

Prediction of *Yeast* Protein–Protein Interactions by Neural Feature Association Rule¹

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Abstract. In this paper, we present an association rule based protein interaction prediction method. We use neural network to cluster protein interaction data and feature selection method to reduce protein feature dimension. After this model training, association rules for protein interaction prediction are generated by decoding a set of learned weights of trained neural network and association rule mining. For model training, the initial network model was constructed with existing protein interaction data in terms of their functional categories and interactions. The protein interaction data of *Yeast* (*S.cerevisiae*) from MIPS and SGD are used. The prediction performance was compared with traditional simple association rule mining method. According to the experimental results, proposed method shows about 96.1% accuracy compared to simple association mining approach which achieved about 91.4%.

1 Introduction

A variety of attempts have been tried to predict protein functions and interactions with various data such as gene expression, protein–protein interaction (PPI) data, and literature analysis. Analysis of gene expression data through clustering also adopted to predict functions of un-annotated proteins based on the idea that genes with similar functions are likely to be co-expressed [1]. Park *et al.* [2] analyzed interactions between protein domains in terms of the interactions between structural families of evolutionarily related domains. Iossifov *et al.* [3] and Ng *et al.* [4] inferred new interaction from existing interaction data.

In this paper, we propose an adaptive neural network (ANN) based feature association mining method for PPI prediction. We used additional association rules for PPI prediction. These are generated by decoding a set of learned weights of adaptive neural network. We assumed that these association rules decoded from neural network (NN) would make the whole prediction procedure more robust to unexpected error factors by accounting relatively robust characteristic of NNs.

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