

Abstract Preview of 'signature profiling' (D9Q9GH)

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Preview of your abstract

Prediction of protein-protein interactions using signature profiling M. A. Mahdavi <maa943@mail.usask.ca> and **Y.-H. Lin** <yenhan.lin@usask.ca>, Department of Chemical Engineering, University of Saskatchewan, Saskatoon, SK S7N 5A9, Canada

Protein-protein interaction is the key element of cellular activities. Proteins interact with each other through functional units such as domains, binding sites, etc that are collectively called signatures. Signatures are main interfaces in each interaction at the protein level. Each protein contains one or more signatures in its primary structure. In this study we present a method to identify protein relationships through their signature contents. Briefly, we introduce a feature vector representing each protein in the genome of an organism where each feature corresponds to a signature. Using a statistical measure, Binary Similarity Function, we score the similarity of each potential pair of proteins regarding their feature vectors. Considering a similarity threshold, the proteins in the pair will be 'interacting' provided that the threshold is satisfied. The method is compared to phylogenetic profile and gene expression profile, and shows that the probability of interaction in our prediction is 3 times better than that in phylogenetic profile, and 11 times better than that in gene expression profile. The false positive rate of this method is significantly lower. It is ~60% lower than phylogenetic profile, and ~90% lower than that in gene expression profile.

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