

CHONG WU

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RESEARCH INTEREST

Statistical genetics (TWAS, GWAS, Mendelian randomization, risk prediction)
 Machine learning (unsupervised learning, supervised learning)

EMPLOYMENT

Assistant Professor Aug. 2018–Present
 Department of Statistics, Florida State University

EDUCATION

University of Minnesota (UMN) Minneapolis, MN
Ph.D., Biostatistics Jun. 2018
 Advisors: Drs. Weihua Guan & Wei Pan
 Thesis: Statistical methods for high-dimensional genetic and genomic data

Huazhong University of Science & Technology Wuhan, China
B.S., Applied Mathematics Jun. 2013
 Advisor: Dr. Xiaoyang Zhou

PEER-REVIEWED ARTICLES

* Corresponding author; †Co-first author.

—Methodology

1. He, Y., Xu, G., **Wu, C.**, & Pan, W. (2021). Asymptotically independent U-statistics in high-dimensional testing. *Annals of Statistics*, 49(1), 154–181.
2. **Wu, C.***, Bradley, J., Li, Y., Wu, L., & Deng, H. (2021). A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. Accepted by *Bioinformatics*.
3. **Wu, C.***, Xu, G., Shen, X., & Pan, W.* (2020). A regularization-based adaptive test for high-dimensional generalized linear models. *Journal of Machine Learning Research*, 21, 1–67.
 (This paper won the 2019 ENAR Distinguished Student Paper Award.)
4. Xue, H., **Wu, C.**, & Pan, W. (2020). Leveraging existing GWAS summary data to improve power for a new GWAS. *Genetic Epidemiology*, 44(7), 717–732.
5. **Wu, C.** (2020). Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank. *Genetics*, 215(4), 947–958.
 (This paper won a platform presentation at the American Society of Human Genetics (ASHG) 2019 Annual Meeting; highlight in *Genetics* August issue)
6. Yang, T., **Wu, C.**, Wei, P., & Pan, W. (2020). Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. *Human Molecular Genetics*, 29(3), 515–526.
7. Yang, T., Kim, J., **Wu, C.**, Ma, Y., Wei, P., & Pan, W. (2020). An adaptive test for meta-analysis of rare variant association studies. *Genetic Epidemiology*, 44(1), 104–116.

8. **Wu, C.***, & Pan, W.* (2020). A powerful fine-mapping method for transcriptome-wide association studies. *Human Genetics*, 139, 199–213.
9. **Wu, C.***, & Pan, W.* (2019) Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes. *Bioinformatics*, 35(19), 3576–3583.
10. **Wu, C.***, Xu, G., & Pan, W.* (2019). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, 29, 2163–2186.
11. **Wu, C.**, & Pan, W. (2018). Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways. *Genetics*, 209(3), 699–709.
12. Zhu, L., Li, Y., Chen, Y., Carrera, C., **Wu, C.**, & Fork, A. (2018). Comparison between two post-dentin bond strength measurement methods. *Scientific Reports*, 8(1), 2350.
13. **Wu, C.**, & Pan, W. (2018). Integrating eQTL data with GWAS summary statistics in pathway-based analysis. *Genetic Epidemiology*, 42(3), 303–316.
(Highlight by IGES. This paper won a poster talk at ASHG 2017 Annual Meeting.)
14. Park, J.Y., **Wu, C.**, Basu, S., McGue, M., & Pan, W. (2018). Adaptive SNP set association testing in generalized linear mixed models with application to family studies. *Behavior Genetics*, 48(1), 55–66.
15. Xu, Z., **Wu, C.**, Wei, P., & Pan, W. (2017). A powerful framework for integrating eQTL and GWAS summary data. *Genetics*, 207(3), 893–902.
16. Liu, B., **Wu, C.**, Shen, X., & Pan, W. (2017). A novel and efficient algorithm for de novo discovery of mutated driver pathways. *Annals of Applied Statistics*, 11(3), 1481–1512.
17. Xu, Z., **Wu, C.**, Pan, W., & Alzheimer's Disease Neuroimaging Initiative (ADNI). (2017). Imaging-wide association study: integrating imaging endophenotypes in GWAS. *NeuroImage*, 159, 159–169.
(This paper won a platform presentation at the American Society of Human Genetics (ASHG) 2017 Annual Meeting.)
18. **Wu, C.[†]**, Kwon, S.[†], Shen, X., & Pan, W. (2016). A new algorithm and theory for penalized regression-based clustering. *Journal of Machine Learning Research*, 17(188), 1–25.
19. **Wu, C.**, Chen, J., Kim, J., & Pan, W. (2016). An adaptive association test for microbiome data. *Genome Medicine*, 8(1), 1–12.
(This paper won the 2016 Joint Statistical Meetings (JSM) Distinguished Student Paper Award on Statistics in Genomics and Genetics Section.)
20. **Wu, C.**, Demerath, E. W., Pankow, J. S., Bressler, J., Fornage, M., Grove, M. L., Chen, W., & Guan, W. (2016). Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. *Epigenetics*, 11(2), 132–139.

—Applications & Collaborations

21. **Wu, C.***, Wu, L., Wang, J., Lin, L., Li, Y., Lu, Q., & Deng, H. (2021). Systematic identification of modifiable risk factors and drug repurposing options for Alzheimer's disease: Mendelian randomization analyses. Accepted by *Alzheimer's & Dementia: Translational Research & Clinical Interventions (TRCI)*.
22. Zhu, J., **Wu, C.**, & Wu, L. (2020). Associations between genetically predicted protein levels and COVID-19 severity. *The Journal of Infectious Diseases*, 223(1), 19–22.
23. Liu, D., Zhou, D., Sun, Y., Zhu, J., Ghoneim, D., **Wu, C.**, Yao, Q., Gamazon, E.R., Cox, N.J., & Wu, L. (2020). A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic

- Cancer Risk. *Cancer Research*, 80(20), 4346–4354.
24. Wu L., Yang Y., Guo X., ..., **Wu C.**, ..., Haiman C., Eccles R., & Long, J., The Practical Consortium (2020). An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. *Nature Communications*, 11(1), 1–11.
 25. Song, M., Greenbaum, J., Luttrell IV, J., Zhou, W., **Wu, C.**, Shen, H., Gong P., Zhang C., & Deng, H. W. (2020). A Review of Integrative Imputation for Multi-Omics Datasets. *Frontiers in Genetics*, 11.
 26. Zhu, J., Shu, X., Guo, X., Liu, D., Bao, J., Milne, R., Giles, G.G., **Wu, C.**, Du, M., White, E., Risch, E., Malats, N., Duell, E., Goodman, P.J., Li, D., Bracci, P., Katzke, V., Neale, R.E., Gallinger, S., Eeden, S.V., Arslan, A., Canzian, F., Kooperberg, C., Freeman, L., Scelo, G., Visvanathan, K., Haiman, C., Marchand, L.L., Yu, H., Petersen, G., Solomon, R.S., Klein, A., Cai, Q., Long, J., Shu, X., Zheng, W., & Wu L. (2020). Associations between genetically predicted blood protein biomarkers and pancreatic cancer risk. *Cancer Epidemiology, Biomarkers & Prevention*, 29(7), 1501–1508.
 27. Bose, M., **Wu, C.**, Pankow, J. S., Demerath, E. W., Bressler, J., Fornage, M., Grove, M. L., Mosley, T. H., Hicks, C., North, K., Kao, W. H., Zhang, Y., Boerwinkle, E., & Guan, W. (2014). Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics*, 15(1), 1–10.

PEER-REVIEWED PROCEEDINGS

28. Park, J. Y., **Wu, C.**, & Pan, W. (2018). An adaptive gene-level association test for pedigree data. *BMC Genetics*, 19(1), 68.
29. **Wu, C.**, Park, J.Y., Guan, W., & Pan, W. (2018). A powerful gene-based test for methylation data. *BMC Proceedings*, 12(9), 60.

SUBMITTED AND IN PREPARATION

* Corresponding author; ^o Student

30. **Wu, C.***, ..., & Wu, L.* (2020+). Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation: a multi-phased study of prostate cancer. Submitted.
31. Xie, T., Xu, C., Shi, X., **Wu, C.**, Meng, R., Meng, X., Yu, G., Wang, K., Xiao, H., & Deng, H. (2020+). Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. Submitted.
32. Guo, X., Wei, W., **Wu, C.**, & Wang, J. (2021+). Sharp Inference on Selected Subgroups in Observational Studies. Submitted.
33. Zhu J., **Wu, C.**, Zhang, Z., & Wu, L. (2021+) Associations between genetically predicted protein concentrations and Alzheimer's disease risk. Submitted.
34. Bae Y.^o, Wu, L., & **Wu, C.*** (2020+). InTACT: An adaptive and powerful framework for joint-tissue transcriptome-wide association studies. Submitted.
35. Sun, Y., Zhou, D., Rahman, R., **Wu, C.**, Zhu, J., Cox NJ., Beach TG., Wu, C., Gamazon, ER., & Wu, L. (2021+). A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. Submitted.
36. Sun, Y., Zhu, J., Zhou, D., Canchi, S., **Wu, C.**, Cox NJ., Rissman, RA. Gamazon, ER., & Wu, L. (2021+). A transcriptome-wide association study of Alzheimer's disease using prediction models of related tissues identifies novel candidate susceptibility genes. *Genome Medicine*. Under revision.

37. Wu, L.*, Zhu, J., Liu, D., Sun, Y., & **Wu, C.*** (2021+). An integrative multi-omics analysis identifies CCR9 and IFNAR2 as candidate causal genes for COVID-19 severity. *Genome Medicine*. Under revision.
38. Xie, T., Xu, C., Shi, X., **Wu, C.**, Meng, R., Meng, X., Yu, G., Wang, K., Xiao, H., & Deng, H. (2021+). Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. *Nature Communications*. Under revision.
39. Hidalgo, B., Lent, S., ..., **Wu, C.**, ..., Hivert, M.F., & Pankow J.S. for the CHARGE consortium (2021+). DNA methylation associated with glycemic traits and type 2 diabetes in multi-ethnic meta-analyses: CHARGE Consortium. *Nature Communications*. Under revision.

G R A N T S

1. Novel Statistical Methods for Transcriptome-wide Association Studies, First Year Assistant Professor grant (Wu, C.), Florida State University. 05/08/19–08/06/19. Role: PI, Total: \$20,000
2. Novel Machine Learning Methods for Alzheimer's Disease, The Committee on Faculty Research Support (Wu, C.), Florida State University. 05/07/20–06/30/20. Role: PI, Total: \$14,000
3. Novel Statistical Methods for Multi-omics Data Integration in Alzheimer's Disease, NIA R03 (Wu, C. and Bradley, J.). 01/01/21–12/31/22. Role: Contact PI, Total: \$295,903

S O F T W A R E

- Owner and maintainer for the following R packages:
 - prclust: Penalized Regression-Based Clustering Methods;
 - MiSPU: Microbiome Based Sum of Powered Score (MiSPU) Tests;
 - aSPU2: A New Version of Adaptive Sum of Powered Score (aSPU) Test;
 - GLMaSPU: Adaptive Tests on High Dimensional Parameters in Generalized Linear Models;
 - glmtp: Truncated Lasso Regularized Generalized Linear Models.
- Online software tutorial: <http://wuchong.org/software.html>
- Lab GitHub Repo: <https://github.com/ChongWuLab>

T E A C H I N G E X P E R I E N C E

- STA 4321/5323 Introduction to Mathematical Statistics
 - Instructor, Florida State University, Department of Statistics Jan. 2021–April. 2021
 - Instructor, Florida State University, Department of Statistics Jan. 2020–May. 2020
 - Instructor, Florida State University, Department of Statistics Aug. 2019–Dec. 2019
 - Instructor, Florida State University, Department of Statistics Jan. 2019–May. 2019
 - Instructor, Florida State University, Department of Statistics Aug. 2018–Dec. 2018
- STA 5934 Statistical Genetics (New topic course, designed by Wu, C.)
 - Instructor, Florida State University, Department of Statistics Aug. 2020–Dec. 2020
- PUBH 7475/8475 Statistical Learning and Data Mining (Instructors: Drs. Wei Pan and Xiaotong Shen)
 - Guest Lecturer, Division of Biostatistics, University of Minnesota Jan. 2017–May. 2017
- PUBH 6451 Biostatistics (Instructors: Dr. William Thomas)

–Lab Instructor, Division of Biostatistics, University of Minnesota

Jan. 2014–May 2014

•PUBH 6414 Biostatistical Methods (Instructors: Dr. Ann M. Brearley)

–Teaching Assistant, Division of Biostatistics, University of Minnesota

Sept. 2013–Dec. 2013

P R E S E N T A T I O N S

•“An adaptive association test for microbiome data”

–Presentation at Eastern North American Region (ENAR) 2016 Spring Meeting
Austin, TX

Mar. 2016

–Poster presented at School of Public Health Research Day, University of Minnesota
Minneapolis, MN

Apr. 2016

–Poster presented at Minnesota Supercomputing Institute (MSI) Research Exhibition
Minneapolis, MN

Apr. 2016

–Presentation at 2016 Joint Statistical Meetings (JSM)
Chicago, IL

Aug. 2016

•“Iterative PCA in epigenome-wide association studies”

–Poster presented at American Society of Human Genetics (ASHG) 2016 Annual Meeting
Vancouver, BC, Canada

Oct. 2016

•“A gene-level adaptive association test for methylation data”

–Presentation at Genetic Analysis Workshop (GAW) 20
San Diego, CA

Mar. 2017

•“An adaptive test on high dimensional parameters in GLMs”

–Presentation at ENAR 2017 Spring Meeting
Washington, DC

Mar. 2017

–Poster presented at MSI Research Exhibition
Minneapolis, MN

Apr. 2017

–Presentation at 2017 JSM
Baltimore, MD

Aug. 2017

•“Imaging-wide association study: integrating imaging endophenotypes in GWAS”

–Invited presentation at 2017 JSM (On behalf of Dr. Wei Pan)
Baltimore, MD

Aug. 2017

–Invited presentation at Third Annual Kliakhandler Conference (On behalf of Dr. Wei Pan)
Houghton, MI

Aug. 2017

•“Integrating eQTL data with GWAS summary statistics in pathway-based analysis”

–Poster talk at ASHG 2017 Annual Meeting
Orlando, FL

Oct. 2017

•“Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes”

–Oral presentation at IGES 27th Annual Meeting
San Diego, CA

Oct. 2018

- “An adaptive test for high-dimensional generalized linear models with application to detect gene-environment interactions”
 –Presentation at ENAR 2019 Spring Meeting
 Philadelphia, PA Mar. 2019
- “Complex Disease Risk Prediction via a Deep Learning Method”
 –Presentation at JSM 2019
 Denver, CO July. 2019
- “Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank”
 –Platform presentation at ASHG 2019
 Huston, TX Oct. 2019
- “A powerful fine-mapping method for transcriptome-wide association studies”
 –Invited Presentation at JSM 2020
 Virtual Aug. 2020
- “Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation: a multi-phased study of prostate cancer”
 –Department seminar at Florida State University School of Medicine
 Virtual Sep. 2020
- “A gene-level methylome-wide association analysis identifies novel Alzheimer’s disease genes”
 –Poster presented at ASHG 2020
 Virtual Oct. 2020
- “A regularization-based adaptive test for high- dimensional generalized linear models”
 –Department seminar at Shanghai University of Finance and Economics Statistics
 Virtual Dec. 2020
- Department seminar at Washington University Biostatistics
 Virtual Dec. 2020

HONORS & AWARDS

- ENAR Distinguished Student Paper Award, Mar. 2019
 –Eastern North American Region International Biometric Society
- James R. Boen Student Achievement Award May. 2018
 –Division of Biostatistics, University of Minnesota
- Pre-Doctoral Trainee Award Oct. 2017
 –Association of Chinese Geneticists in America (ACGA)
- Poster Award May 2017
 –University of Minnesota Chapter of Sigma Xi
- Elected to Delta Omega (Public Health Honorary Society) May 2017
 –University of Minnesota
- Elected to Sigma Xi (The Scientific Research Society) May 2017
 –University of Minnesota
- Distinguished Student Paper Award, Genomics and Genetics Section Aug. 2016

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- 2016 Joint Statistical Meetings
 - Doctoral Dissertation Fellowship 2016–2017
–University of Minnesota
 - Travel Award, Computational Neuroscience Summer School Jul. 2015
–Statistical and Applied Mathematical Sciences Institute
 - Dean’s Ph.D. Scholarship Sept. 2013
–University of Minnesota
 - Honorable Mention in Mathematical Contest in Modeling Apr. 2012
–Consortium for Mathematics and Its Application
 - National Scholarship Sept. 2011
–Ministry of Education, China
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PROFESSIONAL ACTIVITIES

Manuscript Reviewer

- Journal: *Statistics in Biosciences*, *Journal of Theoretical Biology*, *Plos One*, *Biometrical Journal*, *Computational Statistics and Data Analysis*, *Genetic Epidemiology*, *Bioinformatics*, *Biometrics*, *Journal of the American Statistical Association*, *Journal of Machine Learning Research*, *Statistics in Medicine*, *Genome Biology*, and *Nature Communications*.

Guest Editor, *Frontiers in Genetics*

Grant Reviewer

- Reviewer, NIA Special Emphasis panel, ZAG ZIJ-P J2, Functional genomics, 2020
- Reviewer, NCI ITCR study section, 2020