A gene-regulation network based deep structured framework for psychiatric disease prediction

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Abstract: Genes and gene regulators are important genomic elements in disease studies. Perturbations in gene regulatory networks can lead to major disorders like schizophrenia and cancer. Many statistic models have been developed to identify regulators like enhancers. We developed a matched-filter based model using enhancer-associated patterns from experimental signals. We evaluated our model on several enhancer databases, demonstrating its superior performance compared to the state-of-the-art algorithms.

We used this model to construct gene-regulatory networks in human neural cells. To understand how genes are dysregulated in psychiatric diseases like schizophrenia and autism spectrum disorder, we developed a deep-learning framework that predicts disorder onset based only on genetic information. We embedded the gene-regulatory network in the deep-learning framework to reflect the underlining molecular interaction networks. The model highlights genes and pathways that are potential therapeutic targets.

Bio: Mengting Gu is graduating with her Ph.D in Computational Biology and Bioinformatics at Yale University. Her thesis work focuses on developing algorithms to understand genome functions. She is interested in finding patterns from large scale biomedical data to understand the complex underlying molecular processes. She has developed tools like Matched-Filter that has been widely used in the genome annotation consortium. Mengting received her M.S. in computer science at Yale University, and B.S. from Tsinghua University in China.