

Yiming Hu

Curriculum Vitae

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Experience and Education

- 2022 - now Voleon Group, Berkeley, CA, USA
Senior Member of Research Staff
- 2018 - 2021 Voleon Group, Berkeley, CA, USA
Member of Research Staff
- 2013 - 2018 **Yale University**, New Haven, CT, USA
Department of Biostatistics
Ph.D. in Biostatistics, Advisor: Dr. Hongyu Zhao
Dissertation: *Integrative analysis of multi-omics data improves genetic risk prediction and transcriptome-wide association analysis*
- 2009 - 2013 **Peking University**, Beijing, China
School of Mathematical Sciences
B.Sc. in Statistics, Advisor: Dr. Ruibin Xi
Thesis: *Bayesian quantile regression based on the empirical likelihood with spike and slab priors*

Honors and Awards

- 2020 Outstanding Statistical Application Award, American Statistical Association
- 2017 First place, Citadel & Citadel Securities Data Open
- 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 of Peking University

Publications

- [14] Bigdeli, T. B., Fanous, A. H., Li, Y., Rajeevan, N., Sayward, F., Genovese, G., Gupta, R., Radhakrishnan, K., Malhotra, A., Sun, N., Lu, Q., **Hu, Y.**, ..., Harvey, P. D. (2021). Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. *Schizophrenia bulletin*, 47(2), 517-529.
- [13] Harvey P., Sun N., Bigdeli T., Fanous A., Aslan M., Malhotra A., Lu Q., **Hu Y.**, ..., Zhao H., Siever L. (2020). Genome-wide association study of cognitive performance in US veterans with schizophrenia or bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, 183(3), 181-194.
- [12] **Hu, Y.**^{*}, Li M.^{*}, Lu Q.^{*}, Wang J., Li B., Muchnik S., Shi Y., Kunkle B., Mukherjee S., Crane P., Zhao H. (2019) A statistical framework for cross-tissue transcriptome-wide association analysis. *Nature Genetics*, 51(3), 568-576.
- [11] Gelernter J., Sun N., Polimanti R., Levey D., Pietrzak R., Bryois J., Lu Q., **Hu Y.**, ..., Zhao H., Stein M., on behalf of the Department of Veterans Affairs Cooperative Studies Program (#575B) and Million Veteran Program. (2019). Genome-wide association study of posttraumatic stress disorder (PTSD) re-experiencing symptoms in

>165,000 US veterans. *Nature Neuroscience*, in press.

[10] Gelernter J., Sun N., Polimanti R., Pietrzak R., Levey D., Lu Q., **Hu Y.**, ..., Zhao H., Stein M., on behalf of the Department of Veterans Affairs Cooperative Studies Program (#575B) and Million Veteran Program. (2019). Genomewide association study of maximum habitual alcohol intake in >140,000 US European- and African-American veterans yields novel risk loci. *Biological Psychiatry*, in press.

[9] **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.

[8] **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.

[7] 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*, 101(6), 939-964.

[6] 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.

[4] **Hu, Y.**, Zhao H. (2016). CCor: a whole genome network-based similarity measure between two genes. *Bioinformatics*, 72(4)-1225.

[3] 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.

[2] 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.

[1] 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.

Conferences and Invited talks

- 02/2018 Invited talk, Department of Biostatistics and Bioinformatics, Duke University, NC
- 02/2018 Invited talk, Department of Statistical Science, University of Toronto, ON
- 01/2018 Invited talk, Department of Statistics, University of Illinois at Urbana-Champaign, IL
- 01/2018 Invited talk, Division of Human Genetics, Department of Psychiatry, Yale University, CT
- 10/2017 Platform presentation, American Society of Human Genetics Annual Meeting, Orlando, FL
- 08/2017 Oral presentation, Joint Statistical Meetings, Baltimore, MD
- 08/2016 Oral presentation, Joint Statistical Meetings, Chicago, IL
- 04/2016 Poster presentation, New England Statistical Symposium, New Haven, CT

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

2017-2019 Member, American Society of Human Genetics (ASHG)
2017-2019 Member, Association of Chinese Geneticists in America (ACGA)
2016-2019 Member, American Statistical Association (ASA)

Journal Referee

- Annals of Applied Statistics
- Bioinformatics
- Nature Genetics
- American Journal of Human Genetics
- PLOS Computational Biology
- Statistical Applications in Genetics and Molecular Biology
- Frontiers in Genetics
- Heredity
- Journal of Genetics and Genomics
- Genetic Testing and Molecular Biomarkers