

YU-RU SU

Biostatistics Unit, Kaiser Permanente Washington Health Research Institute
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EDUCATION

University of California, Davis, Davis, California, USA
Ph.D. in Biostatistics 09/2011

- Dissertation: Survival analysis for incomplete data
- Advisor: Jane-Ling Wang

National Tsing-Hua University, Hsin-Chu City, Taiwan
M.S. in Statistics 06/2005

National Tsing-Hua University, Hsin-Chu City, Taiwan
B.S. in Mathematics 06/2003

PROFESSIONAL POSITIONS

Kaiser Permanente Washington Health Research Institute, Seattle, Washington, USA
Biostatistics Unit
Scientific Investigator 09/2019 - Present

Fred Hutchinson Cancer Research Center, Seattle, Washington, USA
Biostatistics, Public Health Sciences Division
Staff Scientist 04/2016 - 08/2019
Post-Doctoral Research Fellow 09/2013 - 03/2016

National Cheng Kung University, Tainan City, Taiwan
Department of Statistics
Assistant Professor 09/2011 - 08/2013

University of California, Davis, Davis, California, USA
Department of Statistics
Research Assistant 04/2008 - 07/2011
Teaching Assistant 09/2006 - 07/2011

Academia Sinica, Taipei, Taiwan
Institute of Statistical Science
Post-Master Trainee in the Graduate Training Program 07/2005 - 06/2006

MEMBERSHIPS

American Statistical Association; International Biometric Society (the Western North American Region)

PUBLICATIONS

In refereed journals

- K. Kerlikowske, **Y. Su**, B.L. Sprague and others. Association of screening with digital breast tomosynthesis vs digital mammography with risk of interval invasive and advanced breast cancer. *JAMA*. 327(22):2220-2230.
- Y. Tian, A.E. Kim, ..., **Y. Su** and others (2022). Genome-wide interaction analysis of genetic variants with menopausal hormone therapy for colorectal cancer risk. *J Natl Cancer Inst*. 114(8):1135-1148.
- R. Barfield, J.R. Huyghe, M. Lemire, X. Dong, **Y. Su** and others. Genetic regulation of DNA methylation yields novel discoveries in GWAS of colorectal cancer. *Cancer Epidemiology, Biomarkers & Prevention* 31(5), 1068-1076
- K. M. Jordahl, A. E. Kim, **Y. Su** and others (2022). Beyond GWAS of colorectal cancer: Evidence of interaction with alcohol consumption and putative causal variant for the 10q24.2 region. *Cancer Epidemiology, Biomarkers & Prevention* 31(5), 1077-1089.
- J.R. Huyghe, T.A. Harrison, S. A. Bien, ..., **Y. Su** and others (2021). Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut* 70:1325-1334.
- A. N. Archambault, Y. Lin, J. Jeon, T. A. Harrison, D. T. Bishop, H. Brenner, G. Casey, A. T. Chan, J. Chang-Claude, J. C. Figueiredo, ..., **Y. Su** and others (2021). Nongenetic Determinants of Risk for Early-Onset Colorectal Cancer. *JNCI cancer spectrum*, 5(3):pkab029.
- R. van den Puttelaar, R. G Meester, E. F. Peterse, J. Zheng, L. Hsu, A. G. Zauber, R. B. Hayes, **Y. Su**, and others (2021). 121 Personalized screening strategies for colorectal cancer based on genetic and environmental risk: a cost-effectiveness analysis. *Gastroenterology*, 160(6):S-32-S-33.
- X. Guo, W. Lin, W. Wen, J. Huyghe, S. Bien, Q. Cai, T. Harrison, Z. Chen, C. Qu, ..., **Y. Su** and others. (2021) Identifying novel susceptibility genes for colorectal cancer risk from a transcriptome-wide association study of 125,478 subjects. *Gastroenterology*, 160(4):1164-1178.
- M. Thomas, L. C. Sakoda, M. Hoffmeister, E. A. Rosenthal, J. K. Lee, ..., **Y. Su** and others (2020). Genome-wide modeling of polygenic risk score in colorectal cancer risk. *The American Journal of Human Genetics*, 107(3):432-444.
- X. Dong, **Y. Su (Co-first author)**, R. Barfield, S. Bien, Q. He, T. Harrison, J. Huyghe, T. Keku, N. Lindor, C. Schafmayer, and others (2020). A general framework for functionally informed set-based analysis: Application to a large-scale colorectal cancer study. *PLoS Genetics*, 16(8):e1008947.
- X. Wang, **Y. Su**, P. Peterson, A. T. Chan, D. Albanes, S. Bien, S. I. Berndt, H. Brenner, P. T. Campbell, G. Casey, and others (2020). Exploratory genome-wide interaction analysis of non-steroidal anti-inflammatory drugs and predicted gene expression on colorectal cancer risk. *Cancer Epidemiology, Biomarkers & Prevention*, 29(9):1800-1808.
- Z. Xia, **Y. Su**, P. Petersen, L. Qi, A. E. Kim, J. C. Figueiredo, Y. Lin, H. Nan, L. C. Sakoda, D. Albanes and others (2020). Functional informed genome-wide interaction analysis of body mass index, diabetes and colorectal cancer risk. *Cancer Medicine*, 9(10):3563-3573.
- A. Archambault, **Y. Su**, J. Jeon, M. Thomas, Y. Lin, D. V. Conti, A. K. Win, L. C. Sakoda, I. Lansdorp-Vogelaar, E. Peterse and others (2020). Cumulative burden of colorectal cancer-associated genetic variants is more strongly associated with early-onset vs late-onset cancer. *Gastroenterology*. 158:1274-1286.
- S. McNabb, T. Harrison, D. Albanes, S. Berndt, H. Brenner, B. Caan, P. Campbell, Y. Cao, J. Chang-Claude, A. Chan, ..., **Y. Su**, and others (2019). Meta-analysis of 16 studies of the association of alcohol with colorectal cancer. *International Journal of Cancer*, <https://doi.org/10.1002/ijc.32377>.

- S. A. Bien, **Y. Su (Co-first author)**, D. V. Conti, T. A. Harrison, C. Qu, X. Guo, Y. Lu, D. Albanes, P. L. Auer, B. L. Banbury, and others (2019). Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. *Human Genetics*, 138(4), 307-326.
- J. R. Huyghe, S. A. Bien, T. A. Harrison, H. M. Kang, S. Chen, S. L. Schmit, D. V. Conti, C. Qu, J. Jeon, C. K. Edlund, ..., **Y. Su**, and others (2019). Discovery of common and rare risk loci for colorectal cancer. *Nature Genetics*, 51(1), 76-87.
- Y. Su**, C.-Z. Di, S. Bien, L. Huang, X. Dong, G. Abecasis, S. Berndt, S. Bezieau, H. Brenner, B. Caan, and others (2018). A mixed-effects model for powerful association tests in integrative functional genomics. *The American Journal of Human Genetics*. 102(5):904-919.
- Y. Su**, C.-Z. Di, L. Hsu (2017). Hypothesis testing in functional linear models. *Biometrics*. 73(2):551-561.
- Y. Su**, C.-Z. Di, L. Hsu, Genetics and Epidemiology of Colorectal Cancer Consortium (2017). A unified powerful set-based test for sequencing data analysis of GxE interactions. *Biostatistics*. 18(1):119-131.
- Y. Su** and J.-L. Wang (2016). Semiparametric efficient estimation for shared-frailty models with doubly-censored clustered data. *The Annals of Statistics*, 44, 1298-1331.
- J. R. Carey , P. Liedo, C. Xu, J.-L. Wang, H.-G. Muller, Y. Su, J. W. Vaupel (2016). Diet Shapes Mortality Response to Trauma in Old Tephritid Fruit Flies. *PLoS One* 11(7):e0158468.
- Y.-K. Tseng, **Y. Su**, M. Mao, J.-L. Wang (2015). An extended hazard model with longitudinal covariates. *Biometrika*, 102, 135-150.
- W.-T. Chang, W.-H. Lee, W.-T. Lee, P.-S. Chen, **Y. Su**, P.-Y. Liu, Y.-W. Liu, W.-C. Tsai (2015). Left ventricular global longitudinal strain is independently associated with mortality in septic shock patients. *Intensive Care Med.*, 41(10), 1791-1799.
- J.-M. Sung, C.-T. Su, Y.-T. Chang, **Y. Su**, W.-C. Tsai, S.-P. Wang, C.-S. Yang, L.-M. Tsai, J.-H. Chen, Y.-W. Liu (2014). Independent value of cardiac troponin T and left ventricular global longitudinal strain in predicting all-cause mortality among stable hemodialysis patients with preserved left ventricular ejection fraction. *BioMed Research International* 2014:217290.
- Y.-W. Liu, C.-T. Su, Y.-T. Chang, W.-C. Tsai, **Y. Su**, S.-P. Wang, C.-S. Yang, L.-M. Tsai, J.-H. Chen, J.-M. Sung (2014). Elevated serum interleukin-18 level is associated with all-cause mortality in stable hemodialysis patients independently of cardiac dysfunction. *PLoS One* 9(3):e89457.
- Y.-W. Liu, C.-T. Su, J.-M. Sung, S.-P. Wang, **Y. Su**, C.-S. Yang, L.-M. Tsai, J.-H. Chen, W.-C. Tsai (2013). Association of left ventricular longitudinal strain with mortality among stable hemodialysis patients with preserved left ventricular ejection fraction. *Clinical Journal of the American Society of Nephrology* 8(9), 1564-1674.
- Y. Su** and J.-L. Wang (2012). Modeling left-truncated and right-censored survival data with longitudinal covariates. *The Annals of Statistics* 40(3), 1465-1488.
- J.-F. Wu, **Y. Su (Co-first author)**, C.-C. Chen, H.-L. Chen, Y.-H. Ni, H.-Y. Hsu, J.-L. Wang, M.-H. Chang (2012). Predictive effect of serial serum alanine aminotransferase levels on spontaneous HBsAg seroconversion in Children. *Journal of Pediatric Gastroenterology and Nutrition* 54(1), 97-100.
- N. Kouloussis, N. Papadopoulos, B. Katsoyannos, H.-G. Müller, J.-L. Wang, **Y. Su**, F. Molleman, and J. R. Carey (2011). Seasonal trends in *Ceratitiscapitata* reproductive potential derived from live-caught females in Greece. *Entomologia Experimentalis et Applicata* 140, 181-188.

Published Abstracts from Professional Conferences

X. Wang, **Y. Su**, A. T. Chan, S. A. Bien, S. I. Bernt, H. Brenner, G. Casey, J. Chang-Claude, S. J. Gallinger, R. W. Haile, and others (2018). Functionally informed genome-wide interaction analysis of nonsteroidal anti-inflammatory drugs on colorectal cancer risk. *Cancer Research* 2965-2965.

P. S. Petersen, **Y. Su**, S. I. Berndt, S. A. Bien, H. Brenner, G. Casey, A. T. Chan, J. Chang-Claude, J. C. Figueiredo, S. J. Gallinger, and others (2018). Interactions between genetic predictors of gene expression and dietary factors associated with risk of colorectal cancer. *Cancer Research* 5268-5268.

S. A. Bien, X. Guo, **Y. Su**, T. A. Harrison, C. Qu, Y. Lu, J. Long, S. Chen, A. T. Chan, D. V. Conti, and others (2017). Genetic predictors of gene expression associated with risk of colorectal cancer. *Cancer Research* 1300-1300.

Manuscripts submitted

Y. Su, L. Sakoda, J. Jeon and others. Validation of a genetic-enhanced risk prediction model for colorectal cancer in a large community-based cohort. *Submitted*.

Y. Su, D. Buist, J. Lee and others. Performance of statistical and machine learning risk prediction models for surveillance benefits and failures in breast cancer survivors. *Revision submitted*.

C. Lee, C. Krakauer, **Y. Su** and others. Associations between diabetic retinopathy and dementia. *Submitted*.

M. Lu, **Y. Su**, Y. Liu and others. Joint analysis of survival and ancillary outcomes for associations with somatic mutations. *Submitted*.

COMPUTATIONAL PACKAGES

R packages

- MiST: set-based association tests for genetic effects of variants on phenotypes allowing for functional information.
- MiSTi: set-based association tests for GxE interaction effects on phenotypes allowing for functional information.

INVITED TALKS & ORGANIZED CONFERENCE SESSIONS

Recent developments in integrating multiple-omics data in complex diseases

- Invited session, Joint Statistical Meeting 2018. 08/2018
- Role: organizer and chair

Unified powerful set-based tests for genetic associations

- University of California Davis, Division of Biostatistics. (Online due to COVID-19) 05/2020
- University of Washington, Department of Biostatistics. 11/2019
- Topic contributed session, Joint Statistical Meeting 2018. 08/2018

Hypothesis testing in functional linear models.

- Invited session, WNAR Annual Meeting 2021. (Online due to COVID-19) 06/2021
- Invited session, 1st International Conference on Econometrics and Statistics. 06/2017

A unified powerful set-based test for sequencing data analysis of GxE interactions.

- Invited session, The 2017 ICSA Applied Statistical Symposium. 06/2017
- Biostatistics and Biomathematics, Public Health Science Division, Fred Hutchinson Cancer Research Center. 03/2016

An extended hazard model with longitudinal covariates.

- Invited session, Joint Statistical Meeting 2015. 08/2015

Hypothesis testing for functional linear models with scalar responses.

- Invited session, The WNAR/IMS/KISS/JR Annual Meeting 2020. 06/2020
- Invited session, The 4th International Biostatistics Symposium. 07/2016
- University of California, Davis, Department of Statistics. 06/2014

Modeling left-truncated and right-censored survival data with longitudinal covariates.

- Topic-contributed session, Joint Statistical Meeting 2014. 08/2014
- Topic-contributed session, The 3rd IMS Asia Pacific Rim Meeting. 07/2014
- Invited session, The 9th ICSA international conference. 12/2013
- Fred Hutchinson Cancer Research Center, Biostatistics Program. 11/2013

Nonparametric MLE for doubly-censored data with frailty

- Topic-contributed session, Joint Statistical Meeting 2010. 08/2010