

## CHONG WU

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## RESEARCH INTEREST

Statistical genetics (gene-based test, TWAS, GWAS); 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 GPA: 3.8/4.0  
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 GPA: 3.9/4.0; Ranking: 1/29

## PEER-REVIEWED PUBLICATIONS

\* Corresponding author; †Co-first author.

1. **Wu, C.\*** and Pan, W.\* (2019) Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes. Accepted by *Bioinformatics*.
2. **Wu, C.\***, Xu, G., and Pan, W.\* (2019+). An adaptive test on high dimensional parameters in generalized linear models. Accepted by *Statistica Sinica*.
3. 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).
4. **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.
5. 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.

6. **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 poster talk (top 24 posters among about 3000 posters) at ASHG 2017 Annual Meeting.)
7. 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.
8. 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.
9. 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.
10. 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.)
11. **Wu, C.**<sup>†</sup>, Kwon, S.<sup>†</sup>, 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.)
12. **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.)
13. **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.)
14. 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.

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## P E E R - R E V I E W E D P R O C E E D I N G S

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15. Park, J. Y., **Wu, C.**, and Pan, W. (2018). An adaptive gene-level association test for pedigree data. *BMC Genetics*, 19(1), 68.
16. **Wu, C.**, Park, J.Y., Guan, W., and Pan, W. (2018). A powerful gene-based test for methylation

data. *BMC Proceedings*, 12(9), 60.

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## S U B M I T T E D   A N D   I N   P R E P A R A T I O N

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\* Corresponding author

17. **Wu, C.\***, Xu, G., Shen, X., and Pan, W.\* (2017+). A regularization-based adaptive test for high-dimensional generalized linear models. Under review.  
(This paper won the 2019 ENAR Distinguished Student Paper Award.)
18. He, Y., Xu, G., **Wu, C.**, and Pan, W. Asymptotically independent U-statistics in high-dimensional testing. Resubmitted.
19. **Wu, C.\*** and Pan, W.\* A powerful fine-mapping method for transcriptome-wide association studies. Under review.
20. **Wu, C.** Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank. Under review.
21. Yang, T., **Wu, C.**, Wei P., and Pan, W. Integration of DNA sequencing and transcriptomic data for association analyses of rare variants and lipid traits. Submitted.
22. Yang, T., Kim, J., **Wu, C.**, Ma, Y., Wei P., and Pan, W. Adaptive test for meta-analysis of rare variant association studies. Under review.
23. Yang, T, Kim, J., **Wu, C.**, Ma, Y., Wei, P., Pan, W. Adaptive test for meta-analysis of rare variant association studies. Submitted.
24. **Wu, C.** and Pan, W. Network-based support vector machines with a new penalty. In Preparation.
25. **Wu, C.**, Kim, J., Wei, P., and Pan, W. Adaptive test for meta-analysis of rare variants in sequencing association studies. In preparation.

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## G R A N T

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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)

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## S O F T W A R E

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- 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.

- Contributor: Theano (Pull request: # 6130).
- Online software tutorial: <http://wuchong.org/software.html>

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## TEACHING EXPERIENCE

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<b>Instructor</b>	Jan. 2019–May. 2019
Course Name: STA 4321/5323 Introduction to Mathematical Statistics	
Department of Statistics, Florida State University	
<b>Instructor</b>	Aug. 2018–Dec. 2018
Course Name: STA 4321/5323 Introduction to Mathematical Statistics	
Department of Statistics, Florida State University	
<b>Guest Instructor</b>	Jan. 2017–May 2017
Course Name: PUBH 7475/8475 Statistical Learning and Data Mining	
Division of Biostatistics, University of Minnesota	
<b>Lab Instructor</b> , Instructor: Prof. William Thomas	Jan. 2014–May 2014
Course Name: PUBH 6451 Biostatistics II	
Division of Biostatistics, University of Minnesota	
<b>Teaching Assistant</b> , Instructor: Prof. Ann M. Brearley	Sept. 2013–Dec. 2014
Course Name: PUBH 6414 Biostatistical Methods I (Online Section)	
Division of Biostatistics, University of Minnesota	

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## PRESENTATIONS

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- “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. 2018

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## HONORS & AWARDS

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- ENAR Distinguished Student Paper Award,** 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

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

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## P R O F E S S I O N A L   A C T I V I T I E S

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### Manuscript Reviewer

- Journal: Statistics in Biosciences, Journal of Theoretical Biology, Biometrical Journal, Computational Statistics and Data Analysis, Genetic Epidemiology, Bioinformatics, Biometrics
- Conference: 2017 Joint Statistical Meetings Student Paper Award Reviewer

### Professional Memberships

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| •Member, American Statistical Association       | 2014–Present |
| •Member, Eastern North American Region          | 2015–Present |
| •Member, The American Society of Human Genetics | 2016–Present |