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RESEARCH INTERESTS

Statistical methods for studying susceptibility genes for complex traits; specific topics include: association analysis, haplotype-similarity methods, haplotype-based analysis, outlier detection, EM algorithm, multiple testing/false discovery rate, Bayes hierarchical modeling

POSITION North Carolina State University Raleigh, NC
Department of Statistics and Bioinformatics Research Center
– Assistant Professor, Fall 2003 - present

EDUCATION **Carnegie Mellon University** Pittsburgh, PA
Ph.D., Department of Statistics, 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, May 2000

National Taiwan University Taipei, Taiwan
M.S., Division of Biostatistics, Graduate Institute of Epidemiology, 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.

PUBLICATIONS

- Tzeng, J.Y., Zhang, D., Chang, S.M., Thomas, D.C., Davidian, M. (2008). Regression-based Multi-marker Analysis for Genome-wide Association Studies Using Haplotype Similarity. *Biometrics*. Accepted.
- Sullivan, P.F., de Geus, E.J.C., Willemsen, G., Smit, J.H., Zandbelt, T. Arolt, V., Baune, B.T. Blackwood, D., Cichon, S., Coventry, W.C. Domschke, K. Dumenil, T., Farmer, A., Fava, M., Gordon, S.D., Heutink, P., Holsboer, F., Hoogendijk, W.J., Hottenga, J.J., James, M.R., Kohli, M. Lin, D.Y., Lucae, S., Maier, W., G. Martin, N.G. McGuffin, P., Nolen, W., Nthen, M.M. Perlis, R. Pirlo, K. Posthuma, D. Rietschel, M. Schosser, A., Smoller, J. Tzeng, J.Y., van Dyck, R., Wray, N.R., Zitman, F.G., Boomsma, D.I., Penninx, B.W.J.H. Genomewide association for major depressive disorder: a possible role for the presynaptic protein PICCOLO. Under Revision.
- 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

- Liu, Y., Li, Y.J., Satten, G., Allen, A.S., Tzeng, J.Y. (2008). A regression-based association test using inferred ancestral haplotype similarity. Under Revision.
- 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.

RESEARCH GRANTS

- 08/2005-07/2009 Principal Investigator, Haplotype-based Association Modeling for Whole-Genome Scan and Candidate Gene Studies, DMS-0504726, NSF,
- 03/2006-02/2008 Subcontract Principal Investigator from UNC-CH, for the NIMH funded project “Replication of Schizophrenia Associations in CATIE” R01-MH074027 (PI: Patrick Sullivan) NIMH.
- 1/2007 - 12/2011 Co-Investigator, Genetic susceptibility to intermediate phenotypes for stroke and myocardial infarction NHRI-Ex96-9607PI, National Health Research Institutes of Taiwan.

PROFESSIONAL ACTIVITIES

Editorial & Referee Work:

- Associate Editor: Biometrics

- Panel referee:
 - NIH Hemostasis and Thrombosis Study Section (Oct 2006; Nov 2006)
 - NIH Erythrocyte & Leukocyte Biology Study Section (Feb 2007)
- 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)

Consortium: The Psychiatric GWAS Consortium (Chair: Dr. Mark Daly).

Teaching (Regular semester courses):

- Fall 2008: ST511 Experimental Statistics for Biological Sciences I
- Spring 2008: ST790G Statistics in Genetic Epidemiology and 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

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

- *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

- ❑ *A Constrained Regression Approach for Haplotype Specific Tests*, Joint Statistical Meeting, Denver, CO (Aug 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*, Spring Meetings of the Eastern North American Region (ENAR) of the International Biometric Society, 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 Gavasakar Thesis Award, Carnegie Mellon University, Pittsburgh, PA (2003)
- ❑ IMS Laha Award, San Francisco, CA (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 MEMBERSHIPS

American Statistical Association
American Society of Human Genetics
Institute of Mathematical Statistics
Sigma Xi