

# Yiming Hu

## Curriculum Vitae

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Address: Department of Biostatistics  
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## Education

- 2013 - 2018 **Yale University**, New Haven, CT, USA  
Department of Biostatistics  
**Ph.D. in Biostatistics**, Advisor: Dr. Hongyu Zhao  
Dissertation: *Improving genetic risk prediction of human complex traits by integrating diverse types of genomic data*
- 2009 - 2013 **Peking University**, Beijing, China  
School of Mathematical Sciences  
**B.Sc. in Mathematics and Statistics**, Advisor: Dr. Ruibin Xi  
Thesis: *Bayesian quantile regression based on the empirical likelihood with spike and slab priors*

## Honors and Awards

- 2017 First place, Citadel & Correlation One Datathon  
2017 Silver medal (Top 4% of 3,307), Kaggle challenge: Quora Question Pairs  
2013 Outstanding Graduate of Peking University  
2012 Xianzi Zeng Scholarship of Peking University  
2011 Outstanding Academic Performance Award in Peking University

## Publications

### Published Papers

- [1] **Hu, Y.**, Lu Q., Liu W., Zhang Y., Li M., Zhao H. (2017). **Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction.** *PLOS Genetics*, 13(6): e1006836.
- [2] **Hu, Y.\***, Lu Q.\*, Powles R., Yao X., Yang C., Fang F., Xu X., Zhao H. (2017). **Leveraging functional annotations in genetic risk prediction for human complex diseases.** *PLOS Computational Biology*, 13(6): e1005589.
- [3] Lu Q., Li B., Ou D., Erlendsdottir M., Powles R., Jiang T., **Hu Y.**, Chang D., Jin C., Dai W., He Q., Liu Z., Mukherjee S., Crane P., Zhao H. (2017). A powerful approach to estimating annotation-stratified genetic covariance using GWAS summary statistics. *American Journal of Human Genetics*, in press.
- [4] Lu Q., Powles R., Abdallah S., Ou D., Wang Q., **Hu Y.**, Lu Y., Liu W., Li B., Mukherjee S., Crane P., Zhao H. (2017). Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease. *PLOS Genetics*, 13(7): e1006933.
- [5] Li M., Foli Y., Liu Z., Wang G., **Hu, Y.**, Lu Q., Selvaraj S., Lam W., Paintsil E. (2017). High frequency of mitochondrial DNA mutations in HIV-infected treatment-experienced individuals. *HIV Medicine*, 18 (1), 45-55.
- [6] **Hu, Y.**, Zhao H. (2016). **CCor: a whole genome network-based similarity measure between two genes.** *Biometrics*, 72(4)-1225.
- [7] Xi, R., Li, Y., **Hu, Y.** (2015). Bayesian quantile regression based on the empirical likelihood with spike and slab priors. *Bayesian Analysis*, Volume 11, 821-855.

- [8] Lu Q., **Hu, Y.**, Sun J., Cheng Y., Cheung K., Zhao H. (2015). A statistical framework to predict functional non-coding regions in the human genome through integrated analysis of annotation data. *Scientific Reports*, 5, 10576.
- [9] Lu, Q., Yao, X., **Hu, Y.**, Zhao, H. (2015). GenoWAP: Post-GWAS Prioritization through integrated analysis of genomic functional annotation. *Bioinformatics*, 32(4), 542-548.

### Submitted & Working Papers

- [1] **Hu, Y.\***, Li M.\*, Lu Q.\*, Wang J., Li B., Muchnik S., Shi Y., Kunkle B., Mukherjee S., Crane P., Zhao H. (2017) **A cross-tissue framework to impute gene expression and identify gene-level associations for complex traits.** (To be submitted)
- [2] Li M., **Hu, Y.**, Lu Q., Zhao H. (2017) Integrative analysis of GWAS summary statistics and imputed gene expression in 44 tissues deciphers genetic architecture for many complex traits. (Working)

### Presentations

- 10/2017 Platform presentation, *Joint prediction of gene expression in 44 tissues identifies context-specific associations for complex traits.*, American Society of Human Genetics Annual Meeting, Orlando
- 08/2017 Oral presentation, *Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction*, Joint Statistical Meetings, Baltimore
- 08/2016 Oral presentation, *Leveraging functional annotations in genetic risk prediction for human complex diseases*, Joint Statistical Meetings, Chicago
- 04/2016 Poster presentation, *CCor: a whole genome network-based similarity measure between two genes*, New England Statistical Symposium, New Haven

### Teaching

#### Teaching Assistant

- Fall 2014-2017 Computational Statistics, Yale University, New Haven, CT
- Spring 2015 Introduction to Statistical Thinking, Yale University, New Haven, CT
- Spring 2016 Multivariate Statistics, Yale University, New Haven, CT
- Spring 2017 Applied Survival Analysis, Yale University, New Haven, CT

### Professional Activities

#### Professional Membership

- 2017-present Member, American Society of Human Genetics (ASHG)
- 2017-present Member, Association of Chinese Geneticists in America (ACGA)
- 2016-present Member, American Statistical Association (ASA)

#### Journal Referee

*Annals of Applied Statistics, PLOS Computational Biology, Statistical Applications in Genetics and Molecular Biology, Heredity, Journal of Genetics and Genomics*