

Curriculum Vitae

Yen-Yi Ho

Office Address

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Education

- 2009 Ph.D., Biostatistics, Johns Hopkins University,
*Thesis Title: Gene Association Networks and Higher-Order Interactions:
Algorithms and Statistical Models.*
Committee: Dr. Giovanni Parmigiani (Advisor), Dr. Leslie Cope,
Dr. Pien-Chien Huang, Dr. Thomas Louis
- 2001 M.S., Epidemiology, National Taiwan University
- 1999 B.S., Double Major in Medical Technology & Public Health,
National Taiwan University

Employment

- Aug 2016 – Present Assistant Professor, Department of Statistics, College of Arts and Sciences,
University of South Carolina
- 2011 – 2016 Assistant Professor, Division of Biostatistics, School of Public Health,
University of Minnesota
- 2011 – 2016 Faculty, Biostatistics and Bioinformatics Shared Resource
Masonic Cancer Center, University of Minnesota
- 2009 – 2011 Postdoctoral Research Fellow
McKusick-Nathans Institute of Genetic Medicine
Johns Hopkins University School of Medicine
- 2006 – 2007 Statistical Consultant, Biostatistics Consulting Center
Department of Biostatistics, Johns Hopkins University
- 2005 – 2009 Statistical Consultant, School of Nursing
Johns Hopkins University
- 2001 – 2003 Research Associate, Bioresource Collection and Research Center
Hsinchu, Taiwan

Honors and Awards

- 2003 – 2005 Government Funded Scholarship for Studying Abroad,
Taiwanese Ministry of Education
- 1999 Research Creativity Award, National Science Council, Taiwan
Awarded for outstanding undergraduate research

Teaching Experience

- 2011 – Member, Statistical Genetics and Bioinformatics Curriculum Committee
Division of Biostatistics, University of Minnesota
- 2012 – 2016 Instructor, Statistics for Human Genetics and Molecular Biology (PUBH7445)
Division of Biostatistics, University of Minnesota
- Fall 2016 – Instructor, Elementary Statistics for the Biological and Life Sciences (STAT205)
Department of Statistics, University of South Carolina
- Spring 2017 – Present Instructor, Introduction to Analysis of Genomic Data Using R (BIOL599)
Department of Biological Sciences, University of South Carolina
- Fall 2017 – Present Instructor, Data Analysis I (STAT704)
Department of Statistics, University of South Carolina
- Fall 2017 Introduction to Biostatistics (BMSC700, Guest Lecture)
School of Medicine, University of South Carolina

Professional Memberships and Service

- American Statistical Association
Institute of Mathematical Statistics
Referee, American Journal of Epidemiology (2014)
Referee, Turkish Journal of Medical Sciences (2015)
Referee, PLOS ONE (2016)
Member, Cancer Protocol Review Committee,
Masonic Cancer Center, University of Minnesota (2011–2015)
Reviewer, ASPIRE II Grant Review Committee (April 2018)
Member, Department of Statistics PhD Qualifying Exam Committee (May 2018)

Software

1. Ho, Y.-Y. (2009). LiquidAssociation: R/Bioconductor package for estimating liquid association using the conditional normal model. Available at <http://www.bioconductor.org>
2. Gunderson T.* (2014). fastLiquidAssociation: R/Bioconductor package for exploring liquid association on a genome-wide scale. Available at <http://www.bioconductor.org>. * Package was developed under Ho's supervision as the author's thesis advisor.

Publications

1. Chen, W.J., Liu P.-H., **Ho Y.-Y.**, and Chien, K.-L., et al. (2003). Sibling recurrence risk ratio analysis of the metabolic syndrome and its components over time. *BMC Genetics* **4**, S33-S28.
2. Lee, W.-C., **Ho Y.-Y.** (2003). Potential for gene-gene confounding bias in case-parental control studies. *Annals of Epidemiology* **13**, 261-266.
3. **Ho Y.-Y.**, Parmigiani, G., Louis, T.A., Cope, L.M. (2010). Modeling Liquid Association. *Biometrics* **67**, 133-141. doi: 10.1111/j.1541-0420.2010.01440.x.
4. Jiang, Q., **Ho Y.-Y.**, Hao L, Nichols Berrios C, Chakravarti, A. (2011). Copy number variants in candidate genes are genetic modifiers of Hirschsprung disease. *PLoS One* **6**, e21219.
5. **Ho Y.-Y.**, Matteini A.M., Beamer B., and Fried L., et al. (2011). Exploring biologically relevant pathways in frailty. *Journal of Gerontology A Biological Sciences and Medical Sciences* **66**, 975-979.
6. Shen A., Baker J., Scott G., Davis Y., **Ho Y.-Y.**, Siliciano R. (2013). Endothelial Cell Stimulation Overcomes Restriction and Promotes Productive and Latent HIV-1 Infection of Resting CD4+ T Cells. *Journal of Virology* **87**, 9768-79. doi: 10.1128/JVI.01478-13.
7. Terrell A.N., Huynh M., Grill A., Kovi R.C., O'Sullivan M.G., Guttenplan J.B., **Ho Y.-Y.**, Peterson L.A. (2014). Mutagenic activity of furan in female Big Blue B6C3F1 mice. *Mutation Research/Genetic Toxicology and Environmental Mutagenesis* **770**, 46-54.
8. **Ho Y.-Y.**, Cope, L.M., Parmigiani, G. (2014). Modular network construction using eQTL data: an analysis of computational costs and benefits. *Frontiers in Genetics* **5**, 40. doi: 10.3389/fgene.2014.00040
9. **Ho Y.-Y.**, Baechler E.C., Ortmann W., Behrens T.W., Graham R.R., Bhangale T.R., Pan W. (2014). Using Gene Expression to Improve the Power of Genome-Wide Association Analysis. *Human Heredity* **78**, 94-103. doi: 10.1159/000362837
10. Abbott, K., Nyre, E., Abrahante, J., **Ho Y.-Y.**, Isaksson, R.V., Starr, T. (2014) The Candidate Cancer Gene Database: a database of cancer driver genes from forward genetic screens in mice. *Nucleic Acids Research* **43**, D844-8. doi: 10.1093/nar/gku770.
11. Gunderson T.*, **Ho Y.-Y.*** (2014) An efficient algorithm to explore liquid association on a genome-wide scale. *BMC Bioinformatics* **15**, 371. *Ho was the corresponding author and the first author's thesis advisor.

12. Gupta M., McCauley J., Farkas A., Gudeloglu A., Neuberger M.M., **Ho Y.-Y.**, Yeung L., Vieweg J, Dahm P. (2014) Clinical practice guidelines on prostate cancer: a critical appraisal. *The Journal of Urology* pii: S0022-5347(14)04811-3. doi: 10.1016/j.juro.2014.10.105.
13. Nho R., Im J., **Ho Y.-Y.**, Hergert P. (2014) MicroRNA-96 inhibits FoxO3a function in IPF fibroblasts on type I collagen matrix. *American Journal of Physiology-Lung Cellular and Molecular Physiology* **307**, 632-42. doi: 10.1152/ajplung.00127.2014.
14. Gavin K., Linde J.A., Pacanowski C.R., French S.A., Jeffery R.W., **Ho Y.-Y.** (2015) Weighing frequency among working adults: cross-sectional analysis of two community samples. *Preventive Medicine Reports* **2**, 44-46. doi: 10.1016/j.pmedr.2014.12.005.
15. **Ho Y.-Y.**, O'Connell M., Guan W., Basu S. (2015) Powerful Association Test Combining Rare Variant and Gene Expression Using Family Data from Genetic Analysis Workshop 19. *Genetic Analysis Workshop 19 Proceedings* **9 Suppl 8**, S33.
16. **Ho Y.-Y.**, LaRue R.S., Timothy T. Starr, Largaespada D.A. (2016) Case-oriented pathways analysis in pancreatic adenocarcinoma using data from a sleeping beauty transposon mutagenesis screen. *BMC Medical Genomics* **9**, 16.
17. **Ho Y.-Y.***, Vo T.N.*, Chu H., LeSage M.G., Luo X., Le C.T. (2016) A Bayesian hierarchical model for demand curve analysis. *These authors contribute equally to this paper. *Statistical Methods in Medical Research*. DOI: 10.1177/0962280216673675
18. Arsoniadis E.G., **Ho Y.-Y.**, Melton G.B., Madoff R.D., Le C., Kwaan M.R. (2017) African Americans and Short Term Outcomes After Surgery for Crohn's Disease: An ACS-NSQIP Analysis. *Journal of Crohn's and Colitis*. **11**, 468-473.
19. Abbott K, **Ho Y.-Y.**, Erickson J. (2017) Automatic Health Record Review to Identify Gravely Ill Social Security Disability Applicants. *Journal of the American Medical Informatics Association* **24**, 709-716.
20. Warlick C., Berge J.M., **Ho Y.-Y.**, Yeazel M. (2017) Impact of a Prostate Specific Antigen Screening Decision Aid on Clinic Function. *Urology Practice* **4**, 448-453.
21. Wang L., Liu S., Ding Y., **Ho Y.-Y.**, Yuan S.-S., Tseng G.C. (2017) Meta-analytic framework for liquid association. *Bioinformatics* **15**, 2140-2147.
22. Fagan D.H, Fettig L.M, Avdulov S, Beckwith H., Peterson M.S, **Ho Y.-Y.** , Wang F., Polunovsky V.A, and Yee D. (2017) Acquired tamoxifen resistance in MCF-7 breast cancer cells requires hyperactivation of eIF4F-mediated translation. *Hormones and Cancer* **8**, 219-229.

23. Pulvers K., Cupertino A. P., Scheuermann T. S., Cox L.S., **Ho Y.-Y.**, Nollen N.L., Cuellar R., Ahluwalia J.S. (2018) Daily and Nondaily Smoking Varies by Acculturation among English-speaking, U.S. Latino Men and Women. [Accepted by Ethnicity and Disease]

Book Chapter

1. **Ho Y.-Y.**, Cope L., Dettling M., and Parmigiani G. (2007). Statistical methods for identifying differentially expressed gene combinations. *Methods in Molecular Biology* **408**, 171-191.

Submitted

2. Kinzy T., Starr T., Tseng G, **Ho Y.-Y***. Bayesian Hierarchical Models for Liquid Association Meta-Analysis. [Under review] *Ho is the corresponding author and the first author's thesis advisor.

In Preparation

1. Peterson L., **Ho Y.-Y.** Genome-wide association study for toxicity outcomes using genome data from International HapMap project.
2. Ma C., Christenson S., Nho R, **Ho Y.-Y***. Genome-Wide Study of miRNA Regulated Gene Expressions Networks in Association with Emphysematous Lung Destruction. *Ho is the corresponding author and the first author's thesis co-advisor.
3. Park, G., **Ho, Y.-Y.**, Baechler, E.C, John C. Gene mechanisms for severe malaria children in Africa.
4. Zichen Ma, Hanson T, **Ho, Y.-Y.** Flexible Bivariate Count Data Regressions for Modeling Dependency Structures.
5. Baek S., **Ho, Y.-Y.**, Ma Y. Using sufficient direction factor model to analyze breast cancer pathway effects.

Presentations

Oral Presentation

1. Statistical Methods for identifying differentially expressed gene combinations (2007). *International Biometric Society Eastern North American Region (ENAR)*.
2. Exploring Liquid Association in Non-Gaussian Multivariate Distributions (2008). *Joint Statistical Meetings*.
3. nPARS: A Comprehensive Search Algorithm for Constructing Bayesian Networks Using Large-Scale Genomic Data (2011), *Joint Statistical Meetings, Miami*.

4. Using Gene Expression to Improve the Power of Genome-Wide Association Analysis (2014). *International Biometric Society Eastern North American Region (ENAR)*.
5. **Ho, Y.-Y.**, O'Connell M., Guan W., Basu S. (2015) Powerful Association Test Combining Rare Variant and Gene Expression Using Family Data from Genetic Analysis Workshop 19. *Genetic Analysis Workshop 19, Vienna, Austria* [Presented by O'Connell M]
6. **Ho Y.-Y.**, LaRue R.S., Timothy T. Starr, Largaespada D.A. (2016) Individual-oriented gene set analysis using insertional mutation data. *Joint Statistical Meetings, Chicago*.
7. **Ho Y.-Y.** Statistical Methods for Integrating Large-Scale Genomic Data and Constructing Gene Association Networks (2017). Department of Mathematical Sciences, Clemson University.
8. **Ho Y.-Y.** Statistical Methods for Integrating Large-Scale Genomic Data and Constructing Gene Association Networks (2018). Center for Colon Cancer Research Annual Retreat, Saluda Shoals Park.
9. **Ho Y.-Y.** Statistical Methods for Integrating Large-Scale Genomic Data and Identifying Higher-Order Interactions (2018). Department of Biostatistics, Arnold School of Public Health, University of South Carolina.

Grants Submitted

1. Genomics of autism-related traits in *Peromyscus* (deer mice)
PI: Dr. Michael Felder (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted Feb, 2017, re-submitted Oct, 2017)
2. Identifying Genetic Loci Associated with Neurocristopathies using the Deer Mouse *Peromyscus maniculatus*
PI: Dr. Shannon Davis (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2017, re-submitted January 2018)
3. Chromatin regulatory mechanisms in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2017)
4. Secondary Analysis and Integration Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes
Role: Principal Investigator
Mechanism: CAS Faculty Research Initiative, 07/2017 – 09/2018
5. A Chemopreventive Strategy Based on Edible MicroRNAs Produced in Plants
PI: Dr. Vicki Vance (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R21 (submitted Feb 2018)
6. Mechanism of Replication Rescue by the Human CST Complex
PI: Dr. Jason Stewart (Department of Biological Sciences)
Role: Statistical Consultant
Mechanism: NIH R01 (submitted Feb 2018)
7. A novel technology for isolating and imaging cell type specific exosomes in inter-organ communication
PI: Dr. Guiren Wang (Department of Mechanical Engineering)
Role: Co-Investigator
Mechanism: ASPIRE II (submitted Feb 2018)

Current Grants

1. Molecular mechanisms of leukemia stem cell persistence in AML relapse

Role: Statistical Mentor

Mechanism: CTSI-KL2 2015 - 2018, University of Minnesota

2. Integrating Somatic Mutation and Gene Expression Data to Identify Active Driver Pathways Associated with Cancer Survival

Role: Principal Investigator

Mechanism: ASPIRE I, University of South Carolina 07/2017 – 09/2018

Status: Funded

3. Secondary Analysis and Integration Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes

Role: Principal Investigator

Mechanism: CAS Faculty Research Initiative, 07/2017 – 09/2018

Status: Funded

Past Grants

1. Models for Tobacco Products Evaluation
Principal investigator: Dorothy Hatsukami, PhD
Mechanism: U19 (NIH/FDA)
2. Transdisciplinary Collaborative Center for Research African American Mens Health
Principal investigator: Selwyn Vickers, PhD
Mechanism: U54
3. Constituent Yields and Biomarkers of Exposure for Tobacco Product Regulation
Principal Investigator: Irina Stepanov, PhD
Mechanism: R01
4. Inducing NK cells to remember and fight cancer
Principal Investigator: Jeff Miller, MD
Mechanism: R01
5. Minnesota Obesity Center
Principal Investigator: Allen Levine, PhD
Mechanism: P30
6. Interactions between tobacco smoke constituents in rodent tumor models
Principal Investigator: Lisa Peterson, PhD
Mechanism: R01
7. Molecular mechanisms of leukemia stem cell persistence in AML relapse
Principal Investigator: Zohar Sachs, PhD
Mechanism: CTSI/KL2