YU-RU SU

Biostatistics Division, 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)

OTHER PROFESSIONAL SERVICE

National services

ASA Biometrics Section Byar Paper Award committee	12/2021 - 01/2022
Journal Club Organizor, IBS-WNAR	01/2022 - Present
Representative-at-large elected, IBS-WNAR	12/2022 - Present

Local services

Admission committee 2022, Biostatistics, University of Washington	12/2021 - 01/2022
KPWHRI Biostatistics Division Cultural Committee	07/2022 - Present

RESEARCH FUNDING

Current External Grant Funding

AD and Eye Disease. R01AG060942. National Institute on Aging, 2019-2024. Total Costs: $5,697,977. Key personnel/Biostatistician. 30% FTE

BCSC P01 Round 3. P01CA154292-11. National Cancer Institute, 2022-2027. Total Costs: $3,818,184. Co-investigator/Biostatistician. 30% FTE

BCSC AI for mammography. R01 CA262023. National Cancer Institute, 2022-2027. Total Costs: $474,839. Co-investigator/Biostatistician. 7.5% FTE

LARCH lung cancer trail. R01 CA262015. National Cancer Institute, 2021-2026. Total Costs: $474,839. Key personnel/Biostatistician. 7.25% FTE

Anticholinergic in ACT. R221134001. University of Washington, 2022-2023. Direct Costs: $29,858. Key personnel/Biostatistician. 3% FTE

MUSE 1A Phase II. LTD10120. Syneos Health, 2016-2022. Direct Costs: $8,447,266. Key personnel/Biostatistician. 10% FTE

PUBLICATIONS

Published/accepted in refereed journals

Y. Su, L. Sakoda, J. Jeon and others. (2023) Validation of a genetic-enhanced risk prediction model for colorectal cancer in a large community-based cohort. *Cancer Epidemiology, Biomarkers & Prevention.* https://doi.org/10.1158/1055-9965.EPI-22-0817

C. Lee, C. Krakauer, **Y. Su** and others. Diabetic Retinopathy and Dementia Association, Beyond Diabetes Severity. *American Journal of Ophthalmology. In press.*

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.

R. Carreras-Torres, A.E. Kim, ... **Y. Su** and others (2022). Genome-wide interaction study with smoking for colorectal cancer risk identifies novel genetic loci related to tumor suppression, inflammation and immune response. *Cancer Epidemiology, Biomarkers & Prevention.* https://doi.org/10.1158/1055-9965.EPI-22-0763.

C. Fernandez-Rozadilla, M. Timofeeva, ... **Y. Su** and others (2022). Deciphering colorectal cancer genetics through multi-omic analysis of 100,204 cases and 154,587 controls of European and east Asian ancestries. *Nature Genetics* https://doi.org/10.1038/s41588-022-01222-9.

C.B. Haas, **Y. Su**, P. Petersen and others. Interactions between folate intake and genetic predictors of gene expression levels associated with colorectal cancer risk. *Scientific reports.* 12(1):1-11.

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.

X. Wang, H. Chen, P.M. Kapoor, **Y. Su** and others (2022). A Genome-Wide Gene-Based Gene–Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications.* 2(4):211-219.

A.N. Archambault, J. Jeon, Y, Lin, ... **Y. Su** and others (2022). Risk Stratification for Early-Onset Colorectal Cancer Using a Combination of Genetic and Environmental Risk Scores: An International Multi-Center Study. *Journal of the National Cancer Institute.* 114(4):528-539.

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 otehrs (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–sssociated 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 HBeAg 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 Ceratitis capitata 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 or provisionally accepted

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. *Provisionally accepted by Cancer Epidemiology, Biomarkers & Prevention.*

M. Lu, **Y. Su (co-1st author)**, Y. Liu and others. Joint analysis of survival and ancillary outcomes for associations with somatic mutations. *Submitted.* Shared co-1st authorship between Lu and Su as these two authors contributed to the method development equally.

B.L. Sprague,R.Y. Coley, K.P. Lowry, ... **Y. Su** and others. Digital breast tomosynthesis versus digital mammography screening performance on successive screening rounds. *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