

# Deep Learning with Graph Structure in Small Samples

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**Abstract:** Recently deep learning methods have demonstrated strong capabilities of discovering potential complex patterns for predicting outcomes. They typically need to be trained on a large amount of data. However, biomedical studies often have limited sample sizes but large feature spaces and these features may correlate, interact, and jointly affect an outcome. In this talk, we present a deep learning framework that incorporates the known relationship among variables. In each layer of learning, we focused on multiple local substructures trimmed from the parent feature nodes. We derived a computational-efficient peeling algorithm where features are decomposed into independent components and then summarized for each substructure. Each layer of learning is built upon a gradually reduced tree and the parameters in summary features are optimized through backpropagation. We evaluated the performance of our method through simulations and applied it to two real studies (1) to predict individual response speed using regional cerebral blood flow from functional magnetic resonance imaging data; (2) to predict lung transplantation outcome using gene expression profiles in donors' lungs within several transplant-related pathways. Our method demonstrated improved prediction accuracy in small-scale data, compared to conventional penalized regression, classification trees, and feed forward neural network.