CHONG WU

A460 Mayo Building, MMC 303 420 Delaware St SE, Minneapolis, MN, 55455 ⊠: chongwu@umn.edu; **☎**: 612-516-2222

http://wuchong.org

RESEARCH INTEREST

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

EDUCATION

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

RESEARCH EXPERIENCE

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

TEACHING EXPERIENCE

Jan. 2017-May 2017 Guest Instructor

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

PEER-REVIEWED PUBLICATIONS

- 1. 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)
- 2. Liu, B., Wu, C., Shen, X., and Pan, W. (2017+). A novel and efficient algorithm for de novo discovery of mutated driver pathways. Accepted by *Annals of Applied Statistics*, early online.
- 3. 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 <u>platform presentation</u> at the American Society of Human Genetics (ASHG) 2017 Annual Meeting.)
- 4. 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.)
- 5. 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.)
- 6. 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.)
- 7. 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. (IF: 2.4)

PEER-REVIEWED PROCEEDINGS

- 8. 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).
- 9. 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).

SUBMITTED AND IN PREPARATION

- 10. **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.)
- Wu, C. and Pan, W. (2017+). Integrating eQTL data with GWAS summary statistics in pathway-based analysis. Submitted.
 (This paper won a poster talk (top 24 posters among about 3000 posters) at ASHG 2017 Annual Meeting.)
- 12. Wu, C.*, Xu, G., and Pan, W.* (2017+). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, revised and resubmitted. (* Corresponding author)
- 13. Zhu, L., Li, Y., Chen, Y., Carrera, C., Wu, C., and Fork, A. (2017+). Comparison between two post-dentin bond strength measurement methods. *Scientific Reports*, revised and resubmitted.
- 14. Park, J.Y., **Wu**, C., Basu, S., McGue, M., and Pan, W. (2017+). Adaptive SNP set association testing in generalized linear mixed models with application to family studies. *Behavior Genetics*, revised and resubmitted.
- 15. Wu, C., Xu, G., and Pan, W. An adaptive and powerful test for high dimensional covariance matrices. In Preparation.
- 16. Wu, C. and Pan, W. Network-based support vector machines with a new penalty. In Preparation.
- 17. **Wu**, **C**., Kim, J., Wei, P., and Pan, W. Adaptive test for meta-analysis of rare variants in sequencing association studies. In preparation.

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).

PRESENTATIONS

- "An adaptive association test for microbiome data."
 - Presentation at Eastern North American Region (ENAR) 2016 Spring Meeting

Αι	ustin, TX	Mar.	2016
	oster presented at School of Public Health Research Day, University of Minnesota Iinneapolis, MN	Apr.	2016
	oster presented at Minnesota Supercomputing Institute (MSI) Research Exhibition Iinneapolis, MN	Apr.	2016
	resentation at 2016 Joint Statistical Meetings (JSM) hicago, IL	Aug.	2016
- Po	ntive PCA in epigenome-wide association studies." oster presented at American Society of Human Genetics (ASHG) 2016 Annual Medancouver, BC, Canada		2016
– Pr	rne-level adaptive association test for methylation data." resentation at Genetic Analysis Workshop (GAW) 20 an Diego, CA	Mar.	2017
– Pr	ndaptive test on high dimensional parameters in GLMs." resentation at ENAR 2017 Spring Meeting Vashington, DC	Mar.	2017
	oster presented at MSI Research Exhibition Iinneapolis, MN	Apr.	2017
	resentation at 2017 JSM altimore, MD	Aug.	2017
– In	ging-wide association study: integrating imaging endophenotypes in GWAS" wited presentation at 2017 JSM (On Prof. Wei Pan's behalf) altimore, MD	Aug.	2017
	evited presentation at Third Annual Kliakhandler Conference (On Prof. Wei Pan's b Toughton, MI		f) 2017
- Po	grating eQTL data with GWAS summary statistics in pathway-based analysis" oster talk at ASHG 2017 Annual Meeting orlando, FL	Oct.	2017
	HONORS & AWARDS		
	er Award niversity of Minnesota Chapter of Sigma Xi	May	2017
	ed to Delta Omega (Public Health Honorary Society) niversity of Minnesota	May	2017
	ed to Sigma Xi (The Scientific Research Society) niversity of Minnesota	May	2017

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

WORK EXPERIENCE

Biostatistics Intern, Advisor: Dr. Jeff Budd

May 2014-Aug. 2014

Roles: Developed programs in S+ for statistical analysis

Beckman Coulter, Chaska, MN

PROFESSIONAL ACTIVITIES

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++