

# CHONG WU

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## RESEARCH INTEREST

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High-dimensional data, big data, machine learning, statistical genetics

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## EDUCATION

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**University of Minnesota (UMN)** Minneapolis, MN  
**Ph.D., Biostatistics** May 2018 (Expected)  
Advisors: Prof. Weihua Guan & Prof. 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: Prof. Xiaoyang Zhou GPA: 3.9/4.0; Ranking: 1/29

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## RESEARCH EXPERIENCE

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**Graduate Research Assistant**, Advisor: Prof. Wei Pan Sept. 2014–Present  
Research areas: high-dimensional genetic and genomic data, machine learning, statistical genetics  
Division of Biostatistics, University of Minnesota

**Graduate Research Assistant**, Advisor: Prof. Weihua Guan Sept. 2013–May 2017  
Research areas: statistical genetics, methylation data  
Division of Biostatistics, University of Minnesota

**Undergraduate Research Assistant**, Advisor: Prof. Xiaoyang Zhou 2011–2013  
Research areas: data mining on regional economic indicators  
School of Mathematics and Statistics, Huazhong University of Science & Technology

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## TEACHING EXPERIENCE

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**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

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PEER-REVIEWED PUBLICATIONS

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1. Zhu, L., Li, Y., Chen, Y., Carrera, C., **Wu, C.**, and Fork, A. (2018). Comparison between two post-dentin bond strength measurement methods. Accepted by *Scientific Reports*. (IF: 4.3)
2. **Wu, C.** and Pan, W. (2017+). Integrating eQTL data with GWAS summary statistics in pathway-based analysis. Accepted by *Genetic Epidemiology*.  
(This paper won a poster talk (top 24 posters among about 3000 posters) at ASHG 2017 Annual Meeting.)
3. **Wu, C.\***, Xu, G., and Pan, W.\* (2017+). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, minor revision. (\* Corresponding author)
4. 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. (IF: 2.4)
5. Xu, Z., **Wu, C.**, Wei, P., and Pan, W. (2017+). A powerful framework for integrating eQTL and GWAS summary data. Accepted by *Genetics*, early online. (IF: 4.6)
6. 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*, 17(3):1481–1512.
7. 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.  
(IF: 5.8. This paper won a platform presentation at the American Society of Human Genetics (ASHG) 2017 Annual Meeting.)
8. **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.  
(\* Co-first author. IF: 5.0, a leading journal in machine learning area.)
9. **Wu, C.**, Chen, J., Kim, J., and Pan, W. (2016). An adaptive association test for microbiome data. *Genome Medicine*, 8(1):1–12.  
(IF: 7.1. This paper won the 2016 Joint Statistical Meetings (JSM) Distinguished Student Paper Award on Statistics in Genomics and Genetics Section.)
10. **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.  
(IF: 4.4, the official journal of the DNA Methylation Society.)
11. 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

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Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics*, 15(1):1–10. (IF: 2.4)

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### PEER-REVIEWED PROCEEDINGS

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12. Park, J. Y., **Wu, C.**, and Pan, W. (2017+). An adaptive gene-level association test for pedigree data. Accepted by *BMC Proceedings*, a special issue for the Genetic Analysis Workshop (GAW 20).
  13. **Wu, C.**, Park, J.Y., Guan, W., and Pan, W. (2017+). A powerful gene-based test for methylation data. Accepted by *BMC Proceedings*, a special issue for the Genetic Analysis Workshop (GAW 20).
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### SUBMITTED AND IN PREPARATION

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14. **Wu, C.** and Pan, W. (2017+). Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways. Submitted.
  15. **Wu, C.**, Xu, G., Shen, X., and Pan, W. (2017+). An adaptive test on a high-dimensional parameter in the presence of a high-dimensional nuisance parameter in GLM with application to detect gene-environment interactions. Manuscript.  
(Job talk manuscript, to be submitted to *Journal of the American Statistical Association*.)
  16. Gaeckle, N., Pragman A., Gould T., **Wu, C.**, and Criner, G. (2017+). Current smoking alters the oral microbiome in subjects with COPD. Submitted.
  17. Steven 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., Demerath, and E.W. (2017+) Epigenome-wide association study of moderate-vigorous physical activity in African-American adults. Submitted.
  18. **Wu, C.**, Xu, G., and Pan, W. An adaptive and powerful test for high dimensional covariance matrices. In Preparation.
  19. **Wu, C.** and Pan, W. Network-based support vector machines with a new penalty. In Preparation.
  20. **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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### SOFTWARE

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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;
  - glmTLP: Truncated Lasso Regularized Generalized Linear Models.
- Contributor: Theano (Pull request: # 6130).

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

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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

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## H O N O R S & A W A R D S

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- **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

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## WORK EXPERIENCE

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**Biostatistics Intern**, Advisor: Dr. Jeff Budd May 2014–Aug. 2014  
 Roles: Developed programs in S+ for statistical analysis  
 Beckman Coulter, Chaska, MN

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## PROFESSIONAL ACTIVITIES

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### Manuscript Reviewer

- Journal: Statistics in Biosciences, Journal of Theoretical Biology, Biometrical Journal, Computational Statistics and Data Analysis, Genetic Epidemiology, Bioinformatics
- 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

### Programming Skills

- R, Python, MATLAB, C++