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

Professor   2015-present
Department of Biostatistics, University of Florida

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

Professor   2012 ~ present
Department of Biostatistics, University of North Carolina, Chapel Hill
Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill

Associate Professor   2007 ~ 2012
Department of Biostatistics, University of North Carolina, Chapel Hill
Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill

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

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

Honors
  1. David P. Byar Young Investigator Award (2001), 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

<u>Book Chapters</u>

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.

<u>Peer reviewed papers</u>

(* student first author advised or co-advised)

1. 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*. Accepted.

2. Yin, Z.*, Xia, K., Chung, W., Sullivan, F.P., and **Zou, F.** (2015) Fast eQTL Analysis for Twin Studies. *Genetic Epidemiology*. 39: 357–365.

3. 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* accepted.

4. 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, accepted.

5. 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.)

6. 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.

7. 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.

8. 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.

9. 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.

10. 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.

11. **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..

12. 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.

13. Chung, W.*, and **Zou, F.** (2014) Mixed effects models for GAW18 longitudinal blood pressure data. *BMC proceedings.* 8: S87.

14. 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.

15. Ghosh, Arpita*, **Zou, F.,** and Wright, F.A. (2013) Unified Analysis of Secondary Traits in Case-Control Association Studies. *JASA*. 108: 566-576.

16. 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.*

17. Gong, Y.*, and **Zou, F**. (2012) Varying coefficient models for mapping quantitative trait loci using recombinant inbred intercrosses. *Genetics,* 190:475-486.

18. 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.

19. 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.

20. Collaborative Cross Consortium (2012) The genome architecture of the Collaborative Cross mouse genetics reference population. *Genetics,* 190:389-402.

21. 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.

22. Lee, S.*, Wright, F.A., and **Zou, F.** (2011) Control of population stratification by correlation-selected principal components. *Biometrics,* 67: 967-974.

23. Liu, F., Dunson, D., and **Zou, F.** (2011) High-dimensional variable selection in meta analysis for censored data. *Biometrics,* 67:504–512.

24. 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).

25. 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.

26. 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.

27. Yuan, Z., **Zou, F.,** and Liu, Y. (2011) Bayesian multiple quantitative trait loci mapping for recombinant inbred intercrosses. *Genetics,* 188:189-195.

28. 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.

29. **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.

30. 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

31. 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.

32. Zhang, X., Pan, F., Xie, Y., **Zou, F.,** and Wang, W. (2010) A General approach for efficient genome-wide two-locus epispastic test in disease association study. *Journal of Computational Biology,* 17**:**401-415.

33. 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

34. 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.

35. **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.

36. 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.

37. 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.

38. **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

39. 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.

40. Zhang, X, **Zou, F.,** and Wang, W. (2009) FastChi: an efficient algorithm for analyzing gene-gene interactions**.** *Pacific Symposium on Biocomputing*, 14:528-39.

41. 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.

42. **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.

43. 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

44. 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.

45. 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.

46. 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.

47. Huang, C., Qin, J., and **Zou, F**. (2007) Empirical likelihood-based inference for genetic mixture models. *The Canadian Journal of Statistics*, 35:563-574.

48. Gelfond, J.*, Ibrahim, J. G. and **Zou, F.** (2007) Proximity model for expression trait loci detection. *Biometrics,* 63:1108–1116.

49. 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.

50. 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.

51. 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.

52. 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.

53. **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.

54. Hu, J., Wright, F.A., and **Zou, F.** (2006) Information-enhanced SVD approaches to estimate expression indexes for oligonucleotide arrays. *JASA*, 101:41-50.

55. **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.

56. 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.

57. 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.

58. 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.

59. Hu, J., **Zou, F.**, and Wright, F.A. (2005) Practical FDR-based sample size calculations in microarray experiments. *Bioinformatics*, 21:3264-3272.

60. **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.

61. 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.

62. Lin, D., and **Zou, F.** (2004) Resampling approach to assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology*, 27:202-214.

63. Diao, G., Lin, D., and **Zou, F**. (2004)   Mapping quantitative trait loci with censored observations. *Genetics,* 168:1689-1698.
64. Churchill, G. A. *et al*. (2004). The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics*, 36:1133-1137.
65. **Zou, F.**, Yandell, B.S., and Fine, J.P. (2003)   Rank based statistical methodologies for QTL mapping. *Genetics,* 165:1599-1605.
66. Flaherty, L. *et al.* (2003). The nature and identification of quantitative trait loci: a community's view. *Nature Genetics Review*, 4:911-916.
67. 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
68. 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.
69. 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.
70. **Zou, F.**, and Fine, J.P. (2002) Note on a partial empirical likelihood. *Biometrika,* 89:958-961.
71. **Zou, F.**, Fine, J.P., and Yandell, B.S. (2002) On empirical likelihood for a semiparametric mixture model. *Biometrika*, 89:61-75.
72. 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.
73. **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 Biostatistics, University of Pennsylvania, 2014
2. Joint Applied Statistics Symposium of International Chinese Statistical Association & Korean International Statistical Society**,** Portland, Oregon, 2014
3. Science at the Edge seminar, Michigan state university, 2013
4. Department of Biostatistics, University of Florida, 2013
5. Department of Genetics, University of North Carolina at Chapel Hill, 2013
6. Triangle Statistical Genetics Conference, RTP, 2012
7. The 34th Finnish Summer School on Probability Theory and Statistics, Finland, 2012
8. Second Joint Biostatistics Symposium, Beijing, China 2012
9. Centers of Excellent in Genomic Science (CEGS) 9th Annual meeting, 2011

10. Department of Mathematics and Statistics. Wuhan University, China, 2011
11. Department of Statistics, George Mason University, 2011
12. IMS China, Xi'an, China, 2011
13. Statistical Society of Canada meeting. Canada, 2011
14. ICSA 2011 APPLIED STATISTICS SYMPOSIUM, New York, 2011
15. Royal Netherlands Academy of Sciences and Arts (KNAW): Genomics of gene expression, 2010
16. Department of Biostatistics, Yale University, 2010
17. Department of Mathematics and Statistics, Bowling Green State University, 2010
18. Joint statistical meetings, Vancouver, Canada, 2010
19. Plant and Animal Genome XVII Conference. San Diego, CA, 2009
20. Statistical Genomics workshop, Institute for Mathematical Sciences. Singapore, 2009
21. Department of Statistics, Duke University, 2008
22. Departments of Statistics and Biostatistics, University of Wisconsin at Madison, 2008
23. Department of Mathematics and Statistics. Wuhan University, China, 2007
24. Bioinformatics Center, MD Anderson, 2007
25. International Chinese Statistical Association (ICSA) meeting, 2007
26. The Banff International Research Station for Mathematical Innovation and Discovery workshop: Statistical Analysis of High-Throughput Genetic Data. Canada, 2007
27. 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

Guidance of Doctoral Research
1. Kyungsu Kim, PhD candidate, Dept of Bios.
2. Li Dong, PhD candidate, Dept of Bios.
3. James Xenakis, PhD candidate, Dept of Bios.
4. Zhaoyu Yin, 2014 PhD, Dept of Bios. *"Statistical Analyses of High Throughput Genetics and Genomics Data"*
   Current position: Biostatistician, Bristol-Myers Squibb.
5. Wonil Chung, 2013 PhD, Dept. of Bios. *"Bayesian Multiple Quantitative Trait Loci (QTL) Mapping For Longitudinal Data"*
   Current position: Postdoc, Harvard University
6. 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
7. Yi Gong, 2011 PhD, Dept. of Bios. "*Variable Selection in Varying Coefficient Models for Mapping Quantitative Trait Loci*".
   Current position: Mathematical Statistician, SAS
8. 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.
9. 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
10. 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
11. 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*".
2. Joe Rigdon 2010 "*The Hamming Distance as a Measure of Genetic Heterogeneity*".
3. Tania Robbins, 2004 "*Combining Microarrays with QTL Analysis*".
4. Niki Arya, 2002 "*QTL Analysis of Body Weight Gain in Recombinant Inbred Intercross Mice*".

Service on Doctoral Committee
1. Chen-Ping Fu, PhD candidate, Department of Computer Science
2. Angela Yanyi. Liu, PhD candidate, Department of Epidemiology
3. Alison Wise DrPH candidate, Department of Biostatistics
4. Ting-huei Chen, PhD 2014, Department of Biostatistics

5. Ja-an Lin, PhD, 2013 Department of Biostatistics
6. David Kessler, 2013 Department of Biostatistics
7. Zhaowei Hua, PhD, 2011 Department of Biostatistics
8. Chaeryon Kang, PhD, 2011 Department of Biostatistics
9. Yihui Zhou, PhD, 2011 Department of Biostatistics
10. Shiliang Wang, PhD, 2011 Department of Cell & Molecular Physiology
11. Xiang Zhang, PhD, 2011 Department of Computer Science
12. Rong Jiang, PhD, 2010 Department of Environment Sciences & Engineer
13. Vonn Walter, PhD, 2010 Department of Biostatistics
14. John Schwarz, PhD, 2010 Department of Biostatistic
15. Lindsey Ho, DrPh, 2010 Department of Biostatistics
16. Tsui-Shan (Eva) Lu, PhD, 2009 Department of Biostatistics
17. Chevonne Eversley, PhD, 2009 Department of Genetics
18. Emily Kistner, PhD, 2005 Department of Biostatistics
19. Guoqing Diao, PhD, 2005 Department of Biostatistics
20. Andrew Sterrett, PhD, 2005 Department of Biostatistics
21. Chaehyung Ahn, PhD, 2005 Department of Biostatistics
22. Szu–Yun Leu, PhD, 2005 Department of Biostatistics
23. 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 (2011-2015)
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. R01-MH092335 (PI: Santelli) "Genome-wide Identification of Variants Affecting Early Human Brain Development" NIH (2011-2016) Role: Investigator.
2. R01 GM105785-01A1(PI: Sun) "Statistical Methods for RNA-seq Data Analysis" NIH (2014-2018) Role: Co-investigator.

3. R21 MH097173-02 (PI: Sullivan) "Biomarkers of Olanzapine-induced Weight Gain in Mice" NIH (2012-2015) Role: Investigator.

4. R01-ES019315 (PI: Fry) "In Utero Exposure to Arsenic, Links to Epigenetic Alterations and Disease" NIH (2010-2015) Role: Investigator.

5. P50-HG006582 (PI: Pardo-Manuel de Villena) "An Interdisciplinary Program for Systems Genomics of Complex Behaviors" NIH (2011-2014) Role: Co-investigator.

6. R01-DE018104 (PI: Everett) "Genetic Determinants of Physiological Responses to Fluoride in Bone" NIH (2008-2013) Role: Co-Investigator.

7. R01-CA132887 (PI: Olshan) "Genetic Susceptibility Factors in the Etiology of Neuroblastoma" NIH (2008-2013). Role: Co-Investigator.

8. R01-HL095396 (PI: Knowles) "Molecular Phenotypes for Cystic Fibrosis Lung Disease" NIH (2008-2012) Role: Investigator.

9. GIL (PI: Lin) Gillings Innovation Laboratory (2009-2012) Role: Investigator.

10. RC2-MH089951(PI: Sullivan) "Integration of Genomics & Transcriptomics in Normal Twins & Major Depression" NIH (2009-2011) Role: Investigator.

11. R01-DK066368 (PI: Knowles) "Genetic Modifiers of CF Liver Disease" NIH (2004-2009) Role: Co-Investigator.

12. R01-CA082659 (PI: Lin) "Statistical Methods in Current Cancer Research" NIH (2004-2008) Role: Co-Investigator.

13. R01-CA082659 (PI: Lin) "Statistical Methods in Current Cancer Research" (2000-2004) Role: Co-Investigator.

14. U54-MH066418(PI: Piven) "Gene-Brain-Behavior Relationships in Autism" NIH (2002-2007) Role: Investigator.

15. P30 ES10126-01A1(PI: Swenberg) "UNC-CH Center for Environmental Health & Susceptibility" NIH (2001-2005) Role: Biostatistician.

14. P30-ES010126(PI: Swenberg) "UNC-CH Center for Environmental Health & Susceptibility" NIH (2005-2010) Role: Biostatistician.

15. R01-DA023690(PI: Tarantino) "Organismal and Genetic Networks in Drug Reward and Reinforcement" NIH (2009-2018) Role: Investigator.

16. P50-MH090338(PI: Pardo-Manuel de Villena) "An Interdisciplinary Program for Systems Genomics of Complex Behaviors" NIH (2009-2011) Role: Investigator.

17. P20-RR020751(PI: Wilhelmsen) "The Carolina Center Exploratory Genetic Analysis" NIH (2004-2007) Role: Co-Investigator.

18. RD-83272001(PI: Wright) Computational Toxicology-EPA Center (2005-2011) Role: Co-Investigator.

Service

NIH Reviewer

1. Ad hoc member of the Genetic Variation and Evolution (GVE) Study Section (2011 & 2012).

2. Reviewer of NIH Center for Scientific Review Special Emphasis Panel (2014).

Editorial Activities

1. Associate Editor: Genetics

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
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 Department of Biostatistics
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