Curriculum Vitae

Yen-Yi Ho

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University of South Carolina,
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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
Committee: Dr. Wen-Chung Lee (Advisor), Dr. Wei J Chen,
Dr. Chuhsing Kate Hsiao, Dr. Chien-Jen Chen

1999   B.S., Double Major in Medical Technology & Public Health,
National Taiwan University

Employment

Aug 2022 – Present	Associate Professor, Department of Statistics, College of Arts and Sciences, University of South Carolina
Aug 2022 – Present	Joint appointment Associate Professor, Department of Biological Sciences, College of Arts and Sciences, University of South Carolina
Aug 2016 – Aug 2022	Assistant Professor, Department of Statistics, College of Arts and Sciences, University of South Carolina
Aug 2016 – Aug 2022	Joint appointment Assistant Professor, Department of Biological Sciences, 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 McKusic-Nathans Institute of Genetic Medicine Johns Hopkins University School of Medicine
2006 – 2007	Statistical Consultant, Biostatistics Consulting Center Department of Biostatistics, Johns Hopkins University

Employment

2005 – 2009	Statistical Consultant, School of Nursing Johns Hopkins University
2001 – 2003	Research Associate, Bioresource Collection and Research Center Hsinchu, Taiwan

Honors and Awards

2017	ASA/Kutner Travel Award
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 – 2016	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 – Spring 2020	Instructor, Introduction to Analysis of Genomic Data Using R (STAT599) Department of Biological Sciences, University of South Carolina
Fall 2017 – Fall 2022	Instructor, Data Analysis I (STAT704) Department of Statistics, University of South Carolina
Fall 2017 – Fall 2022	Introduction to Biostatistics (BMSC700, Guest Lecture) School of Medicine, University of South Carolina
Spring 2019	Instructor, Data Analysis II (STAT705) Department of Statistics, University of South Carolina
Spring 2021	Instructor, Genomic Data Science (STAT588/BIOL588) Department of Statistics, University of South Carolina
Spring 2022 – Spring 2023	Instructor, Data Analysis II (STAT705) Department of Statistics, University of South Carolina
Fall 2023	Instructor, Genomic Data Science (STAT588/BIOL588) Department of Statistics, 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)
Referee, PLOS Computational Biology (2017)
Referee, Nucleic Acids Research (2017)
Reviewer, UofSC ASPIRE II Grant Review Committee (April 2018)
Referee, Journal of Gerontology: Biological Sciences (2018)
Referee, Journal of the Royal Statistical Society C (2018)
Referee, BMC Bioinformatics (2018)
Referee, Journal of the Royal Statistical Society C (2019)
Member, ASA/ICS Mentoring Program (2019-Present)
Referee, Drug and Alcohol Dependence (2020)
Referee, BMC Bioinformatics (2020)
Review Panel, UofSC Big Data Health Science Center Pilot Project (April 2020)
Member, ASA/Caucus for Women Member Needs Assessment Committee (October 2020)
Early Career Reviewer, GCAT Study Section, NIH (June 2021)
Referee, Biometrics (2021)
Referee, Physiological Genomics (2021)
Mentor, ASA/ Statistics and Data Science Education Mentoring Program (2021)
Review Panel, NIH/NCI special emphasis panel grant review (2022)
Review Panel, NIH/NCI special emphasis panel grant review (Set-Aside) (2022)
Referee, Translational Research (2022)
Referee, Biostatistics (2022)
Referee, Human Molecular Genetics (2022)
Review Panel, NIH/NCI special emphasis panel grant review (2023)
Review Panel, NIH/NCI special emphasis panel grant review (Set-Aside) (2023)
Review Panel, Canadian Statistical Sciences Institute Grant Program (2023)
Referee, BMC Pulmonary Medicine (2023)

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.

3. Yang, Z.* (2020) ZENCO: Modeling dynamic correlation in zero-inflated count

data. Available at https://github.com/zheny714/ZENCO. *Package was developed under Ho's supervision as the author's thesis advisor.

4. Ma Z.* (2022). Flexible copula model for integrating correlated multi-omics data from single-cell experiments. Available at https://github.com/ZichenMa-USC/FlexibleCopulaModel. *Package was developed under Ho's supervision as the author's thesis advisor.

5. Bussing A., Yang Z., Ma Z., **Ho, Y.-Y.** scDECO: a novel statistical framework to identify differential co-expression gene combinations systematically using single-cell RNA sequencing data. Available at https://github.com/YenYiHo-Lab/scDECO.

Publications

Published Articles

* indicates methodological contribution

<u>Underlined</u> indicates student mentored and/or supervised by Dr. Ho

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.

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.**, Cope L., Dettling M., and Parmigiani G. (2007). Statistical methods for identifying differentially expressed gene combinations. In: Ochs M.F. (eds) *Gene Function Analysis. Methods in Molecular Biology* **408**, 171-191. Humana Press.

4.* **Ho Y.-Y.**, Parmigiani G., Louis T.A., Cope L.M. (2011). Modeling liquid association. *Biometrics* **67**, 133-141. doi: 10.1111/j.1541-0420.2010.01440.x.

5. Jiang Q., **Ho Y.-Y.**, Hao L., Berrios C.N., Chakravarti A. (2011). Copy number variants in candidate genes are genetic modifiers of Hirschsprung disease. *PLoS One* **6**, e21219.

6. **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* **66A**, 975-979.

7. Shen A., Baker J., Scott G.L., Davis Y.P., **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.

8. Terrell A.N., Huynh M., Grill A.E., Kovi R.C., O'Sullivan M.G., Guttenplan J.B., **Ho Y.-Y.**, Peterson L.A. (2014). Mutagenicity of furan in female Big Blue B6C3F1 mice. *Mutation Research/Genetic Toxicology and Environmental Mutagenesis* **770**, 46-54.

9.* **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

10.* **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

11. Abbott K.L., Nyre E., Abrahante J., **Ho Y.-Y.**, Isaksson Vogel R., 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-D848. doi: 10.1093/nar/gku770.

12.* 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 master thesis advisor.

13. Nho R.S., 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**, L632-L642. doi: 10.1152/ajplung.00127.2014.

14. Gupta M., McCauley J., Farkas A., Gudeloglu A., Neuberger M.M., **Ho Y.-Y.**, Yeung L., Vieweg J., Dahm P. (2015) Clinical practice guidelines on prostate cancer: a critical appraisal. *The Journal of Urology* **193**, 1153-1158. doi: 10.1016/j.juro.2014.10.105.

15. 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.

16.* **Ho Y.-Y.**, O'Connell M., Guan W., Basu S. (2016) Powerful association test combining rare variant and gene expression using family data from Genetic Analysis Workshop 19. *BMC Proceedings* **10**, 26.

17.* **Ho Y.-Y.**, Starr T.K., LaRue R.S., 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.

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., Yuan S.-S., **Ho Y.-Y.**, Tseng G.C. (2017) Meta-analytic framework for liquid association. *Bioinformatics* **33**, 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. doi:10.1007/s12672-017-0296-3.

23.* **Ho Y.-Y.***, Vo T.N.*, Chu H., Luo X., Le C.T. (2018) A Bayesian hierarchical model for demand curve analysis. *Statistical Methods in Medical Research* **27**, 2038-2049. doi: 10.1177/0962280216673675. *These authors contribute equally to this paper.

24. 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. *Ethnicity and Disease* **28**, 105-114. doi: 10.18865/ed.28.2.105.

25. Nallandhighal S., Park G.S., **Ho Y.-Y.**, Opoka R.O., John C.C., Tran T.M. (2019) Whole-blood transcriptional signatures composed of erythropoietic and NRF2-regulated genes differ between cerebral malaria and severe malarial anemia. *The Journal of Infectious Disease* **219**, 154-164.

26.* Kinzy T.G., Starr T.K., Tseng G.C., **Ho Y.-Y.*** (2019) Meta-analytic framework for modeling gene coexpression dynamics. *Statistical Applications in Genetics and Molecular Biology* **18**, 1- 12. doi: 10.1515/sagmb-2017-0052. *Ho is the corresponding author and the first author's master thesis advisor.

27. Peterson L.A., Ignatovich I.V., Grill A.E., Beauchamp A., **Ho Y.-Y.**, DiLernia A.S., Zhang L. (2019) Individual differences in the response of human β-lymphoblastoid cells to the cytotoxic, mutagenic and DNA-damaging effects of a DNA methylating agent, N-methylnitrosourethane. *Chemical Research in Toxicology* **32**, 2214-2226.

28.* Baek S., **Ho Y.-Y.**, Ma Y. (2020) Using sufficient direction factor model to analyze latent activities associated with breast cancer survival. *Biometrics* **76**, 1340-1350. doi: 10.1111/biom.13208

29. Krizek B.A., Blakley I.C., **Ho Y.-Y.**, Freese N., Loraine A.E. (2020) The Arabidopsis transcription factor AINTEGUMENTA orchestrates patterning genes

and auxin signaling in the establishment of floral growth and form. *The Plant Journal* **103**, 752-768.

30.* <u>Ma Z.</u>, Hanson T.E., **Ho Y.-Y.*** (2020) Flexible bivariate correlated count data regressions. *Statistics in Medicine* **39**, 3476-3490. doi: 10.1002/sim.8676. *Ho is the first author's thesis co-advisor.

31. Peterson L.A., Oram M.K., Flavin M., Seabloom D., Smith W.E., O'Sullivan M.G., Vevang K.R, Upadhyaya, P., Stornetta A., Floeder A.C., **Ho Y.-Y.**, Zhang L, Hecht S.S, Balbo S., Wiedmann T.S. (2021) Coexpresure to inhaled aldehydes or carbon dioxide enhances the carcinogenic properties of the tobacco specific nitrosamine 4-methylanitrosamino-1-(3-pyridyl)-1-butanone (NNK) in the A/J mouse lung. *Chemical Research in Toxicology* **34**, 723-732.

32.* <u>Yang Z.</u>, **Ho Y.-Y.*** (2022) Modeling dynamic correlation in zero-inflated bivariate count data with applications to single-cell RNA sequencing data. *Biometrics* **78**, 766-776. *Ho is the first author's thesis advisor.

33. Lieberman B., Kusi M., Hung, C.-N., Chou C.-W., He N., **Ho Y.-Y.**, Taverna J.A., Huang T.H.M., Chen C.-L. (2021) Toward uncharted territory of cellular heterogeneity: advances and applications of single-cell RNA-seq. *Journal of Translational Genetics and Genomics* **5**, 1-21.

34.* <u>Ma Z.</u>, Davis S.W., and Ho Y.-Y. (2022). Flexible copula model for integrating correlated multi-omics data from single-cell experiments. *Biometrics* (To appear) *Ho is the first author's thesis advisor.

35. <u>Zhang W.</u>[†], Ma Z.[†] Wang L., Fan D., **Ho, Y.-Y.** (2023) Genome-wide search algorithms for identifying dynamic gene co-expression via Bayesian variable selection. *Statistics in Medicine* [To Appear] [†]These authors contribute equally to this paper.

36. <u>Zhang W.</u>[†], Ma Z.[†], **Ho, Y.-Y.**, Yang S., Habiger J.D., Huang H.-H., Huang Y. (2024) Multi-omics Integrative Analysis for Incomplete Data Using Weighted p-value Adjustment Approaches. *Journal of Agricultural, Biological, and Environmental Statistics* (To appear) [†]These authors contribute equally to this paper.

Submitted

2. <u>Bussing A.</u>, **Ho Y.-Y.**, Fan D. (2024+) FAST-CoExpress: Flexible and Adaptive Scalable Tool for single-cell differential CoExpression analysis with application to spatial single-cell transcriptomic data. (Submitted to Statistics in Medicine).

In Preparation

3. <u>Yang S.</u>, <u>Bussing A.</u>, **Ho Y.-Y.**, (2024+) Temporal Trajectory Modeling of Non-Linear Dynamic Gene Co-expression Patterns Using single-cell transcriptomics data.

Presentations

Oral Presentation

1. **Ho Y.-Y.**, Cope L., Dettling M., and Parmigiani G. (2007) Statistical methods for identifying differentially expressed gene combinations. *International Biometric Society Eastern North American Region (ENAR).*

2. **Ho Y.-Y.**, Cope L., and Parmigiani G. (2008) Exploring liquid association in non-gaussian multivariate distributions. *Joint Statistical Meetings.*

3. **Ho Y.-Y.**, Cope L., and Parmigiani G. (2011) nPARS: A comprehensive search algorithm for constructing Bayesian networks using large-scale genomic data. *Joint Statistical Meetings, Miami.*

4. **Ho Y.-Y.** (2014) 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.** (2017) Statistical methods for integrating large-scale genomic data and constructing gene association networks. *Department of Mathematical Sciences, Clemson University.*

8. **Ho Y.-Y.** (2017) Case-oriented pathway analysis using data from a sleep beauty transposon mutagenesis screen. Lighting Talk, *Research Computing Symposium, University of South Carolina.*

9. **Ho Y.-Y.** (2018) Statistical methods for integrating large-scale genomic data and constructing gene association networks. *Center for Colon Cancer Research Annual Retreat, Saluda Shoals Park.*

10. **Ho Y.-Y.** (2018) Statistical methods for integrating large-scale genomic data and identifying higher-order interactions. *Department of Epidemiology and Biostatistics, Arnold School of Public Health, University of South Carolina.*

11. **Ho Y.-Y.** (2019) Invited Talk: p-value adjustment procedure using empirical weights. *Lifetime Data Science, Pittsburgh, Pennsylvania.*

12. **Ho Y.-Y.** (2019) Invited Talk: p-value adjustment procedure using empirical weights. *Applied Statistics Symposium, International Chinese Statistical Association, Raleigh, North Carolina.*

13. **Ho Y.-Y.** (2020) Modeling dynamic dependence structure in zero-inflated bivariate count data with application to single-cell RNA sequencing data. *Joint Statistical Meetings Philadelphia, Pennsylvania. (Virtual Conference Due to COVID-19).*

14. Baek S., **Ho Y.-Y.**, Ma Y. (2021) Invited Talk: Using sufficient direction factor model to analyze latent activities associated with breast cancer survival. *International Biometric Society Journal Club.*

15. Ma Z., **Ho Y.-Y.** (2021) Flexible Copula Model for Integrating Correlated Multi-Omics Data from Single-Cell Experiments *Joint Statistical Meetings (Virtual Conference Due to COVID-19).*

16. Ma Z., Davis S.W. **Ho Y.-Y.** (2022) Contributed Talk: Modeling Dynamic Correlation Structure in Multi-Omics Data from Single-Cell Experiments. *The Western North American Region of The International Biometric Society (Virtual Conference Due to COVID-19).*

17. Zhang W., Habiger J., Huang H.-H., **Ho Y.-Y.** (2022) Invited Talk: Integrative Genomics Analysis for Incomplete Data Using Weighted p-value Adjustment Approaches. *Applied Statistics Symposium, International Chinese Statistical Association, Raleigh, Gainesville, Florida.*

18. **Ho Y.-Y.** (2023) Invited Talk: Modeling Dynamic Correlation Structure in Multi-Omics Data from Single-Cell Experiments. *Division of Biostatistics and Bioinformatics, University of Cincinnati College of Medicine. (Virtual Seminar)*

19. **Ho Y.-Y.**(2023) Data Science in the Service of Human Health. Lightning Talk, *Department of Statistics, University of South Carolina.*

Grants Submitted

1.Regulation of SIRT6 tumor suppressor in breast cancer by tyrosyl-tRNA synthetase
PI: Dr. Sajish Mattew (College of Pharmacy)
Role: Statistician
Mechanisam: Susan G Komen Foundation (submitted Nov 2016)

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 (submitted Jan 2017)
Status: **Funded**

3. 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)

4. 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/NIDCR R03 (submitted June 2017, re-submitted Jan 2018, re-submitted Aug 2018,
            re-submitted Nov 2018, re-submitted Feb 2019)
Status: **Funded**

5. Chromatin regulatory mechanisms in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2017, re-submitted June 2018)

6. 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**

7. A chemopreventive strategy based on edible microRNAs produced in plants
PI: Dr. Vicki Vance (Department of Biological Sciences)
Role: Statistical Consultant
Mechanism: NIH/NCI R21 (submitted Feb 2018)
Status: **Funded**

8. 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)

Grants Submitted

9. 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, re-submitted Feb 2019)

10. Dysregulation of miR489 expression impacts breast cancer tumorigenesis and heterogeneity
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: Department of Defense (submitted May 2018)

11. Early onset colorectal cancer (EOCRC): A PPG to support our ongoing mission at the center for cancer research at the University of South Carolina
PI: Lorne Hofseth and Frank Berger
Mechanism: UofSC Excellent Initiative (submitted June, 2018)
Role: Co-investigator

12. Mechanism of MHC heterozygote advantage during anti-commensal germinal center B cell selection
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH/NIAID R21 (submitted November, 2018)
Status: **Funded**

13. Playing with data is exhilaratingly fun!
PI: Yen-Yi Ho
Role: **Principal Investigator**
Mechanism: UofSC Center of Teaching Excellence
            2018-2019 Innovative Pedagogy Grants (submitted December 2018)

14. The role of CST in DNA replication origin licensing and activation
PI: Dr. Jason Stewart (Department of Biological Sciences)
Role: Co-Investigator Mechanism: NIH R01 (submitted March 2019)

15. Stress granule protein functions in PNS and CNS axon regeneration
PI: Dr. Jeff Twiss (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted March 2019)

16. Functional evolution of microRNA-489 and microRNA-425
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R01 (submitted June 2019)

Grants Submitted

17. Pathological alteration of lung fibroblasts by e-cig vapor increases the risk
of developing lung fibrosis
PI: Dr. Richard Nho (Department of Medicine, University of Minnesota)
Role: Statistical Consultant
Mechanism: NIH R21 (submitted June 2019)

18. Targeted nanoparticle delivery of microRNA-489 rejuvenates anthracycline-based
    chemotherapy for TNBC
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: DOD (submitted September 2019)

19. miR-96 as a therapeutic target for idiopathic pulmonary fibrosis
PI: Dr. Richard Nho (Department of Department of Medicine, University of Minnesota)
Role: Statistical Consultant
Mechanism: NIH R01 (submitted September 2019)

20. Nanoparticle-delivered miR-489 rejuvenates anthracycline-based chemotherapy
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH/NCI R21 (submitted October 2019)
Status: **Funded**

21. B-cell-intrinsic MHCII Signaling is a Diversifying Force of Selection
    on IgA Repertoires and the Gut Microbiota
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH/NIAID R01 (submitted February, 2020; resubmitted November, 2020)
Status: **Funded**

22. Targeting Interleukin 1α-mediated immune suppression in HER2-positive breast cancer
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: DOD (submitted March 2020)

23. scDECO: A novel statistical framework to systematically identify differential
    co-expression gene combinations using single-cell RNA sequencing data
PI: Yen-Yi Ho (Department of Statistics)
Mechanism: NIH/NCI R21 (submitted November 2020)
Role: Principal Investigator
Status: Pending (Impact Score: 25)

24. Counteracting epigenetic mechanisms in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: Eagle Autism Foundation (Submitted January, 2021)

Grants Submitted

25. Transcriptional and chromatin regulatory programs in epilepsy
and autism in ASH1L-related disorder
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH/NINDS R21 (Submitted Feb, 2021)

26. Epigenetic axis underlying transcriptional programs associated with
intellectual disability and autism in ASH1L associated disorder
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: Jerome Lejeune Foundation (Submitted March, 2021)

27. ASH1L mediated transcription networks in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Collaborator
Mechanism: NIH/NIMH R01 (Submitted July, 2021)

28. Chromatin Regulatory mechanisms underlying severe autism
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Collaborator
Mechanism: Simons Autism Research Foundation (Submitted August, 2021)

Funded Grants (UofSC)

1. B-cell-intrinsic MHCII Signaling is a Diversifying Force of Selection
   on IgA Repertoires and the Gut Microbiota
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH/NIAID R01, 05/25/2021 – 04/30/2026
Total Amount: $2,053,576

2. scDECO: A novel statistical framework to identify differential co-expression
gene combinations systematically using single-cell RNA sequencing data
PI: Yen-Yi Ho
Role: Principal Investigator
Mechanism: NIH/NCI R21, 09/01/2021 – 08/30/2023
Total Amount: $360,498
Status: **Funded**

3. ASH1L mediated transcription networks in autism spectrum disorders
PI: Dr. Sofia Lizarraga (Department of Biological Sciences)
Role: Collaborator
Role: Principal Investigator
Mechanism: NIH R01, 03/01/2022 – 12/31/2026
Status: **Funded**

Past Funded Grants

1. Models for tobacco products evaluation
Principal investigator: Dorothy Hatsukami, PhD (UMN)
Mechanism: U19 (NIH/FDA)

2. Transdisciplinary collaborative eenter for research African American men's health
Principal investigator: Selwyn Vickers, PhD (UMN/UAB)
Mechanism: U54

3. Constituent yields and biomarkers of exposure for tobacco product regulation
Principal Investigator: Irina Stepanov, PhD (UMN)
Mechanism: R01

4. Inducing NK cells to remember and fight cancer
Principal Investigator: Jeff Miller, MD (UMN)
Mechanism: R01

5. Minnesota obesity center
Principal Investigator: Allen Levine, PhD (UMN)
Mechanism: P30

6. Interactions between tobacco smoke constituents in rodent tumor models
Principal Investigator: Lisa Peterson, PhD (UMN)
Mechanism: R01

7. Molecular mechanisms of leukemia stem cell persistence in AML relapse
Principal Investigator: Zohar Sachs, PhD (UMN)
Mechanism: CTSI/KL2

8. Secondary analysis and integration existing data to elucidate the
genetic architecture of cancer risk and related outcomes
Role: Principal Investigator
Mechanism: UofSC CAS Faculty Research Initiative, 07/2017 – 12/2018
Total Amount: $4,100
Amount of Funding to Statistics/Ho: $4,100

9. Integrating somatic mutation and gene expression data to identify
active driver pathways associated with cancer survival
Role: Principal Investigator
Mechanism: UofSC ASPIRE I, University of South Carolina 07/2017 – 09/2019
Total Amount: $14,990
Amount of Funding to Statistics/Ho: $14,990

10. A chemopreventive strategy based on edible microRNAs produced in plants
PI: Dr. Vicki Vance (Department of Biological Sciences)
Role: Statistical Consultant
Mechanism: NIH R21, 07/2018 – 06/2020
Total Amount: $182,726
Amount of Funding to Statistics/Ho: $7,351

Past Funded Grants

11. Mechanism of MHC heterozygote advantage during anti-commensal germinal center
    B cell selection
PI: Dr. Jason Kubinak (School of Medicine)
Role: Co-Investigator
Mechanism: NIH R21, 07/2019 – 06/2021
Total Amount: $223,500
Amount of Funding to Statistics/Ho: $18,288

12. 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 R03, 07/2019 – 06/2021
Total Amount: $277,157
Amount of Funding to Statistics/Ho: $35,875

13. Nanoparticle-delivered miR-489 rejuvenates anthracycline-based chemotherapy
PI: Dr. Hexin Chen (Department of Biological Sciences)
Role: Co-Investigator
Mechanism: NIH R21, 06/01/2020 – 05/31/2022
Total Amount: $267,215
Amount of Funding to Statistics/Ho: $6,250

August, 2024