Jung-Ying Tzeng

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Professor, Department of Statistics and Bioinformatics Research Center, North Carolina State University, Raleigh NC, USA
Visiting Professor, Institute of Epidemiology and Preventive Medicine, National Taiwan University, Taipei, Taiwan
Visiting Professor, Department of Statistics, National Cheng-Kung University, Tainan Taiwan

Mailing Address:
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EDUCATION

Ph.D., Department of Statistics, Carnegie Mellon University, Pittsburgh PA, August 2003
- — Dissertation: Identification of Mutations Affecting Liability to Complex Disease by the Analysis of Haplotypes
- — Advisor: Dr. Kathryn Roeder

M.S., Department of Statistics, Carnegie Mellon University, Pittsburgh PA, May 2000

M.S., Division of Biostatistics, Graduate Institute of Epidemiology, National Taiwan University, Taiwan, January 1997
- — Thesis: Spatial Model Selection Using Bayes Factor and Ratio of Variabilities
- — Advisor: Dr. Chuhsing Kate Hsiao & Dr. Chieh-Jen Chen

B.A., Department of Public Health, June 1994. Major in epidemiology.

POSITIONS AND EMPLOYMENT

Professor, 2016 – present, Department of Statistics and Bioinformatics Research Center, NC State University, Raleigh NC

Visiting Professor, 2016-present, Institute of Epidemiology and Preventive Medicine, National Taiwan University

Visiting Professor, 2016-present, Department of Statistics, National Cheng-Kung University, Tainan Taiwan

Visiting Associate Professor, 2013-2016, Department of Statistics, National Cheng-Kung University, Tainan Taiwan

Associate Professor, 2010 – 2016, Department of Statistics and Bioinformatics Research Center, NC State University, Raleigh NC

Faculty, 2008 – present, Master of Veterinary Public Health Program, NC State University, NC

Faculty, 2005 – present, Genomic Science Graduate Program, NC State University, NC

Assistant Professor, 2003 – 2010, Department of Statistics and Bioinformatics Research Center, NC State University, Raleigh NC

RESEARCH INTRESTS

Statistical methods for understanding genetic mechanisms for complex traits; specific topics include: polygenic approaches based on variance components, genetic similarity, kernel machines, tensor regressions, and penalized regressions; statistical modeling of marker-set and gene-set association analysis for diseases and pharmacogenetics, CNV analysis, allele-specific expression, epigenomic analysis, integrative analysis of multi-omic data, network-guided inference on global and local variant identification in genomic studies, joint screening of whole genome main and interactive effects.

PUBLICATIONS

Published/In press:

1. Wang, C., **Tzeng, J.Y.***, Wu, P.Z., Preisig, M., Hsiao, C.K.* (2018) Re-examining dis/similarity-based tests for rare-variant association with case-control samples. *Genetics,* 209:105-113 (*:co-corresponding authors). PMCID: PMC5937191
2. Luo, Y., Maity, A., Wu, M.C., Smith, C., Duan, Q., Li, Y., **Tzeng, J.Y.** (2018) On the substructure controls in rare variant analysis --- principal components or variance components? *Genetic Epidemiology,* 42:276-287. PMCID: PMC5851819
3. Green, A.J., Hoyo, C., Mattingly, C.J., Luo, Y., **Tzeng, J.Y.**, Murphy, S.K., Buchwalter, D.B., Planchart, A. (2018) Cadmium Exposure Increases the Risk of Juvenile Obesity: A Human and Zebrafish Comparative Study. *International Journal of Obesity,* in press
4. Maity, A., Zhao, J., Sullivan, P.F., **Tzeng, J.Y.** (2018). Inference on phenotype-specific effects of genes using multivariate kernel machine regression. *Genetic Epidemiology,* 42:64-79*.* PMCID: PMC5768462*.*
5. Kong, D., Maity, A., Hsu, F.C., **Tzeng, J.Y.** (2018) Rejoinder to "A note on testing and estimation in marker-set association study using semiparametric quantile regression kernel machine". *Biometrics*, in press. PMCID: PMC5932282
6. Chang, S.M., **Tzeng, J.Y.**, Chen, R.B. (2017) Fast Bayesian variable screenings for binary response regressions with small sample size. *Journal of Statistical Computation and Simulation*, 87, 2708-2723*.* PMCID: PMC5653235
7. Davenport, C.A., Maity, A., Sullivan, P.F., **Tzeng J.Y.** (2017) A powerful test for SNP effects on multivariate binary outcomes using kernel machine regression. *Statistics in Biosciences*, in press. NIHMSID: NIHMS895665
8. Lou, Y.*, McCullough, L.E.*, **Tzeng, J.Y.**#, Darrah, T., Vengosh, A., Maguire, R.L., Maity, A., Hodge, C., Murphy, S.K.,. Mendez, M.A., Hoyo, C.# (2017) Maternal blood cadmium, lead and arsenic levels, nutrient combinations, and offspring birthweight. *BMC Public Health*, 17:354. PMCID: PMC5402649. (*: equal contribution; #: co-corresponding authors)
9. Jeng, X.J., Daye, Z.J., Lu, W., **Tzeng, J.Y.** (2016) Rare variants association analysis in large-scale sequencing studies at the single locus level. *PloS Computational Biology,* 12(6):e1004993*.* PMCID: PMC4927097
10. Kong, D., Maity, A., Hsu, F.C., **Tzeng, J.Y.** (2016) Testing and estimation in marker-set association study using semiparametric kernel quantile regression. *Biometrics*, 72:364-71. PMCID: PMC4870165
11. Hung, H., Lin, Y.T., Chen, P., Wang C.C., Huang, S.Y., **Tzeng, J.Y.** (2016) Detection of gene-gene interactions by multistage sparse and low-rank regression. *Biometrics,* 72:85-94. PMCID: PMC4760921

12. Zhang, G., Huang, K.C., Xu, Z., **Tzeng, J.Y.**, Conneely, K.N., Guan, W., Kang, J., Li Y. (2016) Across-platform imputation of DNA methylation levels incorporating non-local information using penalized functional regression. *Genetic Epidemiology,* 40:333-40. PMCID: PMC4862742
13. **Tzeng, J.Y.**, Magnusson, P.K.E., Sullivan, P.F., the Swedish Schizophrenia Consortium, Szatkiewicz, J. (2015). A new method for detecting associations with rare copy-number variants. *PLOS Genetics,* 11:e1005403. PMCID: PMC4592002
14. Marceau, R., Lu W. Sale, M.M., Bradford, B.M., Williams, S.R., Hsu, F.C., **Tzeng, J.Y.** (2015). A fast multiple-kernel method with applications to detect gene-environment interaction. *Genetic Epidemiology,* 39:456-68. PMCID: PMC4544636
15. Hu, Y., Sun, W., **Tzeng, J.Y.**, Perou, C.M. (2015). Proper use of allele-specific expression improves statistical power for cis-eQTL mapping with RNA-Seq data, *Journal of tshe American Statistical Association,* 110:962-974. PMCID: PMC4642818
16. Neely, M.L., Bondell, H.D., **Tzeng, J.Y.** (2015) A penalized likelihood approach for pharmacogenetic studies via understanding haplotype effect structures for gene and gene-drug interactions. *Biometrics,* 71:529-37. PMCID: PMC4480191.
17. Zhao, G., Marceau, R., Zhang, Z., **Tzeng, J.Y.** (2015). Assessing gene-environment interactions for common and rare variants with binary traits using gene-trait similarity regression. *Genetics,* 199:695-710. [This paper is a highlighted article in *Genetics*.]
18. Wang, Z., Maity, A., Luo, Y., Neely, M.L., and **Tzeng, J.Y.** (2015). Complete effect-profile assessment in association studies with multiple genetic and environmental factors. *Genetic Epidemiology*, 39:122-33
19. Wang, Z., Maity, A., Hsiao, C.K., Voora, D., Kaddurah-Daouk, R., **Tzeng, J.Y.** (2015). Module-based association analysis for omics data with network structure. *PLOS One,* 10:e0122309
20. Network and Pathway Analysis Subgroup of Psychiatric Genomics Consortium. (2015) Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience,* 18:199-209.
21. Maier R, Moser G, Chen GB, Ripke S; Cross-Disorder Working Group of the Psychiatric Genomics Consortium, Coryell W, Potash JB, Scheftner WA, Shi J, Weissman MM, Hultman CM, Landén M, Levinson DF, Kendler KS, Smoller JW, Wray NR, Lee SH. (2015) Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *Am J Hum Genet.* 96:283-94.
22. Byrne EM; Psychiatric Genetics Consortium Major Depressive Disorder Working Group, Raheja UK, Stephens SH, Heath AC, Madden PA, Vaswani D, Nijjar GV, Ryan KA, Youssufi H, Gehrman PR, Shuldiner AR, Martin NG, Montgomery GW, Wray NR, Nelson EC, Mitchell BD, Postolache TT. (2015) Seasonality shows evidence for polygenic architecture and genetic correlation with schizophrenia and bipolar disorder. *J Clin Psychiatry.* 76:128-34.
23. **Tzeng, J.Y.***, Lu, W.*, Hsu, F.C. (2014). Gene-level pharmacogenetic analysis on survival outcomes by gene-trait similarity regression. *Annals of Applied Statistic,* 8:1232-1255. (*= equal contribution)
24. Wang, X., Zhang, D., **Tzeng, J.Y.** (2014) Pathway-guided Identification of Gene-Gene Interaction. *Annals of Human Genetics.* 78:478-491.
25. Hu, J., **Tzeng, J.Y.** (2014) Integrative gene set analysis of multi-platform data with sample heterogeneity. *Bioinformatics. 30:1501-7. PMID: 24489370*
26. Wright, F.A., Sullivan, P.F., Brooks, A.I., Zou, F., Sun, W., Xia, K., Madar, V., Jansen, R., Chung, W., Zhou, Y.H., Abdellaoui, A., Batista, S., Butler, C., Chen, G., Chen, T.H., D'Ambrosio, D., Gallins, P., Ha, M.J., Hottenga, J.J., Huang, S., Kattenberg, M., Kochar, J., Middeldorp, C.M., Qu, A., Shabalin, A., Tischfield, J., Todd, L., **Tzeng, J.Y.**, van Grootheest, G., Vink, J.M., Wang, Q., Wang, W., Wang, W., Willemsen, G., Smit,

J.H., de Geus, E.J., Yin, Z., Penninx, B.W., Boomsma, D.I. (2014) Heritability and genomics of gene expression in peripheral blood. *Nature Genetics.* 46:430-7

27. Wang, X., Epstein M.P., **Tzeng, J.Y.** (2014) Analysis of gene-gene interactions using gene-trait similarity regression. *Human Heredity, 78:17-26.*
28. Zhang, A.J., **Tzeng, J.Y.**, Chow, S.C. (2013) Establishment of reference standards in biosimilar studies. *Generics and Biosimilars Initiative Journal*. 2.
29. Zhang, A.J., **Tzeng, J.Y.**, Chow, S.C. (2013) Statistical considerations in biosimilar assessment using biosimilarity index. *Journal of Bioequivalence and Bioavailability.* 5: 209-214.
30. Cross-Disorder Group of the Psychiatric Genomics Consortium (2013) Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*. 45:984-94.
31. Cross-Disorder Group of the Psychiatric Genomics Consortium. (2013) Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. *Lancet.* 381:1371-9.
32. Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium. (2013) A mega-analysis of genome-wide association studies for major depressive disorder. *Molecular Psychiatry.* 18:497-511.
33. Maity, A., Sullivan, P.F., **Tzeng, J.Y.** (2012). Multivariate Phenotype Association Analysis by Marker-Set Kernel Machine Regressions. *Genetic Epidemiology.* 36:686-95. PMCID: PMC3703860
34. Pongpanich, M., Neely, M.L., **Tzeng, J.Y.** (2012). On the aggregation of multimarker information for marker-set and sequencing data analysis: genotype collapsing vs. similarity collapsing. Invited submission to *Frontiers in Statistical Genetics and Methodology.* 2:110.
35. Sullivan, P. 96 Psychiatric Genetics Investigators. (2012) Don't give up on GWAS. *Mol Psychiatry*. 17:2-3.
36. **Tzeng, J.Y.**, Zhang, D., Pongpanich, M., Smith, C., McCarthy, M.I., Sale, M.M., Bradford, B.M., Hsu, F.C., Thomas, D.C., Sullivan, P.F. (2011). Detecting gene and gene-environment effects of common and rare variants on quantitative traits: A marker-set approach using gene-trait similarity regression. *The American Journal of Human Genetics*. 89:277-288.
37. Lee, M.H., **Tzeng, J.Y.**, Huang, S.Y., Hsiao, C.K. (2011) Combining an evolution-guided clustering algorithm and haplotype-based likelihood ratio test in family-based association studies. *BMC Genetics.* 12:48.
38. Koehler, M., Bondell, H. **Tzeng, J.Y.** (2010). Evaluating haplotype effects in case-control studies via penalized-likelihood approaches: prospective or retrospective analysis? *Genetic Epidemiology*. 34:892-911.
39. Pongpanich, M., Sullivan, P.F., **Tzeng, J.Y.** (2010). A quality control algorithm for filtering SNPs in genome-wide association studies. *Bioinformatics.* 15:1731-1737.
40. **Tzeng, J.Y.***, Lu, W.*, Farmen, M.W., Liu, Y., Sullivan, P.F. (2010). Haplotype-based Pharmacogenetic analysis for longitudinal quantitative traits in the presence of dropout. *Journal of Biopharmaceutical Statistics*. Invited submission for special issue "Statistical Genomics in Clinical Trials." 20:334-350. (*= equal contribution)
41. **Tzeng, J.Y.**, Bondell, H. (2010) A comprehensive approach to haplotype specific analysis via penalized likelihood. *European Journal of Human Genetics*. 18:95-103.
42. Liu, Y., Li, Y.J, Satten, G., Allen, A.S., **Tzeng, J.Y.** (2009). A regression-based association test for case-control studies that uses inferred ancestral haplotype similarity. *Annals of Human Genetics.* 73:520-526.

43. **Tzeng, J.Y.**, Zhang, D., Chang, S.M., Thomas, D.C., Davidian, M. (2009) Gene-Trait Similarity Regression for Multimarker-Based Association Analysis. *Biometrics*. 65:822-832. PMCID: PMC2748404
44. Sullivan, P.F., de Geus, E.J., Willemsen, G., James, M.R., Smit, J.H., Zandbelt, T., Arolt, V., Baune, B.T., Blackwood, D., Cichon, S., Coventry, W.L., Domschke, K., Farmer, A., Fava, M., Gordon, S.D., He, Q., Heath, A.C., Heutink, P., Holsboer, F,, Hoogendijk, W.J., Hottenga, J.J., Hu, Y., Kohli, M., Lin, D., Lucae, S., Macintyre, D.J., Maier, W., McGhee, K.A., McGuffin, P., Montgomery, G.W., Muir, W.J., Nolen, W.A., Nothen, M.M., Perlis, R.H., Pirlo, K., Posthuma, D., Rietschel, M., Rizzu, P., Schosser, A., Smit, A.B., Smoller, J.W., **Tzeng, J.Y.**, van Dyck, R., Verhage, M., Zitman, F.G., Martin, N.G., Wray, N.R., Boomsma, D.I., Penninx, B.W.. (2009) Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. *Molecular Psychiatry*. 14:359-75.
45. Jones, M.L., Epstein M.P., Kao, J.T., Satten, G., Allen, A.S., **Tzeng, J.Y.** (2008). A regression-based association test using inferred ancestral haplotype similarity. Institute of Statistics Mimeo Series No.2611
46. Psychiatric GWAS Consortium Coordinating Committee. (2009). Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *The American Journal of Psychiatry*. 166:540-556.
47. Sullivan, P.F., Lin, D., **Tzeng, J.Y.**, van den Oord, E.J.C.G.,Perkins, D., Stroup, T.S., Wagner, M., Lee, S., Wright, F.A., Zou, F., Liu, W., Downing, A.C., Lieberman, J.A., Close, S.L. (2008) Genomewide association for schizophrenia in the CATIE study. *Molecular Psychiatry*. 13:570-84
48. **Tzeng, J.Y.**, Zhang, D. (2007). Haplotype-based Association Analysis via Variance Component score test. *The American Journal of Human Genetics*, 81:939-963.
49. Wen, S.H , **Tzeng, J.Y.**, Kao, J.T., and Hsiao, C.K. (2006). A Two-stage Design for Multiple Testing in Large-scale Association Studies. *Journal of Human Genetics*. 51:523-532.
50. **Tzeng, J.Y.**, Wang, C.H., Kao, J.T., and Hsiao, C.K. (2006). Regression-based association analysis with clustered haplotypes using genotypes. *The American Journal of Human Genetics*, 78:231-242.
51. **Tzeng, J.Y.** and Roeder, K. (2006). Invited Discussion of Likelihood-Based Inference on Haplotype Effects in Genetic Association Studies by Lin and Zeng. *Journal of the American Statistical Association*, 101:111-114
52. **Tzeng, J.Y.** (2005). Evolutionary-based Grouping of Haplotypes in Association Analysis. *Genetic Epidemiology*, 28:220-231.
53. **Tzeng, J.Y.**, Byerley, W., Devlin, B., Roeder, K. Wasserman, L. (2003). Outlier detection and false discovery rates for whole-genome DNA matching. *Journal of the American Statistical Association*, 98:236-246.
54. **Tzeng, J.Y.**, Devlin, B., Wasserman, L. and Roeder, K. (2003). On the identification of disease mutations by the analysis of haplotype similarity and goodness-of-fit. *The American Journal of Human Genetics*, 72:891-902.
55. Hsiao, C.K., **Tzeng, J.Y.**, and Wang, C.H. (2000). Comparing the performance of two indexes for spatial model selection: applications to two mortality data. *Statistics in Medicine*, 19:1915-1930.
56. **Tzeng, J.Y.**, Hsiao, C.K. and Chen, C.J. (1998). Spatial model selection using Bayes factor and ratio of variabilities for asthma mortality data. *Chinese Journal of Public Health*, 17:158-169.

Submitted:

57. Marceau West, R., Lu, W., Rotroff, D. M., Kuenemann, M., Chang, S.M., Wagner, M.J., Buse, J.B., Motsinger-Reif, A., Fourches, D., **Tzeng, J.Y.** (2018) Identifying individual risk rare variants using protein structure-guided local tests. *Submitted.*

58. Jeng, X.J., Zhang, T., **Tzeng, J.Y.** (2018) Adaptive false negative control under dependence with genomic applications. *Submitted.*
59. Rhyne, J., **Tzeng, J.Y.,** Zhang, T., Jeng, X.J. (2018) eQTL Mapping via Effective SNP Ranking and Screening. *Submitted.*
60. Yao, T.C., Chung, R.H., Lin, C.Y., Tsai, P.C., Chang, W.C., Yeh, K.W., Tsai, M.H., Liao, S.L., Hua, M.C., Lai, S.H., Chang, S.W., Yu, Y.W., Hsu, J.Y., Chang, S.C., Cheng, W.C., Hu, D., Hong, X., Burchard, E.G., Wang, X., **Tzeng, J.Y.**, Tsai, H.J., Huang, J.L. (2018) Genetic loci determining total immunoglobuline levels from birth through adulthood. *Submitted.*

Book Chapters

61. **Tzeng, J.Y.** and Maity, A. (2017) Marker-set approaches for assessing gene-environment and gene-gene interactions at gene level". In *Complex Phenotypes: Methodological Issues in Gene-Environment Interactions*", edited by Windle, M. MIT Press.
62. **Tzeng, J.Y.** (2007). EM Algorithm. In *the Encyclopedia of Measurement and Statistics*, edited by Neil Salkind. Sage Publications.
63. Hsiao, C.K., Chen, C.J., Shih, Y.-F., Lin, LL.-K., Hung, P.T., Yao, C.L., Su, T.C., Lin, T.C., **Tzeng, J.Y.**, and Chen, Y. (2000). Design and statistical analysis for the myopia intervention trial in Taiwan. In *Myopia Updates II* (pp. 161-164), edited by Lin, L.L.-K., Shih, Y.-F. and Hung, P.T. Springer-Verlag, Tokyo.
64. Cheng, Y.H. and **Tzeng, J.Y.** (1997). Chinese version of "*Primer of Biostatistics* (4th ed.) by Glantz, S.A.", McGraw-Hill, Taipei.

REASERCH GRANTS

Current:

04/2010-03/2020 P01CA142538 (Davidian, Kosorok, Owzar) National Institutes of Health. *Statistical Methods for Cancer Clinical Trials.* Role: Co-Investigator

02/2017- 01/2019 GRIP (Wright) RTI International. *The NCSU/RTI Program In Genetic Discovery and Prediction (PGDP)*. Role: Co-Investigator

Completed:

08/2014–07/2017 MOST 103-2314-B-002-039-MY3 (Hsiao) Ministry of Science and Technology of Taiwan. *Using Similarity Measure to Cluster Genetic Markers for Genomewide Association Studies and Integrative Analysis*. Role: Co-Investigator

07/2015-06/2016 2015-2866 (Tzeng) NCSU Faculty Research and Professional Development Grant. *Statistical Methods for Integrative Gene-Set Analysis of Multi-platform Data.* Role: Principle Investigator

04/2012–03/2016 R01HL110380 (Buse and Wagner) National Heart, Lung and Blood Institute. *Exome-Wide Association Study of ACCORD Lipid Trial.* Role: Co-Investigator

07/2014-06/2015 2014-2812 (Tzeng) NCSU Faculty Research and Professional Development Grant. *Statistical Methods for Polygenic Genomic Data Analysis.* Role: Principle Investigator (PI)

04/2009-03/2013 R01MH084022 (Tzeng) National Institutes of Health. *Genome-wide Haplotype Association Analysis in Mental Disorders*. Role: PI

07/2009-06/2012 K23MH085165 (Meltzer-Brody) National Institutes of Health. *HPA Stress Reactivity and Genetic Influences in Postpartum Depression*. Role: Consultant.

03/2006-02/2009 R01MH074027 (Sullivan) National Institutes of Health. *Replication of Schizophrenia Associations in CATIE*. Role: Subcontract PI from UNC-CH.

01/2007-12/2011 NHRI-Ex96-9607 (Juo) National Health Research Institutes of Taiwan. *Genetic Susceptibility to Intermediate Phenotypes for Stroke and Myocardial Infarction*. Role: Co-Investigator.

08/2005-07/2009 DMS-0504726 (Tzeng) National Science Foundation. *Haplotype-based Association Modeling for Whole-Genome Scan and Candidate Gene Studies*. Role: PI

HONORS

- Fellow, American Statistical Association (2018)
- Receipt of the NCSU "*Thank a Teacher*" program (for the Fall teaching of 2012, 2013, 2014, 2015, 2016, 2017)
- Elected Full Member of Sigma Xi Science Research Society (2004)
- Umesh Gavasakar Thesis Award, Carnegie Mellon University, Pittsburgh, PA (2003)
- IMS Laha Award, San Francisco, CA (2003)
- Graduate Scholarship, Carnegie Mellon University, Pittsburgh, PA (1998-2003)
- Professor Wen-Chen Chen Scholarship, Pittsburgh, PA (1998)
- Graduate Thesis Award of the National Public Health Association, Taipei, Taiwan (1997)
- Li-Ching Graduate Thesis Scholarship, Taipei, Taiwan (1996)
- Honorary member of the Phi Tau Phi Scholastic Honor Society at National Taiwan University, Taipei, Taiwan (1994)
- President Awards, National Taiwan University, Taipei, Taiwan (1991-1994, six times)

PROFESSIONAL SERVICES & ACTIVITIES

Editorial & Referee Work:

- Associate Editor: *Biometrics* (2007-present)
- Associate Editor: *Journal of Biopharmaceutical Statistics* (2012-present)
- Guest Associate Editor: *Statistica Sinica* (May-Aug 2014)
- Statistical Advisory Board: *PLOS One* (2013-present)
- Review Editorial Board: *Frontiers in Statistical Genetics and Methodology* (2010-present)
- Editorial board: *Journal of Clinical Bioinformatical Science* (2010-present)
- Editorial board: *ISRN Genetics* (2012-2014)
- Panel referee:
  — NIH *Special Emphasis Panel* for PRAT Fellowship application (Mar 2018)
  — NIH *Biostatistical Methods and Research Design* (BMRD) study section (Feb 2016)
  — NIH *Special Emphasis Panel* (Mar 2014)
  — NIH *Genomics, Computational Biology and Technology* (GCAT) study section (Oct 2013)
  — NIH *Genomics, Computational Biology and Technology* (GCAT) study section (Oct 2012)
  — NIH *Genomics, Computational Biology and Technology* (GCAT) study section (Oct 2011)
  — NIH *Genomics, Computational Biology and Technology* (GCAT) study section (Oct 2010)
  — NIMH Grand Opportunities (GO): *Genomic Profiling and Genomic Technologies in Mental Disorders* (June 2009)
  — NIH *Erythrocyte & Leukocyte Biology* study section (Feb 2007)
  — NIH *Hemostasis and Thrombosis* study section (Oct 2006; Nov 2006)
- Journal referee:
  American Journal of Human Genetics, Annals of Human Genetics, Genetic Epidemiology, Genetics, Human Genetics, Journal of the American Statistical Association, Journal of

Biopharmaceutical Statistics, PLOS Genetics, PLOS One, Statistics in Medicine, Theoretical Population Biology, Statistical Applications in Genetics and Molecular Biology

- Other:
  — Fine-mapping group of the Genetic Analysis Workshop 14 (2004)

Committee/Organizer in Conference and Professional Society:

- ASA/ENAR/ICSA Committees
  - — ASA Committee on Award of Outstanding Statistical Application (2017-2019), Chair
  - — ENAR program committee, ASA Section representative of Statistics in Genomics and Genetics, 2018 ENAR
  - — ASA Committee on Student Paper Awards, American Statistical Association (ASA) Section on Nonparametric Statistics, 2016 JSM
  - — ICSA Nomination and Election Committee (2011-2013)
- Conference Session Organizer
  - — 2017 JSM Invited Session *"Recent Statistical Advances in Single-Cell RNA-seq Analysis*," for the ASA Committee on Award of Outstanding Statistical Application, JSM, Baltimore, MD (August 2017).
  - — 2017 ICSA Invited Session "*Statistical Methods for Modelling Data Complexity in Genomics Studies*", ICSA Applied Statistics Symposium, Raleigh NC (June 2017)
  - — 2016 NC-ASA AISC Conference Invited Session "*Recent development in statistical genetics and genomics*," AISC, Greensboro, NC (October 2016)
  - — 2015 JSM Invited Session *"Emerging Statistical Challenges in Revealing Hidden Heritability*," JSM, Seattle, WA (August 2015).
  - — 2013 JSM Invited Session "*Recent Methodological Development in Genomic Studies of the Post-GWAS Era*," Montreal Canada (August 2013)
  - — 2012 JSM Topic-Contributed Session "*Methods Advancement in Complex Genomic Analysis*," San Diego, CA (August 2012).
  - — 2012 ENAR Topic-Contributed Session "*Advanced Statistical Modeling for Complex Omics Data*", Washington DC (Apr 2012).
  - — 2011 JSM Invited Session "*Statistical Modeling of Genetic Sequence Data*," Miami FL (August 2011).
  - — 2010 EITC Invited Session "*Bioinformatics and Biotechnology*," the 10th Emerging information and Technology Conference, Stanford University, San Francisco CA (August 2010)
  - — 2009 EITC Invited Session "*Bioinformatics and Biotechnology*," the 9th EITC Workshop, MIT (August 2009)
  - — 2007 ICSA Invited Session "*Haplotype Analysis in Genome-wise Association Studies*", ICSA Applied Statistics Symposium, Raleigh NC (June 2007)
- Other Services
  - — Co-founder and co-organizer of the *Triangle Statistical Genetics Conference*, North Carolina
    - Founding and Organizing Committee
      - 2011 Triangle Statistical Genetics Conference (Oct 2011), NC State University, Raleigh NC
    - Organizing Committee
      - 2012 Triangle Statistical Genetics Conference (Sep 2012), UNC-Chapel Hill, Chapel Hill NC
      - 2013 Triangle Statistical Genetics Conference (Oct 2013), Duke University, Durham NC

- 2014 Triangle Statistical Genetics Conference (Oct 2014), SAS Inc., Cary, NC
- 2015 Triangle Statistical Genetics Conference (Nov 2015), SAS Inc., Cary, NC
- 2016 Triangle Statistical Genetics Conference (Oct 2016), SAS Inc., Cary, NC

— Organizing committee, Conference "*Haplotype Analysis of Population and Pedigree Data in Association Studies*" University of Alabama, Birmingham (May 2008)

Other activities:

- Invited visiting scholar (Spring 2017) Institute of Epidemiology and Preventive Medicine, National Taiwan University, Taipei, Taiwan
- Invited visiting scholar (July 2015) Institute of Statistical Science, Academia Sinica, Taipei, Taiwan
- Invited visiting scholar (December 2014) Department of Statistics, National Cheng-Kung University, Tainan, Taiwan
- Invited visiting scholar (July 2014) Taida Institute for Mathematical Sciences, National Taiwan University, Taipei Taiwan
- Invited visiting scholar (December 2013) Department of Statistics, National Cheng-Kung University, Tainan, Taiwan
- Invited visiting scholar (July 2012) Taida Institute for Mathematical Sciences, National Taiwan University, Taipei Taiwan
- Invited visiting scholar (July 2011) Taida Institute for Mathematical Sciences, National Taiwan University, Taipei Taiwan
- Faculty Fellow, 2008 – 2009, Statistical and Applied Mathematical Sciences Institute, NC

TEACHING

Regular Semester Courses:

• 2018 Spring	PP610/810G	Genomic Science Journal Club
• 2017 Fall	ST305	Statistical Methods
• 2017 Fall	ST/GN721	Genetic Data Analysis
• 2016 Fall	ST305	Statistical Methods
• 2016 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2016 Spring	ST305	Statistical Methods
• 2016 Spring	PP610/810G	Genomic Science Journal Club
• 2015 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2015 Spring	PP610/810G	Genomic Science Journal Club
• 2015 Spring	ST/GN721	Genetic Data Analysis
• 2014 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2014 Spring	ST361	Introduction to Statistics for Engineers
• 2013 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2013 Spring	ST/GN721	Genetic Data Analysis
• 2013 Spring	PP610/810G	Genomic Science Journal Club
• 2012 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2011 Spring	ST/GN721	Genetic Data Analysis
• 2011 Spring	PP610/810G	Genomic Science Journal Club
• 2010 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2009 Fall	ST361	Introduction to Statistics for Engineers
• 2009 Fall	ST511	Experimental Statistics for Biological Sciences I
• 2008 Fall	ST511	Experimental Statistics for Biological Sciences I

- 2008 Spring ST361 Introduction to Statistics for Engineers
- 2008 Spring ST790G Statistics in Genetic Epidemiology
- 2007 Fall ST361 Introduction to Statistics for Engineers
- 2007 Spring PP610/810G Genomic Science Journal Club
- 2006 Fall ST361 Introduction to Statistics for Engineers
- 2005 Fall ST790G Statistics in Genetic Epidemiology
- 2005 Spring ST361 Introduction to Statistics for Engineers
- 2004 Fall ST361 Introduction to Statistics for Engineers

Short Courses:

- 2017 August Taipei Summer Institute in Statistical Genetics (Module: Association Mapping), National Taiwan University, Taipei Taiwan
- 2017 Spring Statistical Analysis of Genetic Data, National Taiwan University, Taipei Taiwan
- 2016 July Statistical Genomics Workshop on Sequence and Genotype Data Analysis, National Taiwan University, Taipei Taiwan
- 2015 May NCSU Summer Short Course in Statistical Genetics, *Association Mapping*, North Carolina State University, Raleigh, NC
- 2007 July Summer Workshop in Genetic Epidemiology, National Taiwan University, Taipei, Taiwan
- 2005 July Asian Institute in Statistical Genetics (Module: Population Genetic Data Analysis), Yonsei University, Seoul, Korea
- 2005 June Summer Institute in Statistical Genetics (Module: Human Population Genetic Data), North Carolina State University, Raleigh, NC.
- 2004 June Summer Institute in Statistical Genetics (Module: Population Genetic Data Analysis), North Carolina State University, Raleigh, NC

PRESENTATIONS AND SEMINARS

Invited Presentations

1. [Upcoming] Department of Statistics, University of Southern Carolina, Columbia, SC. *Rare variant prioritization using structure-supervised locus-specific tests.*
2. Joint Statistical Meeting, Vancouver, Canada (July 2018): *Rare variant prioritization using structure-supervised locus-specific tests.*
3. Institute of Epidemiology and Preventive Medicine, National Taiwan University (July 2018): Identifying individual risk rare variants using protein structure-guided local tests.
4. Department of Biostatistics, the State University of New York at Buffalo, Buffalo, NY. (March 2018): *Rethinking Single-Locus Analysis in Rare Variant Association Tests.*
5. 2018 IMPACT Symposium, Research Triangle Park, NC (February 2018): *Identifying individual risk rare variants using structure guided local test.*
6. Department of Biostatistics, University of North Carolina-Chapel Hill, Chapel Hill, NC. (October 2017): *Rethinking Single-Locus Analysis in Rare Variant Association Tests.*
7. NCSU-RTI GRIP Meeting, Research Triangle Institute (RTI) Bioinformatics, Research Triangle Park, NC (August 2017): *Marker-set methods for analysis of gene and gene-environment effects*
8. 61st World Statistics Congress, Marrakech, Morocco (July 2017): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
9. International Conference on Advances in Interdisciplinary Statistics and Combinatorics, Greensboro, NC (Oct 2016): *Rare variants association analysis in large-scale sequencing studies at the single locus level*

10. International Indian Statistical Association (IISA) Conference, Corvallis, OR (Aug 2016): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
11. Institute of Epidemiology and Preventive Medicine, National Taiwan University (July 2016): *Set-based association tests for sequence data*
12. ENAR, Austin TX (Mar 2016): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
13. Bioinformatics Research Center Coffee Talk, NCSU (Mar 2016): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
14. Institute of Statistical Science, Academia Sinica, Taipei, Taiwan (July 2015): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
15. Institute of Epidemiology and Preventive Medicine, National Taiwan University (July 2015): *Rare variants association analysis in large-scale sequencing studies at the single locus level*
16. Joint ICSA Applied Statistics Symposium and Graybill Conference, Fort Collins, Colorado (June 2015): *Detection of gene-gene interactions using tensor regression*
17. Department of Statistics, National Cheng-Kung University, Tainan, Taiwan (Dec 2014): *A kernel machine approach for rare copy number variants*
18. SAMSI Bioinformatics Workshop, RTP, NC (October 2014): *Regression methods for genomic data analysis*
19. Taida Institute for Mathematical Sciences, Department of Mathematics, National Taiwan University, Taiwan (July 2014): *Advanced regression methods for genomic data analysis---tensor regression kernel machine regression*
20. The 3rd IMS Asian Pacific Rim Meeting, Taipei Taiwan (July 2014) *A novel collapsing method for rare copy number variants*
21. Banff International Research Station (BIRS) Workshop --- Emerging Statisticall Challenges and Methods for Analysis of Massive Genomic Data in Complex Human Disease Studies, Alberta, Canada (June 2014): *A novel collapsing method for rare copy number variants*
22. Biostatistics Seminar Series, Department of Biostatistics and Epidemiology, University of Pennsylvania (Mar 2014): *Advanced regression methods for genomic data analysis---tensor regression for gene-gene interaction and kernel machine regression for rare cnv analysis.*
23. ENAR, Baltimore, MD (Mar 2014): *A novel collapsing method for rare copy number variants (CNVs)*.
24. Department of Statistics, National Cheng-Kung University (Dec 2013): *Gene-trait similarity regression for aggregation analysis*
25. Genomic Seminar, Wake Forest University (April 2013): *Robust similarity regression for population substructure in rare variant aggregation analyses*,
26. Department of Biostatistics, Yale University (March 2013): *Robust similarity regression for population substructure in rare variant aggregation analyses*,
27. AISC, Greensboro, NC (October 2012): *Robust similarity regression for population substructure in rare variant aggregation analyses*
28. Joint Statistical Meeting, San Diego (August 2012): *Detecting common and rare variants for general traits: gene-trait similarity regression for gene-level analysis.*
29. Taida Institute for Mathematical Sciences, Department of Mathematics, National Taiwan University, Taiwan (July 2012): *Robust similarity regression for population substructure in rare variant aggregation analyses*
30. The 2nd Institute of Mathematical Statics Asia Pasic Rim Meeting, Tsukuba Japan (July 2012): *Similarity collapsing approach for gene-level analysis on common and rare variants with general traits.*
31. NIEHS Symposium, "Emerging Issues in Analysis and Design of Large-Scale Genetic Studies", RTP, NC (May 2012): *Similarity collapsing approach for gene-level analysis on common and rare variants with general traits.*

32. ENAR, Washington DC (Apr 2012): *Similarity collapsing approach for gene-level analysis on common and rare variants with general traits.*
33. IMPACT Symposium, Durham, NC (November 2011): *Gene-trait similarity regression method for gene-level pharmacogenetic analysis*.
34. Department of Statistics and Probability, Michigan State University, East Lansing, MI (November 2011): *Detecting and comprehending marker-set association for common and rare variants*.
35. Jeffrey L. Houpt Lectures in Genome Sciences, Carolina Center for Genome Sciences, University of North Carolina-Chapel Hill, NC, Chapel Hill (October 2011). *Detecting and comprehending marker-set association for common and rare variants*.
36. Division of Biostatistics, Department of Preventive Medicine, University of Sothern California, Los Angeles CA (August 2010). *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*,
37. Workshop on High-Dimensional Data Modeling, Taida Institute for Mathematical Sciences (TIMS), Department of Mathematics, National Taiwan University, Taiwan (July 2011). *A gene-trait similarity regression method for common and rare variants with general trait values.*
38. Workshop on Statistical Frontiers, Institute of Statistical Science, Academia Sinica, Taiwan (December 2010). *Penalized likelihood approaches for haplotype specific analysis in pharmacogenomics,*
39. 2010 Annual Meeting of Chinese Statistical Society and International Statistical Conference, Jhongli, Taiwan (December 2010). *Detecting gene and gene-environment effects of common and rare variants on quantitative traits: A marker-set approach using gene-trait similarity regression*,
40. The 10th Emerging information and Technology Conference, Stanford University, San Francisco CA (August 2010). *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*.
41. The First Joint Biostatistics Symposium, Renmin University, Beijing, China (July 2010). *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*.
42. Department of Biostatistics, Columbia University, New York NY (March 2010). *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression.*
43. Joint seminar of the Institute of Preventive Medicine, Institute of Epidemiology and Research , and Center for Genes, Environment and Human Health, National Taiwan University, Taiwan (January 2010). *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*.
44. Institute of Statistical Science, Academia Sinica, Taiwan (December 2009). *A gene-trait similarity regression for genetic main and interaction effects in genomewide association haplotype analysis*
45. DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University, Piscataway NJ (Aug 2008). A *constrained regression approach for studying haplotype specific effects*
46. University of Alabama at Birmingham, Birmingham, AL (May 2008). *A gene-trait similarity regression for haplotype analysis in genome-wide association studies*
47. National Institute of Environmental Health Sciences, RTP NC (Dec 2007). *Regression-based multi-marker analysis for genome-wide association studies using haplotype similarity*,
48. Department of Biostatistics, University of North Carolina, Chapel Hill NC (Dec 2007). *Regression-based multi-marker analysis for genome-wide association studies using haplotype similarity*

49. Institute of Statistical Science, Academia Sinica, Taiwan (July 2007). *Regression-based multi-marker analysis for genome-wide association studies using haplotype similarity*
50. National Taiwan University, Taiwan (July 2007). *Model-based association analysis via haplotype similarity for genome-wide studies*
51. Department of Statistics, University of Georgia, Athen GA (Feb 2005). *On the improvement of efficacy of haplotype-based association analysis*
52. Department of Statistics, North Carolina State University, Raleigh NC (Aug 2004). *Cladistic clustering of haplotypes in association analysis*
53. Center for Statistical Sciences, Brown University, Providence RI (Feb 2004). *A haplotype-similarity based approach for detecting genetic association*
54. Graduate Institute of Epidemiology, National Taiwan University, Taiwan (Dec 2003). *Identification of disease mutations by the analysis of haplotypes*
55. Institute of Statistical Science, Academia Sinica, Taiwan (Dec 2003). *A haplotype-similarity based approach for detecting genetic association*
56. Division of Biostatistics, University of Southern California, Los Angeles, CA (Nov 2003). *The use of haplotype similarity in detecting genetic association*.

Contributed Presentations

57. *Rare variants association analysis in large-scale sequencing studies at the single locus level*, Annual Meeting of the American Society of Human Genetics, San Francisco, CA (Nov 2015)
58. *Robust similarity regression for population substructure in rare variant aggregation analyses*, Annual Meeting of the American Society of Human Genetics, San Francisco, CA (Nov 2012)
59. *Detecting gene and gene-environment effects of common and rare variants on quantitative traits: A marker-set approach using gene-trait similarity regression*, Annual Meeting of the American Society of Human Genetics, Washington DC (Nov 2010)
60. *A gene-trait similarity regression for genetic main and interaction effects in genomewide association haplotype analysis.* The 3rd Annual Conference in Quantitative Genomics, Harvard University, Boston MA (Oct 2009).
61. *Penalized likelihood approach to haplotype specific analysis*. Joint Statistical Meeting, Denver, CO (August 2008)
62. *Haplotype-based association analysis via variance component score test*, Conference on Emerging Design and Analysis Issues in Genomic Studies in Population Sciences at Harvard University, Boston MA (Oct 2007)
63. *Regression-based association approach using genetic similarity for genomewide association scans*, Joint Statistical Meeting, Salt Lake City UT (Aug 2007)
64. *Model-based association analysis via haplotype similarity for genome-wide studies*, the International Chinese Statistical Association, Raleigh NC (June 2007)
65. *Regression-based association analysis with clustered haplotypes using genotypes*, Joint Statistical Meeting, Minneapolis MN (Aug 2005)
66. *Regression-based association analysis with grouped haplotypes*, Biometric Society ENAR Spring Meeting, Austin TX (Mar 2005)
67. *Evolutionary-based grouping of haplotypes in association analysis*, Taipei Symposium on Statistical Genome, Taipei Taiwan(Dec 2004)
68. *Evolutionary-based grouping of haplotypes in association analysis*, Annual Meeting of the American Society of Human Genetics, Toronto, Canada (Oct 2004)
69. *Pruning reconstructed haplotype frequencies in association analysis*, Spring Meetings of the Eastern North American Region (ENAR) of the International Biometric Society, Pittsburgh, PA (Mar 2004)

70. *Identification of mutations affecting liability to complex disease by the analysis of haplotypes*, Joint Statistical Meetings of the American Statistical Association, San Francisco, CA (Aug 2003)
71. *Outlier detection and false discovery rates for whole genome association studies*, Annual Meeting of the American Society of Human Genetics, San Diego, CA (Nov 2001)
72. *Bayesian tests of spatial autocorrelation*, Joint Statistical Meetings of the American Statistical Association, Anaheim, CA (Aug 1997)

Other --- Conference Presentations by Mentored Students (who is underlined**)**

1. *A fast multiple-kernel method with applications to detect gene-environment interaction*, Marceau R, Lu W, Tzeng JY. Joint Statistical Meeting, Seattle (August 2015)
2. *A fast multiple-kernel method with applications to detect gene-environment interaction*, Marceau R, Lu W, Tzeng JY. Annual Meeting of the American Society of Human Genetics, San Francisco, CA (Oct 2014)
3. *Similarity-based marker-set association tests for gene-environment effects in case-control studies*. Zhao G, Zhang D, Tzeng JY. Joint Statistical Meeting, San Diego (August 2012)
4. *Comprehending gene-based association signals: a penalized regression approach for haplotype based analysis with application in pharmacogenetic studies and individual medicine.* Koehler ML, Bondell HD, Tzeng JY. ENAR, Washington DC (Apr 2012)
5. *Kernel machine quantile regression of multi-dimensional genetic data.* Kong D, Maity A, Tzeng JY. ENAR, Washington DC. (Apr 2012)
6. *Comprehending gene-based association signals: a penalized regression approach for haplotype based analysis with application in pharmacogenetic studies and individual medicine.* Koehler ML, Bondell HD, Tzeng JY. Joint Statistical Meeting, Miami Beach FL (August 2011)
7. *Assessing RNA-seq differential expression levels with low-confidence mapped reads.* Pongpanich M, Tzeng JY, Nielsen D. Annual Meeting of the American Society of Human Genetics, Montreal, Canada (October 2011)
8. *A retrospective method for inference on haplotype main effects and haplotype-environment interactions using clustered haplotypes*. Jones M, Epstein M, Satten G, Allen A, Tzeng JY. Joint Statistical Meeting, Denver, CO (August 2008)
9. *Association studies of case-control data with genotyping uncertainty*. Liu Y, Tzeng JY. Biometric Society ENAR Spring Meeting, Arlington, VA (March 2008)
10. *A Bayesian approach for incorporating prior knowledge in genome-wide association studies*. Ouyang H, Tzeng JY. Biometric Society ENAR Spring Meeting, Arlington, VA (March 2008)

GRADUATE STUDENT ADVISING

Current PhD Advisees:

1. Brucker, Amanda (Statistics)
2. Huang, Yueyang (Bioinformatics)
3. Wang, Yaxu (Bioinformatics)
4. Yang, Meng (Statistics; co-advised with Dr. Eric Chi) Interactive multi-platform genomic data analysis

Independent Research Advisee:

5. Ge, Lin (Statistics) Assessment of effect of metal mixtures.

Completed PhD Advisees:

6. McKendry, Colleen (May 2018; Statistics; co-advised with Dr. Arnab Maity) Association study and risk assessment of children's methylation and growth trajectory using functional mixed models

7. Marceau, Rachel (December 2017; Statistics; co-advised with Dr. Wenbin Lu) Flexible kernel machine methods for complex genomic data. University of North Carolina, Chapel Hill, NC
8. Luo, Yiwen (May 2017; co-major in Bioinformatics and Statistics; co-advised with Dr. Arnab Maity) Statistical methods to study association between environmental, epigenetic and genetic risk factors and child health. Merck, Philadelphia, PA
9. Xue, Shang (May 2017; Bioinformatics; co-advised with Dr. Jim Holland) Genetic Architecture of Domestication and other Complex Traits in Maize. IBM, Philadelphia, PA
10. Zhang, Teng (June 2016; Statistics; co-advised with Dr. Jessie Jeng) Weak signal detection with applications in high-throughput genomic data analysis.
11. Hu, Jun (December 2014; Bioinformatics) integrative analysis of multi-platform genomic data. Omicsoft Inc., Cary, NC
12. Zhao, Jing (December 2014; Bioinformatics; co-advised with Dr. Arnab Maity). Kernel machine regression in presence of multivariate response with application to genetic data.
13. Zhang, Aijing (December 2013; Statistics; co-advised with Dr. Shein-Chung Chow). Statistical methods for assessment of biosimilarity of follow-on biologics. Quantile, Bejing, China
14. Wang, Xin (December 2013; co-major in Bioinformatics and Statistics; co-advised with Dr. Daowen Zhang). Statistical methods for gene-gene interaction: detections and classifications. Omicsoft Inc., Cary, NC
15. Wang, Zhi (December 2013; Bioinformatics). Module-based analysis for "omics" data. quantitative analyst, Fuzzy Logix, Charlotte, NC
16. Zhao, Guolin (August 2013; Statistics; co-advised with Dr. Daowen Zhang). Statistical methods for assessing gene-gene and gene-environment interactions. Biogen Idec, Boston MA
17. Pongpanich, Monnat (May 2012; Bioinformatics). On the SNP-based and sequence-based whole genome studies for complex traits. Faculty, Department of Mathematics and Computer Science. Chulalongkorn University, Thailand
18. Koehler, Meg (August 2011, Statistics; co-advised with Dr. Howard Bondell). Penalized likelihood approaches for haplotype identification and estimation. Faculty, Department of Biostatistics and Bioinformatics, Duke University, Durham, NC
19. Ouyang, Haojun (August 2009, Bioinformatics; co-advised with Dr. Sujit Ghosh) Bayesian approach for nonlinear dynamic system and genome-wide association study. Eli Lilly, Philadelphia, PA
20. Liu, Youfang (December 2008; Bioinformatics) Analytical tools for population-based association studies. Research associate, UNC-Chapel Hill, Chapel Hill, NC
21. Jones, Marti (December 2007; Statistics) A retrospective method for inference on haplotype main effects and haplotype-environment interactions using clustered haplotypes. Biostatistician, PRA Health Sciences, Raleigh, NC

PhD Committee Member:

- Statistics PhD Major
    1. Jacob Rhyne (Current)
    2. Jonathan Leirer (Current)
    3. Mityl Biswas (Current)
    4. Huimin Peng (Summer 2017)
    5. Sarah Hale (Summer 2016)
    6. Adrian Cole (December 2014)
    7. Clemontina Davenport (December 2013)
    8. Chad Brown (December 2012)
    9. Yen-Wei Li (January 2012)
    10. Stacey Jean Winham (May 2011)
    11. Yuhua Su (December 2010)

12. Suraj Anand (December 2008)
13. Miao Yu (August 2007)
14. Amada Helpler (December 2005)

- Bioinformatics PhD Major
  15. Tao Jiang (Current)
  16. Jun Ma (Current)
  17. Patrick Perkins (Current)
  18. Kyle Roell (Current)
  19. Sarah Wisotsky (Current)
  20. Siamak Mahmoudiandehkordi (Fall 2017)
  21. Michele Balik-Meisner (Fall 2017)
  22. Wenjing Lu (December, 2015)
  23. Skylar Marvel (December 2014)
  24. Rachel Myers (December 2010)
  25. Sunil Suchindran (May 2010)
  26. Christine Duarte (December 2009)
  27. Samuel Dickson (Bioinformatics and co-major Statistics, December 2009)
  28. Yunjung Kim (December 2008)
  29. Li Zhang (December 2007)
  30. Jessica Maia (August 2007)
  31. Hao Mei (Bioinformatics and co-major Statistics, August 2007)
  32. Ren-Hua Chung (December 2006)

- Other PhD Major
  33. Sarah Park (Biological Science, Current)
  34. Bolin Dong (Microbiology, Current)
  35. Ali Yahya Almalki (Civil Engineering, May 2018)
  36. Yang Bian (Crop Science, May 2016)
  37. Charlotte Wang (Biostatistics, National Taiwan University, August 2015)
  38. Dorothy Nelson (Textile, May 2015)
  39. Huei-Ting Tsai (Epidemiology, UNC-CH, December 2007)
  40. Peter Marcus Buff (ECE, May 2006)

MS as Chair or Co-Chair

1. Hsin-Yen Wu (Bioinformatics, May 2016), Department of Biochemistry and Molecular Biology, Michigan State University
2. Guowei Li (Statistics, May 2015)
3. Wei Ran (Statistics, May 2014)
4. Ching Wen Lo (Statistics, May 2014)
5. Rongrong Zhou,(Statistics, May 2012)
6. Murilo Machado Brizzotti (Statistics, May 2011)
7. Dong Wang (Statistics, May 2009)

MS as Committee Member

1. Christina Radder (Statistics, May 2013)
2. Ralph Russell Barbare (Statistics, May 2011)
3. Yan Zheng (Bioinformatics Master, May 2010)
4. Christine Finger (Statistics, May 2005)
5. Hillary Chaney (Statistics, October 2015)
6. Ju Chen (Textile, 2011)

7. Joyce Curry (Biomath, May 2008)

DEPARTMENT/UNIVERSITY SERVICES

1. Graduate Faculty Member, 2003 - present
2. Ph.D. Course and Curriculum Committee, Statistics Department, 2006 - 2007
3. Graduate Student Admission Committee, Bioinformatics PhD Program, 2006 - 2008
4. Ph.D. Written Prelim Exam Committees, Statistics Department, 2007
5. Graduate Student Advisory Committee, Bioinformatics PhD Program, 2008 - 2010
6. January Ph.D. and Master Basic Exam Committee, Statistics Department, 2009
7. Faculty Search Committee, Statistics Department, 2007 - 2008
8. Organizer of Student Research Presentation, Bioinformatics PhD Program, 2008 - 2009
9. Faculty Research and Professional Development Grant Committee, Statistics Department, 2011
10. Prelim paper reviewer, Written Prelim Exam, Statistics Department, 2011
11. Faculty Search Committee, Bioinformatics Cluster, Bioinformatics Research Center, Spring 2012
12. Bioinformatician Search Committee, Bioinformatics Consulting and Service Core, 2012
13. Beach Committee, Statistics Department, 2012
14. January Ph.D. and Master Basic Exam Committee, Statistics Department, 2013
15. Ph.D. Written Prelim Exam Committee, Statistics Department, 2013
16. Faculty Search Committee, Bioinformatics Cluster, Bioinformatics Research Center, 2012-2013
17. Peer teaching review (for Drs. Arnab Maity and Ana-Maria), Department of Statistics, Fall 2012
18. New ST512 Section Group (for non-CALS graduate students), Statistics Department, Fall 2013
19. Faculty Search Committee, Statistics Department, 2013 - 2014
20. Faculty Search Committee, Bioinformatics Cluster, 2013 - 2014
21. Post-Tenure Review Committee, Statistics Department, 2013 - 2016
22. Graduate Program Admission Committee, Statistics Department, 2014 - 2015
23. August Ph.D. Basic Exam Committee, Statistics Department, 2015
24. Teaching Mentor: Dr. Rui Song (2014 - 2016)
    Teaching Mentor: Dr. Eric Chi (2015 -)
25. Peer teaching review (for Dr. Jon Stallings), Department of Statistics, Fall 2015
26. Graduate Program Admission Committee, Statistics Department, 2015 – 2016
27. Events Committee, CHHE Symposium, Center for Human Health and the Environment (CHHE) 2016 - 2017
28. Faculty Search Committee, Statistics Department, 2017 - 2018
29. Advancement Committee, Statistics Department: 2018