomics of gene expression, 2010
19. Department of Biostatistics, Yale University, 2010
20. Department of Mathematics and Statistics, Bowling Green State University, 2010
21. Joint statistical meetings, Vancouver, Canada, 2010
22. Plant and Animal Genome XVII Conference. San Diego, CA, 2009
23. Statistical Genomics workshop, Institute for Mathematical Sciences. Singapore, 2009
24. Department of Statistics, Duke University, 2008
25. Departments of Statistics and Biostatistics, University of Wisconsin at Madison, 2008
26. Department of Mathematics and Statistics. Wuhan University, China, 2007
27. Bioinformatics Center, MD Anderson, 2007
28. International Chinese Statistical Association (ICSA) meeting, 2007
29. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007
30. Department of Mathematics and Statistics. York University, Canada, 2006

Teaching Activities

###### Courses

Statistical Methods in Quantitative Genetics (Bios 783), Spring 2003, Spring 2004, Spring 2006, Spring 2008 and Spring 2010 Instructor

Intermediate Linear Models (Bios663) Spring 2009, Spring 2011 and Spring 2013 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, Spring 2010. Co-instructor

Statistical Methods in Human Genetics (Bios 781), Fall 2012, and Fall 2014, Instructor

###### Guidance of Post-Doctoral Research

###### Hanwen Huang, 2004~2010

Current position: Assistant Professor, University of Georgia

Yize Zhao 2014-2016 (Joint with Dr. Hongtu Zhao)

Current position: Assistant Professor, *Cornell University*

###### Guidance of Doctoral Research

1. Li Dong, PhD candidate, Dept of Bios. (joint with Xiaojing Zheng)
2. Vasyl Zhabotynsky, DrPD candidate, Dept of Bios. (joint with Wei Sun)
3. Laura Zhou, PhD candidate, Dept of Bios. (joint with Wei Sun)
4. Meichen Dong, PhD candidate, Dept of Bios. (joint with Yuchao Jiang)
5. Xinlei Mi, 2018 PhD, Dept of Bios., University of Florida.
6. Yeonil Kim, 2019 Dept of Bios., University of Florida. (joint with Chi,Yueh-Yun)
7. James Xenakis, 2018 PhD, Dept of Bios
8. Zhaoyu Yin, 2014 PhD, Dept of Bios. *“Statistical Analyses of High Throughput Genetics and Genomics Data”*

Current position: Biostatistician, [Bristol-Myers Squibb](http://www.thelabrat.com/jobs/companies/BristolMyersSquibb.shtml).

1. Wonil Chung, 2013 PhD, Dept. of Bios. *“Bayesian Multiple Quantitative Trait Loci (QTL) Mapping For Longitudinal Data”*

Current position: Postdoc, Harvard University

1. Gregory Mayhew, 2013, DrPH, Dept of Bios. joint with Fred Wright. “*Genotype-Phenotype Similarity Testing and Methods for Integrating Multiple Data Sources in Genetic Association*”

Current position: Postdoc, Duke University

1. Yi Gong, 2011 PhD, Dept. of Bios. “*Variable Selection in Varying Coefficient Models for Mapping Quantitative Trait Loci*”.

Current position: Mathematical Statistician, SAS

1. Seunggeun Lee, 2010 PhD, Dept. of Bios., joint with Dr. Fred Wright “*Principal Component Analysis in High Dimensional Data: Application for Genomewide Association Studies*”.

Current position: Assistant Professor, University of Michigan.

1. Arpita Ghosh, 2009 PhD, Dept. of Bios., joint with Dr. Fred Wright. *“Conditional Likelihood for Risk Estimation in Genome Scans and Coefficient Shrinkage”*.

Current position: Postdoctoral Fellow, National cancer institute

1. Yu-Ling Chang, 2008 PhD, Dept of Bios., joint with Dr. Fred Wright. “*Fast Bayesian Methods for Genetic Mapping with Applications to eQTL Analysis*”. Current position: Mathematical Statistician at Division of Oncology, CDER, FDA
2. Jonathan Gelfond, 2007 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*”

Current position: Assistant Professor, University of Texas Health Science Center at San Antonio, TX

###### Guidance of Master’s Research

1. Shiliang Wang 2011 “*QTL Underlying Voluntary Exercise in Mice*”.

###### Joe Rigdon 2010 “*The Hamming Distance as a Measure of Genetic Heterogeneity*”.

###### Tania Robbins, 2004 “*Combining Microarrays with QTL Analysis***”.**

###### Niki Arya, 2002 “QTL Analysis of Body Weight Gain in Recombinant Inbred Intercross Mice”.

###### Service on Doctoral Committee

1. Bocha Jia, PhD candidate, Dept of Bios.
2. Qianyun Li, PhD candidate, Dept of Bios
3. Suwan Xu, PhD 2017, Dept of Bios
4. Sinjini Sikar, PhD candidate, Dept of Bios
5. Choi, Wan Suk, 2017 PhD, Dept of Bios.
6. Xu,Yunan, Phd candidate, Dept of epidemiology
7. Chen-Ping Fu, PhD candidate, Department of Computer Science
8. Angela Yanyi. Liu, PhD candidate, Department of Epidemiology
9. Alison Wise DrPH candidate, Department of Biostatistics
10. Ting-huei Chen, PhD 2014, Department of Biostatistics
11. Ja-an Lin, PhD, 2013 Department of Biostatistics
12. David Kessler, 2013 Department of Biostatistics
13. Zhaowei Hua, PhD, 2011 Department of Biostatistics
14. Chaeryon Kang, PhD, 2011 Department of Biostatistics
15. Yihui Zhou, PhD, 2011 Department of Biostatistics
16. Shiliang Wang, PhD, 2011 Department of Cell & Molecular Physiology
17. Xiang Zhang, PhD, 2011 Department of Computer Science
18. Rong Jiang, PhD, 2010 Department of Environment Sciences & Engineer
19. Vonn Walter, PhD, 2010 Department of Biostatistics
20. John Schwarz, PhD, 2010 Department of Biostatistic

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1. Lindsey Ho, DrPh, 2010 Department of Biostatistics
2. Tsui-Shan (Eva) Lu, PhD, 2009 Department of Biostatistics
3. Chevonne Eversley, PhD, 2009 Department of Genetics
4. Emily Kistner, PhD, 2005 Department of Biostatistics
5. Guoqing Diao, PhD, 2005 Department of Biostatistics
6. Andrew Sterrett, PhD, 2005 Department of Biostatistics
7. Chaehyung Ahn, PhD, 2005 Department of Biostatistics
8. Szu–Yun Leu, PhD, 2005 Department of Biostatistics
9. Jianhua Hu, PhD, 2003 Department of Biostatistics

Others

1. Alex Vasiljev (BSURE) 2010 joint with Fred Wright
2. Qian Liu, 2010 MS, Department of Environmental Sciences and Engineering, UNC

###### Evita Hollis, 2002, the Summer Pre-Graduate Research Experience Program (SPGRE).

**Contracts & Grants**

Principal Investigator on Grants

1. R01 GM074175-05 “Robust Methods for Complex Trait Mapping with Collaborative Cross”. Natl Inst Gen Medical Sciences (2011-2016)

2. R01 GM074175-01 “Robust Methods for Complex Trait Association Mapping”. Natl Inst Gen Medical Sciences (2006-2011)

3. R03 MH070504 “Statistical Analysis of RIX for Complex Traits” National Inst. of Health (2004-2007)

4. ZOU05P0 “Robust Methods for Complex Trait Association Mapping” Cystic Fibrosis Foundation (2005-2006)

Investigator on Grants

1. 5 P30 ES010126-18 (PI: Troester) **UNC-CH Center for Environmental Health & Susceptibility - Biostatistics & Bioinformatics Facility Core.** NIEHS (2016-2021). Role: Co-Investigator.
2. 5 P30 AI050410-21 (PI: Swanstrom) **The University of North Carolina Center for AIDS Research: Core F – Biostatistics.** National Institute of Allergy and Infectious Diseases (2016-2021). Role: Co-Investigator.
3. 5 R01 AI123535-03 (PI: Wohl) Clinical Sequelae and Urogenital Viral Dynamics in Survivors of Ebola Virus Disease. National Institute of Allergy and Infectious Diseases (2017-2022). Role: Co-Investigator.
4. 5 R01 FD006030-03 (PI: Ataga) The Association of Biomarkers of Endothelial Function with Prospective Changes in Kidney Function in Sickle Cell Anemia. FDA (2017-2022). Role: Co-Investigator.
5. 5 R01 HD092374-02 (PI: O'Shea) Placental Epigenome and Brain Dysfunction after Preterm Birth. E. K. Shriver National Institute of Child Health and Human Development (2017-2022) Role: Co-Investigator.
6. 5 UL1 TR002489-02 (PI: Buse) North Carolina Translational and Clinical Science Institute (NC TraCS) - Biostatistics, Epidemiology, and Research Design (BERD). National Center for Advancing Translational Sciences (2018-2023). Role: Co-Investigator.
7. 1 R01 MH116527-01 (PI: Zhang) Analysis of Big Data Squared in Biomedical Studies. NIH (2018-2023). Role: Co-Investigator.
8. 2 R01 GM105785-06 (PI: Sun) Statistical Methods for RNA-seq Data Analysis. NIH (2019-2022). Role: Contract PI.
9. 1 R01 ES029925-01 (PI: Pardo-Manuel de Villena) Genetic Underpinning of Diabetes Associated with Arsenic Exposure. NIEHS (2019-2024). Role: Co-Investigator.
10. R01-MH092335 (PI: Santelli) “Genome-wide Identification of Variants Affecting Early Human Brain Development” NIH (2011-2016) Role: Co-Investigator.
11. R01 GM105785-01A1 (PI: Sun) “Statistical Methods for RNA-seq Data Analysis” NIH (2014-2018) Role: Co-Investigator.
12. R01-DA023690(PI: Tarantino) “Organismal and Genetic Networks in Drug Reward and Reinforcement” NIH (2009-2018) Role: Co-Investigator.
13. R21 MH097173-02 (PI: Sullivan) “Biomarkers of Olanzapine-induced Weight Gain in Mice” NIH (2012-2015) Role: Co-Investigator.
14. R01-ES019315 (PI: Fry) “In Utero Exposure to Arsenic, Links to Epigenetic Alterations and Disease” NIH (2010-2015) Role: Co-Investigator.
15. P50-HG006582 (PI: Pardo-Manuel de Villena) “An Interdisciplinary Program for Systems Genomics of Complex Behaviors” NIH (2011-2014) Role: Co-investigator.
16. R01-DE018104 (PI: Everett) “Genetic Determinants of Physiological Responses to Fluoride in Bone” NIH (2008-2013) Role: Co-Investigator.
17. R01-CA132887 (PI: Olshan) “Genetic Susceptibility Factors in the Etiology of Neuroblastoma” NIH (2008-2013). Role: Co-Investigator.
18. R01-HL095396 (PI: Knowles) “Molecular Phenotypes for Cystic Fibrosis Lung Disease” NIH (2008-2012) Role: Investigator.
19. GIL (PI: Lin) Gillings Innovation Laboratory (2009-2012) Role: Investigator.
20. RC2-MH089951(PI: Sullivan) “Integration of Genomics & Transcriptomics in Normal Twins & Major Depression” NIH (2009-2011) Role: Investigator.
21. R01-DK066368 (PI: Knowles) “Genetic Modifiers of CF Liver Disease” NIH (2004-2009) Role: Co-Investigator.
22. R01-CA082659 (PI: Lin) “Statistical Methods in Current Cancer Research” NIH (2004-2008) Role: Co-Investigator.
23. R01-CA082659 (PI: Lin) “Statistical Methods in Current Cancer Research” (2000-2004) Role: Co-Investigator.
24. U54-MH066418(PI: Piven) “Gene-Brain-Behavior Relationships in Autism” NIH (2002-2007) Role: Investigator.
25. P30 ES10126-01A1(PI: Swenberg) “UNC-CH Center for Environmental Health & Susceptibility” NIH (2001-2005) Role: Biostatistician.
26. P30-ES010126(PI: Swenberg) “UNC-CH Center for Environmental Health & Susceptibility” NIH (2005-2010) Role: Biostatistician.
27. P50-MH090338(PI: Pardo-Manuel de Villena) “An Interdisciplinary Program for Systems Genomics of Complex Behaviors” NIH (2009-2011) Role: Investigator.
28. P20-RR020751(PI: Wilhelmsen) “The Carolina Center Exploratory Genetic Analysis” NIH (2004-2007) Role: Co-Investigator.
29. RD-83272001(PI: Wright) Computational Toxicology-EPA Center (2005-2011) Role: Co-Investigator.

**Service**

NIH Reviewer

1. Appointed regular member of the Genetic Variation and Evolution (GVE) Study Section 2015-2021
2. Ad hoc member of the Genetic Variation and Evolution (GVE) Study Section (2011 & 2012).
3. Reviewer of NIH Center for Scientific Review Special Emphasis Panels (2014, 2015).

Editorial Activities

1. Associate Editor: Genetics 2010-current

Other Avticities

1. ENAR Education Advisory Committee 2016
2. ENAR Short Course on “Statistical Genetic and Genomic Analysis”

Referee

1. The American Journal of Epidemiology
2. The Annals of Applied Statistics
3. Annals of Statistics
4. Annals of the Institute of Statistical Mathematics
5. TheAustralian and New Zealand Journal of Statistics
6. Biometrics
7. Bioinformatics
8. Biostatistics
9. BMC Bioinformatics
10. BMC Genetics
11. BMC Medical Genetics
12. Canadian Journal of Statistics
13. Computational Statistics and Data Analysis
14. Genetic Epidemiology
15. Genetics
16. Genetics Research
17. Genetic Selection Evolution
18. Genetika
19. Heredity
20. Human Heredity
21. The inter[national Journal of Biostatistics](http://www.bepress.com/ijb/)
22. Journal of American Medical Association
23. Journal of American Statistical Association
24. Journal of Biopharmaceutical Statistics
25. Journal of Computational and Graphical Statistics
26. Lifetime Data Analysis
27. Mammalian Genomics
28. PLOS One
29. Statistics in Biosciences
30. Statistics in Medicine
31. Statistics and Probability Letters
32. Scientific Committee Member, 2002 International Conference on Critical Assessment of Microarray Data Analysis
33. Theoretical and Applied Genetics

Service to the University of North Carolina

1. Faculty of the UNC-CH Bioinformatics and Computational Biology Training Program (2002-current).
2. Bioinformatics and Computational Biology (BCB) curriculum committee (2009-2010).
3. Member of SPH Conflict of Interest Committee (2011-current)

Service to the University of Florida

1. Director of Biostatistics Core of Cancer Center 2016-current

Service to the Department of Biostatistics at UNC

1. Space Committee, Chair 2011-current
2. Graduate Admissions Committee 2003-present
3. Seminar Committee, Chair 2008-2011
4. Faculty Search Committee 2002, 2003, 2005, 2009
5. Graduate Studies Committee 2001-2006
6. Masters Examinations Committee 2006-2011

Service to the Department of Biostatistics at UF

1. PhD qualify examination Committee chair 2015-current