

Name: Qing Lu
PI Name:Qing Lu

Email: lucienq@ufl.edu
PI email: lucienq@ufl.edu

Functional Neural Networks for High-dimensional Genetic Data Analysis

Shan Zhang¹, Yuan Zhou¹, Pei Geng², and Qing Lu¹

¹Department of Biostatistics, University of Florida; ² Department of Mathematics, Illinois State University

Artificial intelligence (AI) is a thriving research field with many successful applications in areas such as computer vision and speech recognition. Machine learning methods, such as neural networks (NN), play a central role in modern AI technology. While NN also holds great promise for genetic research, the high-dimensional genetic data and complex genetic structure bring tremendous challenges. The vast majority of genetic variants on the genome have small or no effects on diseases, and fitting NN on a large number of variants without considering the underlying genetic structure (e.g., linkage disequilibrium) could bring a serious overfitting issue. Furthermore, while a single disease phenotype is often studied in a classic genetic study, in emerging research fields (e.g., imaging genetics), researchers need to deal with different types of phenotypes. To address these challenges, we propose a functional neural networks (FNN) method. FNN uses a series of basis functions to model high-dimensional genetic and a variety of phenotype data and further builds a multi-layer functional neural network to capture the complex relationship between genetic variants and disease phenotypes. Through simulations, we demonstrate the advantages of FNN for high-dimensional genetic data analysis in terms of robustness and accuracy. We also illustrate the method via an application to nicotine dependence.