

# Kunling Huang

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<https://github.com/KunlingHuang/KunlingHuang.github.io>

## EDUCATION

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### University of Wisconsin-Madison

Madison, Wisconsin

*Doctor of philosophy in Statistics*

September 2016 – May 2021

Advisor: Dr. Qiongshi Lu

Dissertation: “**Statistical methods for linking noncoding genetic variations to target genes with application in neurodevelopmental disorders**”

Relative course work: Human Genetics, Machine Learning, Computational Network Biology, Clinical trials, Causal Inference, Experimental Design, Statistical Consulting

### National Taiwan University

Taipei, Taiwan

*Master of Arts in Economics*

September 2013 – May 2016

### National Taiwan University

Taipei, Taiwan

*Bachelor of Arts in Economics*

September 2009 – June 2013

## SKILLS

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Operation systems: Linux/Unix

Programming languages: R, Python, Java

Database tools: MySQL

## PROJECTS

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

- Conducted a trio-based transcriptome-wide association study on GTEx brain tissues on large-scale genetic data to identify autism spectrum disorder (ASD) genes
- Developed and optimized pipeline using R libraries tidyverse and data.table (project code available at: <https://github.com/qlu-lab/TITANS>)
- Designed parallel computing strategy on high-performance computing environment HTCondor
- Implemented pseudo sibling matching and conditional logistic regression models for analyzing ASD trios
- Specified and confirmed the epigenetic role of transcription factor gene *POU3F2* on ASD risk
- Performed DNase-I network analysis and demonstrated excess damaging *de novo* variants in known ASD genes regulated by *POU3F2*
- Identified heritability enrichments in *POU3F2* binding sites using LD score regression
- Evaluated the differential expression in adult and fetal brain for *POU3F2*

### Integrating enhancer-promoter interaction with ASD GWAS signals

- Constructed variance tests for Hi-C enhancer-promoter interaction on GWAS scores to pinpoint genes distantly regulating ASD risks
- Adapted variance quantitative loci (vQTL) methods to denoise the Hi-C interaction data and achieved model robustness
- Processed the Hi-C raw data to interpretable format using Fit-Hi-C

### **Modelling prenatal and postnatal brain eQTLs together via fused LASSO**

- Modelled expression quantitative loci (eQTL) in adult and fetal brain together to boost power in fetal studies using fused LASSO model
- Designed a fast coordinate descent algorithm taking eQTL summary statistics in each developmental stage as input
- Implemented the algorithm as a python scikit-learn compatible module

### **Genome-wide association study for congenital heart disease**

- Curated next generation sequencing (NGS) data using Plink and bcftools
- Combining the association results between microarray and NGS studies using meta-analysis tool METAL and R

### **Identifying ovarian cancer biomarkers with different disease progress**

- Collected RNA-seq data and ovarian cancer progress information using Bioconductor on R
- Performed gene expression cluster analysis using weighted correlation network analysis (WGCNA) on R
- Specified disease associated clusters using Gene Ontology (GO)
- Confirmed the biomarker validity by testing the difference of survival rates in patient groups with different cancer progress

## **RESEARCH EXPERIENCE**

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### **University of Wisconsin-Madison**

*Research Assistant*

**Madison, Wisconsin**

April 2018 – May 2021

- Integrated and curated resources from NCBI and UCSC
- Supervised master students to develop pipelines for mapping metabolite quantitative loci
- Provided high throughput computing and human genetics trainings to undergraduate students

## **PUBLICATIONS**

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- “Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder,” 2019, *bioRxiv*
- “Modelling prenatal and postnatal brain eQTLs together using penalized regression,” 2020, *In progress*
- “Integrating enhancer-promoter interactions and GWAS summary statistics,” 2020, *In progress*