

CHONG WU

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<http://www.tc.umn.edu/~wuxx0845/>

Research Interests: high-dimensional data, big data, machine learning, statistical genetics, microbiome data, methylation data

Education

University of Minnesota (UMN)

Minneapolis, MN

Ph.D., Biostatistics.

May 2017 (Expected)

Advisors: Prof. Weihua Guan & Prof. Wei Pan; GPA: 3.8/4.0

Thesis: Statistical Methods for High-dimensional Genomic Data

Huazhong University of Science & Technology

Wuhan, China

B.S., Applied Mathematics.

June 2013

Advisor: Prof. Xiaoyang Zhou; GPA: 3.9/4.0; Ranking: 1/29

Research Experience

Graduate Research Assistant, Advisor: Prof. Wei Pan

September 2014–Present

Topics: high-dimensional test, machine learning, statistical genetics

Division of Biostatistics, University of Minnesota

Graduate Research Assistant, Advisor: Prof. Weihua Guan

September 2013–Present

Topics: statistical genetics, methylation data

Division of Biostatistics, University of Minnesota

Undergraduate Research Assistant, Advisor: Prof. Xiaoyang Zhou

2011–2013

Topics: data mining on regional economic indicators

School of Mathematics and Statistics, Huazhong University of Science & Technology

Teaching Experience

Lab Instructor, Instructor: Prof. William Thomas,

January 2014–May 2014

Course Name: PUBH 6451 Biostatistics II

Division of Biostatistics, University of Minnesota

Teaching Assistant, Instructor: Prof. Ann M. Brearley,

September 2013–July 2014

Course Name: PUBH 6414 Biostatistical Methods I (Online Section)

Division of Biostatistics, University of Minnesota

Peer-reviewed Publications

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), pp.1–25.

Wu, C., Chen, J., Kim, J. and Pan, W., 2016. An adaptive association test for microbiome data. *Genome Medicine*, 8(1), pp.1–12.

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), pp.132–139.

Bose, M., **Wu, C.**, Pankow, J.S., Demerath, E.W., Bressler, J., Fornage, M., Grove, M.L., Mosley, T.H., Hicks, C., North, K. and Kao, W.H., 2014. Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics*, 15(1), pp.312–322.

Submitted and In Preparation

Wu, C., Xu, G., and Pan W. An Adaptive Test on High Dimensional Parameters in Generalized Linear Models. *Journal of Machine Learning Research*, submitted.

Wu C., Xu G., and Pan W. An adaptive and powerful test for high dimensional covariance matrices.

Wu C. and Pan W. Network-based support vector machines with a new penalty.

Wu C., Pankow J. S., Demerath E. W., Bressler W., Grove M. L., Fornage M., and Guan W. Iterative PCA in epigenome-wide association studies.

Software

Independently developed and maintained the following software

- prclust: R package that makes it incredibly easy to use penalized regression based clustering method. It has been downloaded more than 2,000 times.
- MiSPU: R package that makes it easy to use an adaptive and powerful test in microbiome association studies.
- MethyImpute: R package that makes it easy to impute the missing covariates in methylation studies.
- GLMaSPU: R package that makes it incredibly easy to implement some testing methods in high dimensional generalized linear models framework.
- GitHub repository: <https://github.com/ChongWu-Biostat>.

Presentations

- "An adaptive association test for microbiome data." March 2016
Presentation at ENAR 2016 Spring Meeting, Austin, TX.
- "An adaptive association test for microbiome data." April 2016

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

- "An adaptive association test for microbiome data." April 2016
Poster presented at MSI Research Exhibition, University of Minnesota, Minneapolis, MN.
- "An adaptive association test for microbiome data." August 2016
Presentation at Joint Statistical Meetings, Chicago, IL.
- "Iterative PCA in epigenome-wide association studies." October 2016
Poster presented at ASHG 2016, Vancouver, BC, Canada.

Honors & Awards

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

Work Experience

Biostatistics Intern , Adviosr: Dr. Jeff Budd Roles: Developed programs in S+ for statistical analysis Beckman Coulter, Chaska, MN	May 2014–August 2014
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Professional Activities

Manuscript Reviewer

- Statistics in Biosciences

Professional Memberships

- American Statistical Association 2014–Present
- Eastern North American Region, International Biometric Society 2015–Present
- The American Society of Human Genetics 2016–Present