Yiming Hu

Curriculum Vitae

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Experience and Education

2018 - now Voleon Group, Berkeley, CA, USA
Member of Research Staff
- Developing nonparametric prediction models for non-stationary time series data
- Developing ensemble learning methods to combine multiple forecasting models
- Building optimization frameworks for portfolio construction

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 Mathematics and 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] **Hu, Y.**, Zhao, Z., Lu, Q., Zhao, H. (2019) A cross-trait genetic risk prediction framework leveraging biobank-scale GWAS summary statistics. *In preparation*
[13] **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.
[12] Harvey P., Sun N., Bigdeli T., Fanous A., Aslan M., Malhotra A., Lu Q., **Hu Y.**, Li B., Chen Q., Mane S., Miller P., Rajeevan N., Sayward F., Cheung K., Li Y., Greenwood T., Gur R., Braff D., Consortium on the Genetics of Schizophrenia (COGS), Brophy M., Pyarajan S., Gleason T., Przygodszki R., O'Leary T., Muralidhar S., Gaziano M., Million Veteran Program (MVP), Huang G., Concato J., Zhao H., Siever L. (2019). 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.
[11] Gelernter J., Sun N., Polimanti R., Levey D., Pietrzak R., Bryois J., Lu Q., **Hu Y.**, Li B., Radhakrishnan K., Aslan M., Cheung K., Li Y., Rajeevan N., Sayward F., Harrington K., Chen Q., Cho K., Pyarajan S., Sullivan P., Quaden R., Shi Y., Hunter-Zink H., Gaziano J., Concato J., 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.**, Li B., Radhakrishnan K., Aslan M., Cheung K., Li Y., Rajeevan N., Sayward F., Harrington K., Chen Q., Cho K., Honerlaw J., Pyarajan S., Lencz T., Quaden R., Shi Y., Hunter-Zink H., Gaziano J., Kranzler H., Concato J., 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. ***Biometrics***, 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
- Heredity
- Journal of Genetics and Genomics