

# YING JI

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EDUCATION

<b>Vanderbilt University, Nashville, TN</b>	2015/08 - Present
Ph.D. in Human Genetics	GPA: 3.82
M.S. in Biostatistics	
Coursework: Advanced Statistical Computing; Applied Survival Analysis; Modern Regression Analysis; Contemporary Statistical Inference; Fundamentals of Probability; High Performance Computing	
<b>Tsinghua University, Beijing, China</b>	2011/09 - 2015/07
B.S. in Biological Science	

## EXPERIENCE

Risk gene prediction using machine learning methods

- Leveraged large scale gene expression profiles (including dense and sparse data) as features, built random forest models to characterize risk genes, predicted more than 1000 high risk genes (python, scikit-learn)
  - Quantified disease risk of genes by integrating multi-omics information (including categorical and continuous) data using a Bayesian framework
  - Unveiled spatiotemporal heterogeneity of risk genes by clustering techniques (PCA, t-SNE)

## Predict genetic risk for breast cancer in East Asian population

- Developed pipeline to predict genetic risk in East Asian by leveraging European sample results and conducted meta-analysis using R, increased prediction auROC from 0.56 to 0.62
  - Mentored rotation graduate student on using Linux/unix and implementing models on computer clusters

PROJECTS

## Predict patient readmission from high dimensional hospitalization Data

- Conducted feature engineering of sparse, messy hospital billing data (10,000 subjects)
  - Achieved 70% accuracy (cross validation) to predict readmission within 30 days of discharge through implementing different models (logistic regression, support vector machine, and random forest)

## ACTIVITIES

**Secretary of Human Genetics Graduate Student Association**      2017/08-2018/08  
Took minutes at every meeting and maintained communication between participants.

## **PRESENTATIONS/ AWARDS**

<b>2019 Graduate Leadership Development Institute (GLDI) travel award</b>	2019/05
Travel support for JSM (joint statistics meeting) 2019	
<b>2018 American Society of Human Genetics Oral Presentation</b>	2018/10
Abstract scored in top 8% among more than 3000 participants	