

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. Wohl, D. A., Fischer, W. A., Mei, W., **Zou, F.**, Tozay, S., Reeves, E., ... & Brown, J. (2023). Post-Ebola Symptoms 7 Years After Infection: The Natural History of Long Ebola. *Clinical Infectious Diseases*, 76(3), e835-e840.
2. Peterson, J.J., Lewis, C.A., Burgos, S.D., Manickam, A., Xu, Y., Rowley, A.A., Clutton, G., Richardson, B., **Zou, F.**, Simon, J.M. and Margolis, D.M., 2023. A histone deacetylase network regulates epigenetic reprogramming and viral silencing in HIV-infected cells. *Cell Chemical Biology*, 30(12), pp.1617-1633.
3. Elsherif, L., Derebail, V., Tang, Y., ..., **Zou, F.**, Cai, J., Pollock, D. and Ataga, K. Predictive Capacity of Plasma and Urinary Biomarkers for Persistent Albuminuria in Patients with Sickle Cell Disease (2023) *Blood* 142 (Supplement 1): 3897.
4. Zhang, Tiange P., 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." *Infectious diseases of poverty* 8.04 (2019): 85-95.
5. Zhang, Y., Li, J., Xie, Y., Wu, D., Ong, J., Marley, G., Kamarulzaman, A., Lu, H., **Zou, F.**, Smith, J.S. and Tucker, J.D., 2023. Pay-it-forward incentives for hepatitis virus testing in men who have sex with men: a cluster randomized trial. *Nature medicine*, 29(9), pp.2241-2247.
6. Szempruch, K.R., Martschenko, A.D., Arora, H., Isaak, R.S., Prasad, R., Schmitz, J.L., Liu, C., **Zou, F.** and Rodriguez, P.S., 2023. Normal Saline vs Plasma-Lyte A Use Intra-and Post-Operatively in Adult Kidney Transplant Recipients. *OBM Transplantation*, 7(2), pp.1-16.
7. Zou, B., Mi, X., Stone, E. and **Zou, F.**, 2023. A deep neural network framework to derive interpretable decision rules for accurate traumatic brain injury identification of infants. *BMC medical informatics and decision making*, 23(1), p.58.
8. Shang, B., Venkatratnam, A., Liu, T., Douillet, C., Shi, Q., Miller, M., Cable, P., **Zou, F.**, Ideraabullah, F.Y., Fry, R.C. and Stýblo, M., 2023. Sex-specific

- transgenerational effects of preconception exposure to arsenite: metabolic phenotypes of C57BL/6 offspring. *Archives of toxicology*, 97(11), pp.2879-2892.
9. Zhou, Yi, et al. "Monetary incentives and peer referral in promoting secondary distribution of HIV self-testing among men who have sex with men in China: A randomized controlled trial." *PLoS medicine* 19.2 (2022): e1003928. [PMCID: PMC8887971](#)
 10. Zhao, B., **Zou, F.** and Zhu, H., 2023. Cross-trait prediction accuracy of summary statistics in genome-wide association studies. *Biometrics*, 79(2), pp.841-853.
 11. Feng, Qunqiang, Pan Liu, Pei-Fen Kuan, **Fei Zou**, Jianan Chen, and Jialiang Li. "A network approach to compute hypervolume under receiver operating characteristic manifold for multi-class biomarkers." *Statistics in Medicine* (2023). [PMID: 36597213](#)
 12. Unlu Yazici, M., Marron, J. S., Bakir-Gungor, B., **Zou, F.**, & Yousef, M. (2023). Invention of 3Mint for feature grouping and scoring in multi-omics. *Frontiers in Genetics*, 14. [PMC10050723](#)
 13. Kim, Y., Chi, Y. Y., Shen, J., & **Zou, F.** (2023). Robust genetic model-based SNP-set association test using CauchyGM. *Bioinformatics*, 39(1), btac728.
 14. Zhou, L., **F. Zou**, W. Sun (2023) Prioritizing candidate peptides for cancer vaccines through predicting peptide presentation by HLA-I proteins. *Biometrics*, 79(3), 2664–2676 [PMCID 35833513](#)
 15. Zou, B., **Zou, F.**, & Cai, J. (2023). An efficient machine learning framework to identify important clinical features associated with pulmonary embolism. *Plos one*, 18(9), e0292185.
 16. Dong, Meichen, Yiping He, Yuchao Jiang, and **Fei Zou**. "Joint gene network construction by single-cell rna sequencing data." *Biometrics* 79, no. 2 (2023): 915-925. [PMID: 35184277](#)
 17. Zhabotynsky*, V., Huang, L., Little, P., Hu, Y. J., Pardo-Manuel de Villena, F., **Zou, F.**, & Sun, W. (2022). eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. *PLoS Genetics*, 18(3), e1010076.
 18. Gao, X*., Hudgens, M. G., & **Zou, F.** (2022). Case-Cohort Studies with Time-Dependent Covariates and Interval-Censored Outcome. In *Emerging Topics in Modeling Interval-Censored Survival Data* (pp. 221-234). Cham: Springer International Publishing.
 19. Xia, Kai*, Andrey A. Shabalin, Zhaoyu Yin, Wonil Chung, Patrick F. Sullivan, Fred A. Wright, Martin Styner, John H. Gilmore, Rebecca C. Santelli, and Fei Zou. "TwinEQTL: ultrafast and powerful association analysis for eQTL and GWAS in twin studies." *Genetics* 221, no. 4 (2022): iyac088.
 20. Shang, Bingzhen, Abhishek Venkatratnam, Hadley Hartwell, Christelle Douillet, Peter Cable, Tianyi Liu*, **Fei Zou**, Folami Y. Iderabdullah, Rebecca C. Fry, and Miroslav Stýblo. "Ex vivo exposures to arsenite and its methylated trivalent

- metabolites alter gene transcription in mouse sperm cells." *Toxicology and applied pharmacology* 455 (2022): 116266.
21. Léa Maitre, Jean-Baptiste Guimbaud, Charline Warembourg, Nuria Güil-Oumrait, The Exposome Data Challenge Participant Consortium, Paula Marcela Petrone, Marc Chadeau-Hyam, Martine Vrijheid, Juan R. Gonzalez, Xavier Basagaña (2022) State-of-the-Art Methods for Exposure-Health Studies: results from the Exposome Data Challenge Event. *Environment International*, 168 (2022): 107422.
 22. Xenakis, J., Douillet, C., Bell, T., Hock, P., Farrington, J., Liu, T*.., Murphy, C., Saraswatula, A., Shaw, G., Nativio, G., Shi, Q., Venkatratnam, A., **Zou, F.**, Fry, R., Stýblo, M., and Pardo-Manuel de Villena, F., (2022) An interaction of inorganic arsenic exposure with body weight and composition on type 2 diabetes indicators in Diversity Outbred mice. *Mammalian Genome* (2022): 1-15. PMID: **35819478**
 23. Roque, D. A., Hadar, E., Zhang, Y., **Zou, F.**, & Murrow, R. (2022). Reducing Ataxic Side Effects from Ventral Intermediate Nucleus of the Thalamus Deep Brain Stimulation Implantation in Essential Tremor: Potential Advantages of Directional Stimulation. *Stereotactic and Functional Neurosurgery*, 100(1), 35-43.
 24. Zou, B., Santos, H. P., Xenakis, J. G., O'Shea, M. M., Fry, R. C., & **Zou, F.** (2022). A mixed-effects two-part model for twin-data and an application on identifying important factors associated with extremely preterm children's health disorders. *Plos one*, 17(6), e0269630. [PMC9191696](#)
 25. Zhou Y, Lu Y, Ni Y, Wu D, He X, Ong JJ, Tucker JD, Sylvia SY, Jing F, Li X, Huang S, Shen G, Xu C, Xiong Y, Sha Y, Cheng M, Xu J, Jiang H, Dai W, Huang L, **Zou F**, Wang C, Yang B, Mei W, Tang W. Monetary incentives and peer referral in promoting secondary distribution of HIV self-testing among men who have sex with men in China: A randomized controlled trial. *PLoS Med.* 2022 Feb 14;19(2):e1003928. doi: 10.1371/journal.pmed.1003928. PMID: 35157727; PMCID: PMC8887971.
 26. Zhao, B.*, and **Zou, F.** (2022) On Polygenic Risk Scores for Complex Traits Prediction. *Biometrics*, 78(2), 499-511.
 27. Lee, Sung Hyun, Yajing Hao, Tong Gui, Gianpietro Dotti, Barbara Savoldo, **F Zou**, and Tal Kafri. "Inadvertent transfer of murine VL30 retrotransposons to CAR-T cells." *Advances in Cell and Gene Therapy* 2022 (2022).
 28. Kistler, C.E., Austin, C.A., Liu, J.J.*, Cauble, M., Wise, A., Patel, S.M., Ward, K., Wiltshire, T., **Zou, F.**, Szeto, A.H. and Crona, D.J., (2022). The feasibility and potential of pharmacogenetics to reduce adverse drug events in nursing home residents. *Journal of the American Geriatrics Society*.

29. Zou, B., Mi, X., Tighe, P. J., Koch, G. G., & **Zou, F.** (2021). On kernel machine learning for propensity score estimation under complex confounding structures. *Pharmaceutical Statistics*, 20(4), 752-764.
30. Xie, Jiali, Hunyong Cho, Bridget M. Lin, Malvika Pillai, Lara H. Heimisdottir, Dipankar Bandyopadhyay, **F Zou**, Jeffrey Roach, Kimon Divaris, and Di Wu. "Improved Metabolite Prediction Using Microbiome Data-Based Elastic Net Models." *Frontiers in cellular and infection microbiology* (2021): 972.
31. 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.
32. Mi, X., Tighe, P., **Zou, F.**, & Zou, B. (2021). A deep learning semiparametric regression for adjusting complex confounding structures. *The Annals of Applied Statistics*, 15(3), 1086-1100.
33. 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* 11, no. 5: jkab096.
34. 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.
35. 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.
36. 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
37. 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. PMID: **32694196**

38. 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.
39. Kim, Y.*, Chi, Y. Y., & **Zou, F.** (2020). An efficient integrative resampling method for gene–trait association analysis. *Genetic Epidemiology*, 44(2), 197-207.
40. 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
41. 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.
42. 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
43. 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.
44. 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
45. 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.
46. 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.
47. Zimmerman H, Yin Z, **Zou F**, Everett ET. (2019) Interfrontal bone among inbred strains of mice and QTL mapping. *Frontiers in genetics*, 10:291.
48. Mi X*, **Zou F**, Zhu R. (2019) Bagging and deep learning in optimal individualized treatment rules. *Biometrics*. 75(2): 674-684. PMID: 30365175
49. 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.
50. 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.

51. 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.
52. 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.
53. 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.
54. 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.
55. 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.
56. 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.
57. 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.
58. 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.
59. 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.
60. 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
61. 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.
62. 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.
63. 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. *Inflamm Bowel Dis* 23:641-649
64. 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.
 65. 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.
 66. 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
 67. 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.
 68. 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.
 69. Yin, Z.*, Xia, K., Chung, W., Sullivan, F.P., and **Zou, F.** (2015) Fast eQTL Analysis for Twin Studies. *Genetic Epidemiology*. 39: 357–365.
 70. 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.
 71. 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., Schoovers, R., van Grootenhuis, G., Willemse, 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.
 72. 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.)
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75. 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.
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85. 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.
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90. 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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92. 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.
93. 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.
94. Yuan, Z., **Zou, F.**, and Liu, Y. (2011) Bayesian multiple quantitative trait loci mapping for recombinant inbred intercrosses. *Genetics*, 188:189-195.
95. 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., Zielenki, 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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99. 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.

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102. **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.
103. 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.
104. 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.
105. **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
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108. 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.
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110. 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

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113. 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.
114. Huang, C., Qin, J., and **Zou, F.** (2007) Empirical likelihood-based inference for genetic mixture models. *The Canadian Journal of Statistics*, 35:563-574.
115. Gelfond, J.*, Ibrahim, J. G. and **Zou, F.** (2007) Proximity model for expression trait loci detection. *Biometrics*, 63:1108–1116.
116. 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.
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119. 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.
120. **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.
121. Hu, J., Wright, F.A., and **Zou, F.** (2006) Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101:41-50.
122. **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.

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124. 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.
125. 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.
126. Hu, J., **Zou, F.**, and Wright, F.A. (2005) Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21:3264-3272.
127. **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.
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129. Lin, D., and **Zou, F.** (2004) Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27:202-214.
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132. **Zou, F.**, Yandell, B.S., and Fine, J.P. (2003) Rank based statistical methodologies for QTL mapping. *Genetics*, 165:1599-1605.
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134. 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
135. Lukens, L., **Zou, F.**, Lydiate, D., Parkin, I., and Osborn, T. (2003) Comparison of a *Brassica Oleracea* genetic map with genome of *Arabidopsis Thaliana*. *Genetics*, 164:359-372.
136. 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.
137. **Zou, F.**, and Fine, J.P. (2002) Note on a partial empirical likelihood. *Biometrika*, 89:958-961.
 138. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002) On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89:61-75.
 139. 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.
 140. **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. NIEHS seminar, Semiparametric Deep Learning Based Comparative Effective Analysis and Permutation-based Feature Importance Test, Feb/2022
2. Singapore Statistical Methods in Genetic/Genomic Studies workshop, Joint Gene Network Construction by SingleCell RNA Sequencing Data, Jan/2022
3. Exposome Data Challenge Event, Deep-Exposome: A Predictive and Interpretative Deep Neural Network Ensemble for Exposome Data April 2021
4. ENAR, March 2021
5. ICSA Applied Statistics Symposium, 2020
6. ICSA-China, Hangzhou, China 2019
7. Department of Biostatistics, Columbia University, 2018
8. Big Data and Information Analytics (BigDIA), Houston, Texas, 2018
9. The International Conference on Advances in Finite Mixture, Guiling, China, 2018
10. Summer school in statistical genetics at Laval University, 2018
11. Biostatistics Seminar, MD-Anderson 2017
12. Biostatistics Seminar, UT Health Science Center at Houston 2017
13. ICSA Applied Statistics Symposium, Chicago, IL 2017
14. Department of Statistics, Florida state university, 2017
15. Biostatistics Workshop, University of Florida, 2017
16. ICSA-China, Shanghai, China 2016
17. Department of Statistics, University of Georgia 2016
18. Department of Statistics, Wuhan University, 2016
19. Department of Statistics, Shangdong University, 2016
20. 2016 China Statistics Conference, Qingdao 2016

21. Department of Statistics, Zhongnan University of Economics, 2016
22. Department of Statistics, University of Florida, 2015
23. NC-Tracs, University of North Carolina at Chapel Hill, 2015
24. IMS-China, Yunnan, China, 2015
25. Department of Biostatistics, University of Pennsylvania, 2014
26. Joint Applied Statistics Symposium of International Chinese Statistical Association & Korean International Statistical Society, Portland, Oregon, 2014
27. Science at the Edge seminar, Michigan state university, 2013
28. Department of Biostatistics, University of Florida, 2013
29. Department of Genetics, University of North Carolina at Chapel Hill, 2013
30. Triangle Statistical Genetics Conference, RTP, 2012
31. The 34th Finnish Summer School on Probability Theory and Statistics, Finland, 2012
32. Second Joint Biostatistics Symposium, Beijing, China 2012
33. Centers of Excellent in Genomic Science (CEGS) 9th Annual meeting, 2011
34. Department of Mathematics and Statistics. Wuhan University, China, 2011
35. Department of Statistics, George Mason University, 2011
36. IMS China, Xi'an, China, 2011
37. Statistical Society of Canada meeting. Canada, 2011
38. ICSA 2011 APPLIED STATISTICS SYMPOSIUM, New York, 2011
39. Royal Netherlands Academy of Sciences and Arts (KNAW): Genomics of gene expression, 2010
40. Department of Biostatistics, Yale University, 2010
41. Department of Mathematics and Statistics, Bowling Green State University, 2010
42. Joint statistical meetings, Vancouver, Canada, 2010
43. Plant and Animal Genome XVII Conference. San Diego, CA, 2009
44. Statistical Genomics workshop, Institute for Mathematical Sciences. Singapore, 2009
45. Department of Statistics, Duke University, 2008
46. Departments of Statistics and Biostatistics, University of Wisconsin at Madison, 2008
47. Department of Mathematics and Statistics. Wuhan University, China, 2007
48. Bioinformatics Center, MD Anderson, 2007
49. International Chinese Statistical Association (ICSA) meeting, 2007

50. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007
51. 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 Biostatsitics, 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, 2022 PhD Dept of Bios. (joint with Wei Sun)

5. Meichen Dong, 2021 PhD, 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. Yue Pan, PhD candidate, Dept of Bios
3. Brown, Eric Dwayne Jr, Dept of Environmental Health Science
4. Yutong Liu, PhD candidate, Dept of Bios
5. Bocha Jia, PhD, Dept of Bios, university of Florida
6. Sinjini Sikar, PhD, Dept of Bios, university of Florida

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

36. 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: Swanson) 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).
4. ENAR student paper award committee 2018, 2019

5. AD hoc reviewer as a NIH/SREA reviewer for a CSR study section meeting held on 3/7/2022-3/8/2022.

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