

Abstract of poster presentations

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NRProF: Neural Response Based Protein Function Prediction Algorithm

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A large amount of proteomic data is being generated due to advancements in high-throughput genome sequencing methods. But the rate of the experimental functional characterization falls far behind. To fill the gap between the number of sequences and their annotations, fast and accurate automated annotation methods are required. Many methods, such as GOblet, GOfigure, and Gotcha, are designed based on the BLAST search. Unfortunately, the sequence coverage of these methods is low as they cannot detect the remote homologues. The lack of annotation specificity and high complexity of the existing methods advocate the needs to improve automated protein function prediction method. Here we present a novel automated protein functional assignment method based on the neural response algorithm, which simulates the neuronal behavior of the visual cortex in the human brain. The main idea of this algorithm is to define a distance metric that corresponds to the similarity of the subsequences and reflects how the human brain can distinguish between different sequences. We predicted the most similar target protein for a given query protein using the two layered neural response algorithm and thereby assigned the GO term associated with the target sequence to the query sequence. Our method predicted and ranked the actual leaf GO term among the top 5 probable GO terms with 87.66% accuracy. Results of the 5-fold cross validation and the comparison with PFP and FFPred servers indicate the prominent performance by our method.