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 PUBLICATIONS

* Corresponding author; †Co-first author.

1. **Wu, C.*** , Xu, G., Shen, X., and Pan, W.* (2020+). A regularization-based adaptive test for high-dimensional generalized linear models. Accepted by *Journal of Machine Learning Research*.
(This paper won the 2019 ENAR Distinguished Student Paper Award.)

2. Xue, H., **Wu, C.**, and Pan, W. Leveraging existing GWAS summary data to improve power for a new GWAS. Accepted by *Genetic Epidemiology*.

3. Wu L., Yang Y., Guo X., Shu X., Cai Q., Shu X., Li B., Tao R., **Wu C.**, Nikas J., Sun Y., Zhu J., Roobol M., Giles G., Brenner H., John E., Clements J., Grindedal E., Park J., Stanford J., Kote-Jarai Z., Haiman C., Eeles R., Zheng W., The Practical Consortium. An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Accepted by *Nature Communications*.

4. 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.. Associations between genetically predicted blood protein biomarkers and pancreatic cancer risk. Accepted by *Cancer Epidemiology, Biomarkers & Prevention*.

5. **Wu, C.**. Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank. Accepted by *Genetics*.
(This paper won a <u>platform presentation</u> at the American Society of Human Genetics (ASHG) 2019 Annual Meeting.)

6. He, Y., Xu, G., **Wu, C.**, and Pan, W (2020). Asymptotically independent U-statistics in high-dimensional testing. Accepted by *Annals of Statistics*.

7. Yang, T., *Wu, C.*, Wei, P., and 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.

8. Yang, T., Kim, J., **Wu, C.**, Ma, Y., Wei, P., and Pan, W. (2020). An adaptive test for meta-analysis of rare variant association studies. *Genetic Epidemiology*, 44(1), 104–116.

9. **Wu, C.*** and Pan, W.* (2020). A powerful fine-mapping method for transcriptome-wide association studies. *Human Genetics*, 139, 199–213.

10. **Wu, C.*** and 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.

11. **Wu, C.***, Xu, G., and Pan, W.* (2019). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, 29, 2163–2186.

12. Nguyen, S., Guan, W., **Wu, C.**, Grove, M.L., Xia, R., Roetker, N., Holliday, K., Hibler, E., Zheng, Y., Whitsel, E., Bressler, J., North, K.E., Fornage, M., Boerwinkle, E., Pankow, J.S., and Demerath, E.W. (2018) Abstract P133: Epigenome-wide association study of moderate-vigorous physical activity in adult African-Americans identifies loci near HCCA2. *Circulation*, 137 (Suppl 1).

13. **Wu, C.** and Pan, W. (2018). Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways. *Genetics*, 209(3), 699–709.

14. Zhu, L., Li, Y., Chen, Y., Carrera, C., **Wu, C.**, and Fork, A. (2018). Comparison between two post-dentin bond strength measurement methods. *Scientific Reports*, 8(1), 2350.

15. **Wu, C.** and 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 <u>poster talk</u> (top 24 posters among about 3000 posters) at ASHG 2017 Annual Meeting.)

16. Park, J.Y., **Wu, C.**, Basu, S., McGue, M., and Pan, W. (2018). Adaptive SNP set association testing in generalized linear mixed models with application to family studies. *Behavior Genetics*,

48(1), 55–66.

17. Xu, Z., **Wu, C.**, Wei, P., and Pan, W. (2017). A powerful framework for integrating eQTL and GWAS summary data. *Genetics*, 207(3), 893–902.

18. Liu, B., **Wu, C.**, Shen, X., and Pan, W. (2017). A novel and efficient algorithm for de novo discovery of mutated driver pathways. *Annals of Applied Statistics*, 11(3), 1481–1512.

19. Xu, Z., **Wu, C.**, Pan, W., and 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.)

20. **Wu, C.**[†], Kwon, S.[†], Shen, X., and Pan, W. (2016). A new algorithm and theory for penalized regression-based clustering. *Journal of Machine Learning Research*, 17(188), 1–25.
(A leading journal in machine learning area.)

21. **Wu, C.**, Chen, J., Kim, J., and 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.)

22. **Wu, C.**, Demerath, E. W., Pankow, J. S., Bressler, J., Fornage, M., Grove, M. L., Chen, W., and Guan, W. (2016). Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. *Epigenetics*, 11(2), 132–139.
(The official journal of the DNA Methylation Society.)

23. 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., and 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

24. Park, J. Y., **Wu, C.**, and Pan, W. (2018). An adaptive gene-level association test for pedigree data. *BMC Genetics*, 19(1), 68.

25. **Wu, C.**, Park, J.Y., Guan, W., and Pan, W. (2018). A powerful gene-based test for methylation data. *BMC Proceedings*, 12(9), 60.

SUBMITTED AND IN PREPARATION

* Corresponding author

26. **Wu, C.***, Bradley, J., Li, Y., Wu, L., Deng, H. (2020+). A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. Submitted.

27. **Wu, C.***, Wu, L., Wang, J., Lin, L., Li, Y., Lu, Q., Deng, H. (2020+). Systematic identification of modifiable risk factors and drug repurposing options for Alzheimer's disease: Mendelian randomization analyses. Submitted.

28. **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.

29. 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.

30. Song, M., Greenbaum, J., Luttrell J., Zhou W, **Wu, C.**, Shen, H., Gong, P., Zhang, C., Deng, H. (2020+). A Review of Integrative Imputation for Multi-Omics Datasets. Submitted.

31. Guo, X., Wang, J., **Wu, C.** (2020+). Sharp Inference on Maximal Heterogeneous Treatment Effect in Observational Studies. Submitted.

32. Zhu, J., **Wu, C.**, Wu, L. (2020+). Associations between genetically predicted blood protein biomarkers and COVID-19 severity: analyses of 3,199 hospitalized patients and 897,488 population controls. Submitted.

33. Hidalgo, B., Lent, S., DiCorpo, D., Cardona, A., Guan, W., Chu, A., Wessel, J., Day, F., Absher, D.M., Arnett, D.K., Aslibekyan, S., Assimes, T.L., Baccarelli, A., Bandinelli, S., Bell, J.T., Bielak, L.F., Boerwinkle, E., Bressler, J., Brody, J., Chia, C., Montoro, E.C., Day, F., Deary, I., Djousse, L., Dupuis, J., Egan, J., Feinberg, A., Ferrucci, L., Floyd, J., Gieger, C., Grallert, H., Herder, C., Hernandez, D., Hill, W.D., Horvath, F., Hou, L., Huan, T., Irvin, M.R., Jhun, M., Joehanes, R., Kardia, S., Kriebel, J., Lamichhane, A.P., Lemaitre, R.N., Levy, D., Li, Y., Ligthart, S., Liu, C., Liu, J., Marioni, R.E., Meigs, J., Mendelson, M., Moore, A.Z., Mukamal, K.J., Ong, K., Peters, A., Rathmann, W., Rotter, J.I., Salfati, E.I., Selvin, E., Singleton, A.B., Sotoodehnia, N., Smith, J.A., Starr, J.M., Tanaka, T., Taylor, K.D., Tsai, P., Tsao, P.S., Vandiver, A.S., Duijn, C., Meurs, J., Wareham, N., Whitsel, E.A, **Wu, C.**, Zhang, G., Zhao W., Hivert, M.F., Pankow J.S. for the CHARGE consortium. DNA methylation associated with glycemic traits and type 2 diabetes in multi-ethnic meta-analyses: CHARGE Consortium, submitted.

GRANT

1. PI, Novel Statistical Methods for Transcriptome-wide Association Studies, First Year Assistant Professor grant, Florida State University. 05/08/19–08/06/19. (Cost: $20,000)

2. PI, Novel Machine Learning Methods for Alzheimer's Disease, The Committee on Faculty Research Support, Florida State University. 05/07/20–06/30/20. (Cost: 14,000)

SOFTWARE

- 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;

      –glmtlp: Truncated Lasso Regularized Generalized Linear Models.

- Contributor: Theano (Pull request: # 6130).

- Online software tutorial: http://wuchong.org/software.html

TEACHING EXPERIENCE

Instructor   Jan. 2019–May. 2020
Course Name: STA 4321/5323 Introduction to Mathematical Statistics
Department of Statistics, Florida State University

Instructor   Aug. 2018–Dec. 2018
Course Name: STA 4321/5323 Introduction to Mathematical Statistics
Department of Statistics, Florida State University

Guest Instructor   Jan. 2017–May 2017
Course Name: PUBH 7475/8475 Statistical Learning and Data Mining
Division of Biostatistics, University of Minnesota

Lab Instructor, Instructor: Prof. William Thomas   Jan. 2014–May 2014
Course Name: PUBH 6451 Biostatistics II
Division of Biostatistics, University of Minnesota

Teaching Assistant, Instructor: Prof. Ann M. Brearley   Sept. 2013–Dec. 2014
Course Name: PUBH 6414 Biostatistical Methods I (Online Section)
Division of Biostatistics, University of Minnesota

PRESENTATIONS

- "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 Prof. Wei Pan's behalf)
Baltimore, MD   Aug. 2017

–Invited presentation at Third Annual Kliakhandler Conference (On Prof. Wei Pan's behalf)
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

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
   –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

PROFESSIONAL ACTIVITIES

Manuscript Reviewer

   •Journal: Statistics in Biosciences, Journal of Theoretical Biology, 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.

   •Conference: 2017 Joint Statistical Meetings Student Paper Award Reviewer

Professional Memberships

   •Member, American Statistical Association   2014–Present

   •Member, Eastern North American Region   2015–Present

   •Member, The American Society of Human Genetics   2016–Present