Kunling Huang

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SUMMARY OF QUALIFICATION

- Extensive experience in analyzing large-scale omics data on cloud environments
- Advanced knowledge of GWAS and eQTL drug discovery pipelines
- Familiarity with public variant databases such as NCBI, gnomAD, and Ensembl
- Strong oral and interpersonal skills in a fast-pace and collaborative environment

SKILLS

- Operation systems: Linux/Unix
- Programming languages: R, Python
- Bioinformatics tools: bcftools, GATK, Plink

EDUCATION

Doctor of philosophy in Statistics, *University of Wisconsin-Madison* Sep 2016 – Nov 2022

- Dissertation: "**Statistical methods for linking noncoding genetic variation to target genes with applications in neurodevelopmental disorders**" (Advisor: Dr. Qiongshi Lu)
- Relative course work: Human Genetics, Advanced Bioinformatics, Machine Learning, Computational Network Biology, Clinical trials, Causal Inference, Experimental Design

INTERNSHIPS

Computational Biologist Intern (Remote), *23andMe* June 2021 – Sep 2021

- Established a deep learning prediction pipeline on Amazon Elastic Compute Cloud
- Evaluated the prediction pipeline performance on 43 selected eQTLs across 25 tissues using python package pytorch

PROJECTS

Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder

- Conducted a large-scale transcriptome-wide association study (N associations=750K) on autism spectrum disorder (ASD) genetics data (N samples=18K)
- Designed and optimized parallel computing strategy on high-throughput computing environments
- Developed data analyzing pipeline using R libraries tidyverse and data.table (project code available at: https://github.com/qlu-lab/TITANS)
- Validated novel ASD genes through DNase-I network analysis and *de novo* variant enrichment analysis with collaborators

Multi-biofluid metabolome-wide association study illuminates the molecular basis in complex trait genetics

- Constructed polygenic score models from 2,558 metabolite GWASs for 370K UK biobank individuals
- Performed metabolome-wide association scan across 530 UK biobank traits (N association=170K)
- Predicted functional outcomes for metabolite QTLs using Ensembl tool variant effect predictor (VEP)
- Conducted extensive literature review on top steroid metabolites for cardiovascular diseases and adiposity

Trans-ethnic meta-analysis identifies novel loci for congenital heart disease

- Curated microarray and next-generation sequencing (NGS) family data using Plink and bcftools
- Conducted GWAS on congenital heart disease (CHD) trios based on different CHD subtypes among multiple ethnic groups

A case-only analysis on autism risks with different polygenic background

- Integrated family-based vcf files from multiple whole exome sequencing callers using bcftools and GATK
- Estimated autism risk regulated by different polygenic background and rare disruptive variants using a case-only model

INVITED TALKS

1. **Huang, K., "**Multi-biofluid metabolome-wide association study illuminates the molecular basis in complex trait genetics", *American Society of Human Genetics*, Los Angeles, CA, Oct 2022

PUBLICATIONS

1. **Huang, K.**, Wu, Y., Shin, J., Zheng, Y., Siahpirani, A. F., Lin, Y., Ni, Z., Chen, J., You, J., Keles, S., Wang, D., Roy, S. & Lu, Q., "Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder," 2021, *PLOS Genetics*
2. **Huang, K.**, Liu, J., Song, G., Panyard, D., Wu, Y., Deming, Y., Miao, J., Zhao, Z., Engelman, C., and Lu, Q., "Multi-biofluid metabolome-wide association study illuminates the molecular basis in complex trait genetics," 2022, *In progress*
3. Zhang, Y., Lu, Q., Ye, Y., **Huang, K**., Lu, W., Wu, Y., Zhong, X., Li, B., Yu, Z., Travers, B., Werling, D., Li, J. & Zhao, H., "SUPERGNOVA: Local genetic correlation analysis reveals heterogeneous etiologic sharing of complex traits," 2021, *Genome Biology*
4. Jin, S., Lu, Q., Wu, Y., **Huang, K**., Diab, N., Pereira, A., Gelb, B., Priest, J., Zhao, H., Brueckner, M. & Lifton, R., "Trans-ethnic meta-analysis identifies novel loci for congenital heart disease," 2022, *In progress*
5. Chen, J., You, J., Zhao, Z., Ni, Z., **Huang, K**., Wu, Y., Fletcher, J., Lu, Q., "Gamete simulation improves polygenic transmission disequilibrium analysis," 2020, *biorxiv*