

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

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

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

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

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.

Member of NIH study section GVE 2015 ~ current

Honors

1. 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/Research

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. Mi, X.L.*, Zou, B., Zou, F., and Hu, J. (2021) Permutation-based Identification of Important Biomarkers for Complex Diseases via Machine Learning Models. *Nature Communications*, 2021 May 21;12(1):3008. doi: 10.1038/s41467-021-22756-2.
2. Roque, D.A., Hadar, E., Zhang, Y., Zou, F. and Murrow, R (2021) Reducing Ataxic Side Effects from Ventral Intermediate Nucleus of the Thalamus Deep Brain Stimulation Implantation in Essential Tremor: Potential Advantages of Directional Stimulation. *Stereotact Funct Neurosurg*
3. Miller, B., Morse, A., Borgert, J.E., Liu, Z., Sinclair, K., Gamble, G., **Zou, F.**, Newman, J., Leon-Novelo, L., Marroni, F. and McIntyre, L., (2021). Testcrosses are an efficient strategy for identifying cis regulatory variation: Bayesian analysis of allele specific expression (BASE). *G3: Genes, Genomes, Genetics*. accepted.
4. Zhao, B., and **Zou, F.** (2021) On Polygenic Risk Scores for Complex Traits Prediction. *Biometrics*, accepted.
5. B. Zou, X. Mi, P.J. Tighe, G.G. Koch, **Zou F.** (2021) On Kernel Machine Learning for Propensity Score Estimation under Complex Confounding Structures. *Pharmaceutical Statistics*, accepted.
6. Zhang, J., Xia, K., Ahn, M., Jha, S.C., Blanchett, R., Crowley, J.J., Szatkiewicz, J.P., **Zou, F.**, Zhu, H., Styner, M. and Gilmore, J.H., (2021). Genome-Wide Association Analysis of Neonatal White Matter Microstructure. *Cerebral Cortex*, 31(2), pp.933-948.
7. 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>. 22, pp.416-427. PMID: 31925417
8. Giusti-Rodríguez, P., Xenakis, J. G., Crowley, J. J., Nonneman, R. J., DeCristo, D. M., Ryan, A., ... Sullivan, P. F. and **Zou, F.** (2020). Antipsychotic behavioral phenotypes in the mouse Collaborative Cross recombinant inbred inter-crosses (RIX). *G3: Genes, Genomes, Genetics*, 10(9), 3165-3177.

9. Price, J. T., Vwalika, B., Hobbs, M., Nelson, J. A., Stringer, E. M., **Zou, F.**, ... & Stringer, J. S. (2019). Highly diverse anaerobe-predominant vaginal microbiota among HIV-infected pregnant women in Zambia. *PloS one*, *14*(10), e0223128.
10. Kim, Y.*, Chi, Y. Y., & **Zou, F.** (2020). An efficient integrative resampling method for gene–trait association analysis. *Genetic Epidemiology*, *44*(2), 197-207.
11. 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. *Sci Rep* **10**, 5434. PMID: 32214192
12. 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.
13. 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*. PMID: 31693114
14. Mazul, A.L., Weinberg, C.R., Engel, S.M., Siega-Riz, A.M., **Zou, F.**, Carrier, K.S., Basta, P.V., Vaksman, Z., Maris, J.M., Diskin, S.J. and Maxen, C., 2019. Neuroblastoma in relation to joint effects of vitamin A and maternal and offspring variants in vitamin A-related genes: A report of the Children’s Oncology Group. *Cancer epidemiology*, *61*, pp.165-171.
15. Zhang, T.P., Yang, F., Tang, W. *et al.* Pay-it-forward gonorrhea and chlamydia testing among men who have sex with men in China: a study protocol for a three-arm cluster randomized controlled trial. *Infect Dis Poverty* **8**, 76 (2019). <https://doi.org/10.1186/s40249-019-0581-1> PMID: 32530426
16. Zhao Y*, Zhu H, Lu Z, Knickmeyer RC, & **Zou F.** (2019) Structured Genome-Wide Association Studies with Bayesian Hierarchical Variable Selection. *Genetics*. 212:397-415.
17. 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. *Cereb Cortex*. 29:1139-1149.
18. Zimmerman H, Yin Z, **Zou F**, Everett ET. (2019) Interfrontal bone among inbred strains of mice and QTL mapping. *Frontiers in genetics*, 10:291.
19. Mi X*, **Zou F**, Zhu R. (2019) Bagging and deep learning in optimal individualized treatment rules. *Biometrics*. 75(2): 674-684. PMID: 30365175
20. 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. *Hum Brain Mapp*. 39:4998-5013.
21. 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. *Oncotarget*. 9(34):23704-23717.
22. 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. *Leuk Lymphoma*. 59:2557-2569.

23. Liu Y, Xiong S, Sun W, **Zou F.** (2018) Joint Analysis of Strain and Parent-of-Origin Effects for Recombinant Inbred Intercrosses Generated from Multiparent Populations with the Collaborative Cross as an Example. *G3* 8:599-605.
24. 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.
25. Yang D, **Zou F**, Xiong S, Forde JJ, Wang Y, Draganov PV. (2018) Endoscopic submucosal dissection for early Barrett's neoplasia: a meta-analysis. *Gastrointest Endosc.* 87:1383-1393.
26. 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.
27. 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.
28. 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. *Exp Hematol Oncol.* 6:26.
29. 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.
30. 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.
31. 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
32. 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. *Genetics* 30:1049-1062.
33. 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.
34. Chaudhry, N.A., Rivero, M., Grajo, J.R., Moser, P.P., **Zou, F.**, Homsy, 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. *Inflamm Bowel Dis* 23:641-649
35. 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.
36. 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.
 37. 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. *BMC Med Educ* 21: 297
 38. 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. *Cereb Cortex*: 1-10.
 39. 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.
 40. Yin, Z.*, Xia, K., Chung, W., Sullivan, F.P., and **Zou, F.** (2015) Fast eQTL Analysis for Twin Studies. *Genetic Epidemiology*. 39: 357–365.
 41. 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. *JASA* 110: 975-986.
 42. 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.
 43. 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.)
 44. 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.
 45. 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.
 46. 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.

47. 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.
48. 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.
49. **Zou, F.**, Sun, W., Crowley, J.J., Zhabotynsky, V., Sullivan, P.F., Pardo-Manuel de Villena, F.F. (2014) A Novel Statistical Approach for Jointly Analyzing RNA-seq Data from F1 Reciprocal Crosses and Inbred Lines. *Genetics*, 197:389-99.
50. 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.
51. Chung, W.*, and **Zou, F.** (2014) Mixed effects models for GAW18 longitudinal blood pressure data. *BMC proceedings*. 8: S87.
52. 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 *Stat.* 2: 292-302.
53. Ghosh, Arpita*, **Zou, F.**, and Wright, F.A. (2013) Unified Analysis of Secondary Traits in Case-Control Association Studies. *JASA*. 108: 566-576.
54. 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.
55. Gong, Y.*, and **Zou, F.** (2012) Varying coefficient models for mapping quantitative trait loci using recombinant inbred intercrosses. *Genetics*, 190:475-486.
56. Xia, K., Shabalina, 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.
57. 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.
58. Collaborative Cross Consortium (2012) The genome architecture of the Collaborative Cross mouse genetics reference population. *Genetics*, 190:389-402.
59. 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) Understanding the population structure of North American patients with cystic fibrosis. *Clin Genet.*, 79:136-46. PMC2995003.
60. Lee, S.*, Wright, F.A., and **Zou, F.** (2011) Control of population stratification by correlation-selected principal components. *Biometrics*, 67: 967-974.

61. Liu, F., Dunson, D., and **Zou, F.** (2011) High-dimensional variable selection in meta analysis for censored data. *Biometrics*, 67:504–512.
62. Guo, X., Pace, R.G., Stonebraker, J.R., Commander, C.W., Dang, A.T., Drumm, M.L., Harris, H., **Zou, F.**, Swallow, D.M., Wright, F.A., O'Neal, W.K., and Knowles, M.R. (2011) Mucin variable number tandem repeat polymorphisms and severity of Cystic Fibrosis lung disease: significant association with *MUC5AC*. *PLoS ONE*, 6:e25452 (total 8 pages).
63. 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.
64. 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.
65. Yuan, Z., **Zou, F.**, and Liu, Y. (2011) Bayesian multiple quantitative trait loci mapping for recombinant inbred intercrosses. *Genetics*, 188:189-195.
66. 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.
67. **Zou, F.**, Huang, H., Lee, S., and Hoeschele, I. (2010) Nonparametric Bayesian variable selection with applications to multiple quantitative trait loci mapping with epistasis and gene-environment interaction. *Genetics*, 186:385-94.
68. 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](#)
69. Zhang, X., Huang, S., **Zou, F.**, and Wang, W. (2010) TEAM: Efficient two-Locus epistasis tests in human genome-wide association study. *Bioinformatics*: 26: i217-27. [PMC2881371](#).
70. Zhang, X., Pan, F., Xie, Y., **Zou, F.**, and Wang, W. (2010) A General approach for efficient genome-wide two-locus epistatic test in disease association study. *Journal of Computational Biology*, 17:401-415.
71. 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](#)

72. 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.
73. **Zou, F.**, Huang, H., and Ibrahim, J.G. (2010) A semiparametric Bayesian approach for estimating the gene expression distribution. *Journal of Biopharmaceutical Statistics*, 20:267-280.
74. Sun, W., Ibrahim, J.G., and **Zou, F.** (2010) Genomewide multiple-loci mapping in experimental crosses by iterative adaptive penalized regression. *Genetics*, 185:349-359.
75. 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.
76. **Zou, F.**, Lee, S. Knowles, M., and Wright, F.A. (2010) Control of population stratification using correlated SNPs by shrinkage principal components. *Human Heredity*, 70:9-22. PMC2912642
77. Bartlett, J.R., Friedman, K.J., Ling, S.C., Pace, R.G., Bell, S.C., Bourke, B., Castaldo, G., Castellani, C., Cipolli, M., Colombo, C., Colombo, J.L., Debray, D., Fernandez, A., Lacaille, F., Macek, M.J., Rowland, M., Salvatore, F., Taylor, C.J., Wainwright, C., Wilschanski, M., Zemková, D., Hannah, W.B., Phillips, M.J., Corey, M., Zielenski, J., Dorfman, R., Wang, Y., **Zou, F.**, Silverman, L.M., Drumm, M.L., Wright, F.A., Lange, E.M., Durie, P.R., and Knowles, M.R. (2009) Genetic modifiers of liver disease in Cystic Fibrosis. *JAMA*, 302:1076-1083.
78. Zhang, X, **Zou, F.**, and Wang, W. (2009) FastChi: an efficient algorithm for analyzing gene-gene interactions. *Pacific Symposium on Biocomputing*, 14:528-39.
79. Levy, H., Murphy, A., **Zou, F.**, Gerard, C., Klanderma, 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.
80. **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. PMC2632598.
81. 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. PMC2665019
82. 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)*. 2008:821–829.

83. Sullivan, P.F., Lin, D.Y., Tzeng, J.Y., 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*, 13:570-84.
84. 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.
85. Huang, C., Qin, J., and **Zou, F.** (2007) Empirical likelihood-based inference for genetic mixture models. *The Canadian Journal of Statistics*, 35:563-574.
86. Gelfond, J.*, Ibrahim, J. G. and **Zou, F.** (2007) Proximity model for expression trait loci detection. *Biometrics*, 63:1108–1116.
87. 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.
88. 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.
89. 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.
90. 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.
91. **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.
92. Hu, J., Wright, F.A., and **Zou, F.** (2006) Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101:41-50.
93. **Zou, F.**, Gelfond, J., Airey, D., Lu, L., Manly, K., Williams, W., and Threadgill, D. (2005) Quantitative trait locus analysis using recombinant inbred intercrossoes (RIX): theoretical and empirical considerations. *Genetics*, 170:1299-1311.
94. 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.

95. 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.
96. 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.
97. Hu, J., **Zou, F.**, and Wright, F.A. (2005) Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21:3264-3272.
98. **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.
99. 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.
100. Lin, D., and **Zou, F.** (2004) Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27:202-214.
101. Diao, G., Lin, D., and **Zou, F.** (2004) Mapping quantitative trait loci with censored observations. *Genetics*, 168:1689-1698.
102. Churchill, G. A. *et al.* (2004). The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics*, 36:1133-1137.
103. **Zou, F.**, Yandell, B.S., and Fine, J.P. (2003) Rank based statistical methodologies for QTL mapping. *Genetics*, 165:1599-1605.
104. Flaherty, L. *et al.* (2003). The nature and identification of quantitative trait loci: a community's view. *Nature Genetics Review*, 4:911-916.
105. 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
106. 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.
107. 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.
108. **Zou, F.**, and Fine, J.P. (2002) Note on a partial empirical likelihood. *Biometrika*, 89:958-961.

109. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002) On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89:61-75.
110. 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.
111. **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. ENAR, March 2021
2. ICSA Applied Statistics Symposium, 2020
3. ICSA-China, Hangzhou, China 2019
4. Department of Biostatistics, Columbia University, 2018
5. Big Data and Information Analytics (BigDIA), Houston, Texas, 2018
6. The International Conference on Advances in Finite Mixture, Guilin, China, 2018
7. Summer school in statistical genetics at Laval University, 2018
8. Biostatistics Seminar, MD-Anderson 2017
9. Biostatistics Seminar, UT Health Science Center at Houston 2017
10. ICSA Applied Statistics Symposium, Chicago, IL 2017
11. Department of Statistics, Florida state university, 2017
12. Biostatistics Workshop, University of Florida, 2017
13. ICSA-China, Shanghai, China 2016
14. Department of Statistics, University of Georgia 2016
15. Department of Statistics, Wuhan University, 2016
16. Department of Statistics, Shangdong University, 2016
17. 2016 China Statistics Conference, Qingdao 2016
18. Department of Statistics, Zhongnan University of Economics, 2016
19. Department of Statistics, University of Florida, 2015
20. NC-Tracs, University of North Carolina at Chapel Hill, 2015
21. IMS-China, Yunnan, China, 2015
22. Department of Biostatistics, University of Pennsylvania, 2014
23. Joint Applied Statistics Symposium of International Chinese Statistical Association & Korean International Statistical Society, Portland, Oregon, 2014
24. Science at the Edge seminar, Michigan state university, 2013
25. Department of Biostatistics, University of Florida, 2013
26. Department of Genetics, University of North Carolina at Chapel Hill, 2013
27. Triangle Statistical Genetics Conference, RTP, 2012

28. The 34th Finnish Summer School on Probability Theory and Statistics, Finland, 2012
29. Second Joint Biostatistics Symposium, Beijing, China 2012
30. Centers of Excellent in Genomic Science (CEGS) 9th Annual meeting, 2011
31. Department of Mathematics and Statistics. Wuhan University, China, 2011
32. Department of Statistics, George Mason University, 2011
33. IMS China, Xi'an, China, 2011
34. Statistical Society of Canada meeting. Canada, 2011
35. ICSA 2011 APPLIED STATISTICS SYMPOSIUM, New York, 2011
36. Royal Netherlands Academy of Sciences and Arts (KNAW): Genomics of gene expression, 2010
37. Department of Biostatistics, Yale University, 2010
38. Department of Mathematics and Statistics, Bowling Green State University, 2010
39. Joint statistical meetings, Vancouver, Canada, 2010
40. Plant and Animal Genome XVII Conference. San Diego, CA, 2009
41. Statistical Genomics workshop, Institute for Mathematical Sciences. Singapore, 2009
42. Department of Statistics, Duke University, 2008
43. Departments of Statistics and Biostatistics, University of Wisconsin at Madison, 2008
44. Department of Mathematics and Statistics. Wuhan University, China, 2007
45. Bioinformatics Center, MD Anderson, 2007
46. International Chinese Statistical Association (ICSA) meeting, 2007
47. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007
48. Department of Mathematics and Statistics. York University, Canada, 2006

Teaching Activities

Courses

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

Genetic Data Analysis (Bios781) Spring 2020, 2018 and Fall 2012, 2014 Instructor

Topics in Statistical Genetics and Genomics (BCB723) Spring 2018, 2019, 2020 Co-instructor

Intermediate Linear Models (Bios663) Spring 2009, 2011, 2013, 2015, 2019, 2021 Instructor

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

Biostatistics in Bioinformatics and Computational Biology (Gnet 215), Fall 2003, 2004, 2005 and 2007, Spring 2010. Co-instructor

Genetic Data Analysis (taught at Department of Biostatistics, UF) 2016, 2017

Statistical learning from omics data, SAMSI, 2015 Co-instructor

Guidance of Post-Doctoral Research

1. Hanwen Huang, 2004~2010

Current position: Associate Professor, University of Georgia

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

Current position: Assistant Professor, Yale University

Vasyl Zhabotynsky 2020- current

Guidance of Doctoral Research

1. Kai Xia, PhD candidate, Dept of Bios.

2. Vasyl Zhabotynsky, 2020 DrPD, Dept of Bios. (joint with Wei Sun)

3. Sophie Gao, DrPD candidate, Dept of Bios. (joint with Michael Hudgens)

4. Laura Zhou, PhD candidate, Dept of Bios. (joint with Wei Sun)

5. Meichen Dong, PhD candidate, Dept of Bios. (joint with Yuchao Jiang)

6. Tianyi Liu, PhD candidates, Dept of Bios. (joint with Quefeng Liu)

7. Li Dong, 2019 PhD, Dept of Bios. (joint with Xiaojing Zheng)

8. Xinlei Mi, 2018 PhD, Dept of Bios., University of Florida.
9. Yeonil Kim, 2019 Dept of Bios., University of Florida. (joint with Chi, Yueh-Yun)
10. James Xenakis, 2018 PhD, Dept of Bios
11. Zhaoyu Yin, 2014 PhD, Dept of Bios.
12. Wonil Chung, 2013 PhD, Dept. of Bios.
13. Gregory Mayhew, 2013, DrPH, Dept of Bios. joint with Fred Wright.
14. Yi Gong, 2011 PhD, Dept. of Bios.
15. Seunggeun Lee, 2010 PhD, Dept. of Bios., joint with Dr. Fred Wright
16. Arpita Ghosh, 2009 PhD, Dept. of Bios., joint with Dr. Fred Wright.
17. Yu-Ling Chang, 2008 PhD, Dept of Bios., joint with Dr. Fred Wright.
18. Jonathan Gelfond, 2007 PhD, Dept. of Bios., joint with Drs. Joe Ibrahim and Mayetri Gupta.

Guidance of Master's Research

1. Junjian Liu 2021
2. Shiliang Wang 2011
3. Joe Rigdon 2010
4. Niki Arya, 2002

Service on Doctoral Committee

1. Qianyun Li, PhD candidate, Dept of Bios
2. Yutong Liu, PhD candidate, Dept of Bios
3. Bocha Jia, PhD, Dept of Bios, university of Florida
4. Sinjini Sikar, PhD, Dept of Bios, university of Florida
5. Fang Zhou, PhD, Dept of Bios
6. Ting Wang, PhD, Dept of Bios
7. Benjamin Langworthy, PhD, Dept of Bios
8. Wujuan Zhong, PhD, Dept of Bios
9. Suwan Xu, PhD, Dept of Bios

10. Choi, Wan Suk, 2017 PhD, Dept of Bios.
11. Xu, Yunan, Phd candidate, Dept of epidemiology
12. Chen-Ping Fu, PhD candidate, Department of Computer Science
13. Angela Yanyi. Liu, PhD candidate, Department of Epidemiology
14. Alison Wise, DrPH candidate, Department of Biostatistics
15. Ting-huei Chen, PhD 2014, Department of Biostatistics
16. Ja-an Lin, PhD, 2013 Department of Biostatistics
17. David Kessler, 2013 Department of Biostatistics
18. Zhaowei Hua, PhD, 2011 Department of Biostatistics
19. Chaeryon Kang, PhD, 2011 Department of Biostatistics
20. Yihui Zhou, PhD, 2011 Department of Biostatistics
21. Shiliang Wang, PhD, 2011 Department of Cell & Molecular Physiology
22. Xiang Zhang, PhD, 2011 Department of Computer Science
23. Rong Jiang, PhD, 2010 Department of Environment Sciences & Engineer
24. Vonn Walter, PhD, 2010 Department of Biostatistics
25. John Schwarz, PhD, 2010 Department of Biostatistic
26. Lindsey Ho, DrPh, 2010 Department of Biostatistics
27. Tsui-Shan (Eva) Lu, PhD, 2009 Department of Biostatistics
28. Chevonne Eversley, PhD, 2009 Department of Genetics
29. Emily Kistner, PhD, 2005 Department of Biostatistics
30. Guoqing Diao, PhD, 2005 Department of Biostatistics
31. Andrew Sterrett, PhD, 2005 Department of Biostatistics
32. Chaehyung Ahn, PhD, 2005 Department of Biostatistics
33. Szu-Yun Leu, PhD, 2005 Department of Biostatistics
34. 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
3. 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)
5. R01 (Co-PI) “Novel Multi-View Deep Learning for Complex Human Diseases” Submitted

Investigator on Grants

1. 2 R01 GM105785-06 (PI: Sun) Statistical Methods for RNA-seq Data Analysis. NIH (2019-2022). Role: Contract PI.
2. 1 RF1 AG061022-01 (PI: Gonzalez) Neurocognitive Aging, MCI and Alzheimer's Disease DNA Methylation among Diverse Latinos. NIH (3/15/19-2/29/24). Role: Contract PI.
3. 1 P42 ES031007-01 (PI: Fry) The UNC Chapel Hill Superfund Research Program (UNC-SRP) NIH (12/1/19-11/30/24). Co-director of DMAC.
4. 3-UM1-AI069423-15S1 (MPIs: Eron, Herce, Wohl) HIV/AIDS Clinical Trials Unit (CTU) Covid-19 RadX-UP Supplement. NIH/NIAID (12/1/20-11/30/22) Role: Co-Investigator.
5. 1 R01 HL155986-01 (PI: Kafri) The Circadian Rhythm as a Lentiviral Vector Restriction Factor. NIH (9/1/20-8/31/24) Role: Co-Investigator.
6. 1 R01 AG062686-01A1 (PI: Cene) Implementation and Evaluation of Patient Priorities Care-North Carolina for Older Adults with Multiple Chronic Conditions. NIH (9/15/19-4/30/24). Role: Co-Investigator.
7. 1 R01 AI158826-01 (PI: Tucker) Pay-it-forward gonorrhea testing among men who have sex with men: The PIONEER pragmatic randomized controlled trial. NIH (3/19/21-2/28/26). Role: Co-Investigator.
8. 1 R01 GM138912-01A1 (PI: Pattenden) Development of a Cavitation Enhancement Technology to Access Archived Tissues for Epigenetic-based Biomedical Research. NIH (4/1/21-3/31/25) . Role: Co-Investigator.

9. 5 R34 MH119963-02 (PI: Tucker) Enhancing Partner Services among Men Who Have Sex with Men Living With HIV: A Pilot Randomized Controlled Trial. NIH (8/8/19-6/30/22) Role: Co-Investigator
10. 1 R01 ES029925-01 (PI: Pardo-Manuel de Villena) Genetic Underpinning of Diabetes Associated with Arsenic Exposure. NIEHS (2019-2024). Role: Co-Investigator.
11. 5 P30 ES010126-18 (PI: Troester) UNC-CH Center for Environmental Health & Susceptibility - Biostatistics & Bioinformatics Facility Core. NIEHS (2016-2021). Role: Co-Investigator.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 1 R01 MH116527-01 (PI: Zhang) Analysis of Big Data Squared in Biomedical Studies. NIH (2018-2023). Role: Co-Investigator.
18. R01-MH092335 (PI: Santelli) “Genome-wide Identification of Variants Affecting Early Human Brain Development” NIH (2011-2016) Role: Co-Investigator.
19. R01 GM105785-01A1 (PI: Sun) “Statistical Methods for RNA-seq Data Analysis” NIH (2014-2018) Role: Co-Investigator.
20. R01-DA023690(PI: Tarantino) “Organismal and Genetic Networks in Drug Reward and Reinforcement” NIH (2009-2018) Role: Co-Investigator.
21. R21 MH097173-02 (PI: Sullivan) “Biomarkers of Olanzapine-induced Weight Gain in Mice” NIH (2012-2015) Role: Co-Investigator.
22. R01-ES019315 (PI: Fry) “In Utero Exposure to Arsenic, Links to Epigenetic Alterations and Disease” NIH (2010-2015) Role: Co-Investigator.
23. P50-HG006582 (PI: Pardo-Manuel de Villena) “An Interdisciplinary Program for Systems Genomics of Complex Behaviors” NIH (2011-2014) Role: Co-investigator.
24. R01-DE018104 (PI: Everett) “Genetic Determinants of Physiological Responses to Fluoride in Bone” NIH (2008-2013) Role: Co-Investigator.
25. R01-CA132887 (PI: Olshan) “Genetic Susceptibility Factors in the Etiology of Neuroblastoma” NIH (2008-2013). Role: Co-Investigator.
26. R01-HL095396 (PI: Knowles) “Molecular Phenotypes for Cystic Fibrosis Lung Disease” NIH (2008-2012) Role: Investigator.

27. GIL (PI: Lin) Gillings Innovation Laboratory (2009-2012) Role: Investigator.
28. RC2-MH089951(PI: Sullivan) “Integration of Genomics & Transcriptomics in Normal Twins & Major Depression” NIH (2009-2011) Role: Investigator.
29. R01-DK066368 (PI: Knowles) “Genetic Modifiers of CF Liver Disease” NIH (2004-2009) Role: Co-Investigator.
30. R01-CA082659 (PI: Lin) “Statistical Methods in Current Cancer Research” NIH (2004-2008) Role: Co-Investigator.
31. R01-CA082659 (PI: Lin) “Statistical Methods in Current Cancer Research” (2000-2004) Role: Co-Investigator.
32. U54-MH066418(PI: Piven) “Gene-Brain-Behavior Relationships in Autism” NIH (2002-2007) Role: Investigator.
33. P30 ES10126-01A1(PI: Swenberg) “UNC-CH Center for Environmental Health & Susceptibility” NIH (2001-2005) Role: Biostatistician.
34. P30-ES010126(PI: Swenberg) “UNC-CH Center for Environmental Health & Susceptibility” NIH (2005-2010) Role: Biostatistician.
35. P50-MH090338(PI: Pardo-Manuel de Villena) “An Interdisciplinary Program for Systems Genomics of Complex Behaviors” NIH (2009-2011) Role: Investigator.
36. P20-RR020751(PI: Wilhelmsen) “The Carolina Center Exploratory Genetic Analysis” NIH (2004-2007) Role: Co-Investigator.
37. RD-83272001(PI: Wright) Computational Toxicology-EPA Center (2005-2011) Role: Co-Investigator.

Services

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 2010-2015

Other Activities

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

3. SAMSI workshop organizer on “Program on Beyond Bioinformatics: Statistical and Mathematical Challenges (Bioinformatics)” 2014-2015

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. The Australian 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 international Journal of Biostatistics
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 (2011-2012)
4. LCCC member

Service to the University of Florida

1. Director of Biostatistics Core of Cancer Center 2015-2017

Service to the Department of Biostatistics at UNC

1. Graduate Admissions Committee 2003-present, Director 2017-current
2. PhD Examinations Committee - Applied 2017-current
3. Masters Examinations Committee 2006-2011, 2017 - current
4. Space Committee, Chair 2011-2012
5. Seminar Committee, Chair 2008-2011
6. Faculty Search Committee 2002, 2003, 2005, 2009

7. Graduate Studies Committee 2001-2006

Service to the Department of Biostatistics at UF

1. PhD qualify examination Committee chair 2015-2017