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RESEARCH INTERESTS

Statistical methods for studying susceptibility genes for complex traits; specific topics include: statistical modeling of multimarker/haplotype association for genome-wide and candidate-gene studies, gene/pathway-based analysis for pharmacogenetics, SNP genotyping error and quality control, and sequence-based association analysis.

PROFESSIONAL EXPERIENCE

Associate Professor, 08/2010 – present, Department of Statistics and Bioinformatics Research Center, NC State University, Raleigh NC

Assistant Professor, 08/2003 – present, Department of Statistics and Bioinformatics Research Center, NC State University, Raleigh NC

Faculty, 11/2005 – present, Genomic Science Graduate Program, NC State University, NC

Faculty, 08/2008 – present, Master of Veterinary Public Health Program, NC State University, NC

Faculty Fellow, 2008 – 2009, Statistical and Applied Mathematical Sciences Institute, NC

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.

REASERCH GRANTS

- 04/2009-03/20012 1 R01 MH084022-01A1 (Tzeng) National Institutes of Health. *Genome-wide Haplotype Association Analysis in Mental Disorders*. Role: Principal Investigator
- 04/2010-03/20015 1 P01 CA142538-01 (Kosorok, Davidian, George) National Institutes of Health. *Statistical Methods for Cancer Clinical Trials*. 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: Principal Investigator
- 07/2009 - 06/2012 K23MH085165-01A (Meltzer-Brody) National Institutes of Health. *HPA Stress Reactivity and Genetic Influences in Postpartum Depression*. Role: Consultant.
- 03/2006-02/2009 R01-MH074027 (Sullivan) National Institutes of Health. *Replication of Schizophrenia Associations in CATIE*. Role: Co-Investigator and Subcontract Principal Investigator from UNC-CH.
- 1/2007 - 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.

PUBLICATIONS

- Tzeng, J.Y., Lu, W., Hsu, F.C. (2012). Gene-level pharmacogenetic analysis on survival outcomes by gene-trait similarity regression. *Submitted*.
- Maity, A., Sullivan, P.F., Tzeng, J.Y. (2012). Multivariate Phenotype Association Analysis by Marker-Set Kernel Machine Regressions. *Submitted*.
- 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.
- Pongpanich, M., Neely, M.L., Tzeng, J.Y. (2011). 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*. Accepted.
- 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.
- 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.
- 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.
- 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.

- Tzeng, J.Y., Bondell, H. (2010) A comprehensive approach to haplotype specific analysis via penalized likelihood. *European Journal of Human Genetics*. 18:95-103.
- 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.
- 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.
- 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., Nöthen, 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.
- 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
- Psychiatric GWAS Consortium Coordinating Committee. (2009). Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *The American Journal of Psychiatry*. 166:540-556.
- 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
- Tzeng, J.Y., Zhang, D. (2007). Haplotype-based Association Analysis via Variance Component score test. *The American Journal of Human Genetics*, 81:939-963.
- Tzeng, J.Y. (2007). EM Algorithm. In *the Encyclopedia of Measurement and Statistics*, edited by Neil Salkind. Sage Publications.
- 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.
- 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.
- 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
- Tzeng, J.Y. (2005). Evolutionary-based Grouping of Haplotypes in Association Analysis. *Genetic Epidemiology*, 28:220-231.
- Tzeng, J.Y., Byerley, W., Devlin, B., Roeder, K. and Wasserman, L. (2003). Outlier detection and false discovery rates for whole-genome DNA matching. *Journal of the American Statistical Association*, 98:236-246.
- 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.

- 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.
- Hsiao, C.K., Chen, C.J., Shih, Y.-F., Lin, L.L.-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 Lin, L.L.-K., Shih, Y.-F. and Hung, P.T. (Eds.), *Myopia Updates II* (pp. 161-164). Springer-Verlag, Tokyo.
- 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.
- Cheng, Y.H. and Tzeng, J.Y. (1997). Chinese version of “*Primer of Biostatistics* (4th ed.) by Glantz, S.A.”, McGraw-Hill, Taipei.
- Tzeng, J.Y. (1997). *Spatial Model Selection Using Bayes Factor and Ratio of Variabilities*. Master thesis. Division of Biostatistics, National Taiwan University.

PROFESSIONAL ACTIVITIES

Editorial & Referee Work:

- Associate Editor: *Biometrics* (2007-present)
- Panel referee:
 - 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, Journal of the American Statistical Association, Statistics in Medicine, Theoretical Population Biology, Statistical Applications in Genetics and Molecular Biology
- Other:
 - University of Alabama at Birmingham-Clinical Nutrition Research Center Pilot Grant program (2007)
 - Fine-mapping group of the Genetic Analysis Workshop 14 (2004)

Event Organizer:

- 2nd RTP Statistical Genetics Conference, Raleigh NC (September 2012)
- 1st RTP Statistical Genetics Conference, Raleigh NC, (October 2011)
- Invited Session “Statistical Modeling of Genetic Sequence Data,” JSM, Miami FL (August 2011)
- Invited Session “Bioinformatics and Biotechnology,” the 10th Emerging information and Technology Conference, Stanford University, San Francisco CA (August 2010)
- Invited Session “Bioinformatics and Biotechnology,” the 9th EITC Workshop, MIT (August 2009)
- Conference “Haplotype Analysis of Population and Pedigree Data in Association Studies” University of Alabama, Birmingham (May 2008)

- Invited Session “Haplotype Analysis in Genome-wise Association Studies”, ICSA Applied Statistics Symposium (June 2007)

Committees: ICSA Nomination and Election Committee (2011-2013)

Consortium: The Psychiatric GWAS Consortium

Teaching (Regular semester courses):

- Spring 2011: ST/GN721 Genetic Data Analysis; PP610/810G Genomic Science Journal Club
- Fall 2010: ST511 Experimental Statistics for Biological Sciences I
- Fall 2009: ST511 Experimental Statistics for Biological Sciences I; ST361 Introduction to Statistics for Engineers
- Fall 2008: ST511 Experimental Statistics for Biological Sciences I
- Spring 2008: ST790G Statistics in Genetic Epidemiology; ST361 Introduction to Statistics for Engineers
- Fall 2007: ST361 Introduction to Statistics for Engineers
- Spring 2007: ST635/PP810G Genomic Science Journal Club
- Fall 2006: ST361 Introduction to Statistics for Engineers
- Fall 2005: ST790G Statistics in Genetic Epidemiology
- Spring 2005: ST361 Introduction to Statistics for Engineers
- Fall 2004: ST361 Introduction to Statistics for Engineers
- Fall 2004: ST590D Statistics for Molecular Biology

Teaching (Other):

- Summer Workshop in Genetic Epidemiology, National Taiwan University, Taipei, Taiwan (July 2007)
- Asian Institute in Statistical Genetics (Module: Population Genetic Data Analysis), Yonsei University, Seoul, Korea (July 2005)
- Summer Institute in Statistical Genetics (Module: Human Population Genetic Data), North Carolina State University, Raleigh, NC. (June 2005)
- Summer Institute in Statistical Genetics (Module: Population Genetic Data Analysis), North Carolina State University, Raleigh, NC. (June 2004)

PRESENTATIONS AND SEMINARS

Invited Seminars/Presentations

- *Gene-trait similarity regression method for gene-level pharmacogenetic analysis.* IMPACT Symposium, Durham, NC (November 2011)
- *Detecting and comprehending marker-set association for common and rare variants.* Department of Statistics and Probability, Michigan State University, East Lansing, MI (November 2011)
- *Detecting and comprehending marker-set association for common and rare variants.* Jeffrey L. Houpt Lectures in Genome Sciences, Carolina Center for Genome Sciences, University of North Carolina-Chapel Hill, NC, Chapel Hill (October 2011)
- *A gene-trait similarity regression method for common and rare variants with general trait values.* Workshop on High-Dimensional Data Modeling, Taida Institute for Mathematical Sciences (TIMS), Department of Mathematics, National Taiwan University, Taiwan (July 2011)

- *Penalized likelihood approaches for haplotype specific analysis in pharmacogenomics*, Workshop on Statistical Frontiers, Institute of Statistical Science, Academia Sinica, 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*, the 2010 Annual Meeting of Chinese Statistical Society and International Statistical Conference, Jhongli, Taiwan (December 2010)
- *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*, 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*, Division of Biostatistics, Department of Preventive Medicine, University of Southern California, Los Angeles CA (August 2010)
- *Marker-set analysis for genetic main effects and gene-environment interactions via gene-trait similarity regression*, 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*, 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*, 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)
- *A Gene-Trait Similarity Regression for Genetic Main and Interaction Effects in Genomewide Association Haplotype Analysis*, Institute of Statistical Science, Academia Sinica, Taiwan (December 2009).
- *A constrained regression approach for studying haplotype specific effects*, DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University, Piscataway NJ (Aug 2008)
- *A gene-trait similarity regression for haplotype analysis in genome-wide association studies*, University of Alabama at Birmingham, Birmingham, AL (May 2008)
- *Regression-based Multi-marker Analysis for Genome-wide Association Studies Using Haplotype Similarity*, National Institute of Environmental Health Sciences, RTP NC (Dec 2007)
- *Regression-based Multi-marker Analysis for Genome-wide Association Studies Using Haplotype Similarity*, 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*, Institute of Statistical Science, Academia Sinica, Taiwan (July 2007)
- *Model-based association analysis via haplotype similarity for genome-wide studies*, National Taiwan University, Taiwan (July 2007)
- *On the Improvement of Efficacy of Haplotype-based Association Analysis*, Department of Statistics, University of Georgia, Athen GA (Feb 2005)
- *Cladistic Clustering of Haplotypes in Association Analysis*, Department of Statistics, North Carolina State University, Raleigh NC (Aug 2004)
- *A Haplotype-Similarity Based Approach for Detecting Genetic Association*, Center for Statistical Sciences, Brown University, Providence RI (Feb 2004)
- *Identification of Disease Mutations by the Analysis of Haplotypes*, Graduate Institute of Epidemiology, National Taiwan University, Taiwan (Dec 2003)
- *A Haplotype-Similarity Based Approach for Detecting Genetic Association*, Institute of Statistical Science, Academia Sinica, Taiwan (Dec 2003)

- *The Use of Haplotype Similarity in Detecting Genetic Association*, Division of Biostatistics, University of Southern California, Los Angeles, CA (Nov 2003)

Conference Presentation (Presented by coauthors are marked by *)

- *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)
- *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 (November 2010)
- *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).
- *Penalized Likelihood Approach to Haplotype Specific Analysis.* Tzeng JY, Bondell HD*. Biometric Society ENAR Spring Meeting, San Antonio, TX (March 2009)
- *Penalized Likelihood Approach to Haplotype Specific Analysis.* Joint Statistical Meeting, Denver, CO (August 2008)
- *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)
- *Association Studies of Case-Control Data with Genotyping Uncertainty.* Liu Y*, Tzeng JY. Biometric Society ENAR Spring Meeting, Arlington, VA (March 2008)
- *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)
- *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)
- *Regression-Based Association Approach Using Genetic Similarity for Genomewide Association Scans,* Joint Statistical Meeting, Salt Lake City UT (Aug 2007)
- *Model-based association analysis via haplotype similarity for genome-wide studies,* the International Chinese Statistical Association, Raleigh NC (June 2007)
- *Regression-based Association Analysis with Clustered Haplotypes Using Genotypes,* Joint Statistical Meeting, Minneapolis MN (Aug 2005)
- *Regression-based Association Analysis with Grouped Haplotypes,* Biometric Society ENAR Spring Meeting, Austin TX (Mar 2005)
- *Evolutionary-based Grouping of Haplotypes in Association Analysis,* Taipei Symposium on Statistical Genome, Taipei Taiwan (Dec 2004)
- *Evolutionary-based Grouping of Haplotypes in Association Analysis,* Annual Meeting of the American Society of Human Genetics, Toronto, Canada (Oct 2004)
- *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)
- *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)

- *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)
- *Bayesian Tests of Spatial Autocorrelation*, Joint Statistical Meetings of the American Statistical Association, Anaheim, CA (Aug 1997)

HONORS

- Elected Full Member of Sigma Xi Science Research Society (2004)
- Umesh Gavaskar 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)

CURRENT AND PAST GRADUATE STUDENTS

Current:

- Hu, Jun (Bioinformatics). Sequence-based genomic and transcriptomic analyses
- Pongpanich, Monnat (Bioinformatics). On the SNP-based and sequence-based whole genome studies for complex traits
- Starr, Aijing (Statistics). Integrative genomic analysis in pharmacogenetics
- Wang, Xin (Bioinformatics). Gene-based association tests for pharmacogenetic studies
- Wang, Zhi (Bioinformatics). Statistical mining for pharmacometabolics.
- Zhao, Guolin (Statistics). Statistical methods for assessing gene-gene and gene-environment interactions

Past:

- Jones, Marti (2007, Statistics) A retrospective method for inference on haplotype main effects and haplotype-environment interactions using clustered haplotypes. Biostatistician, PRA International
- Liu, Youfang (2008, Bioinformatics) Analytical Tools for population-based association Studies. Postdoc, UNC-Chapel Hill
- Ouyang, Haojun (2009, Bioinformatics; co-advised with Dr. Sujit Ghosh) Bayesian approach for nonlinear dynamic system and genome-wide association study. Biostatistician, Eli Lilly
- Koehler, Meg (2011, Statistics; co-advised with Dr. Howard Bondell). Penalized likelihood approaches for haplotype identification and estimation. Assistant professor, Department of Biostatistics and Bioinformatics, Duke University.