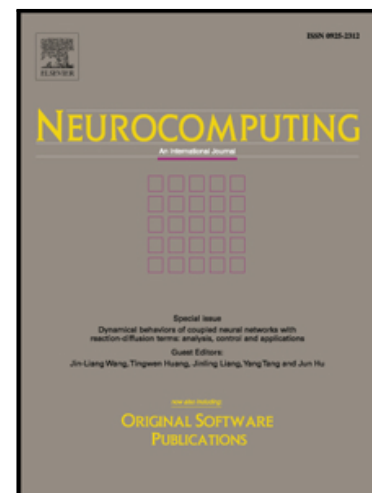


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## Prediction of Protein-Protein Interactions Using An Effective Sequence Based Combined Method

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### Abstract

Proteins and their interactions play a key role in the realization of all cellular biological activities of organisms. Therefore, prediction of protein-protein interactions is crucial for elucidating biological processes. Experimental studies are inadequate for some reasons such as the time required to reveal interactions, the fact that it is an expensive way and the number of yet unknown interactions is too great. Thus, a number of computational methods have been developed to predict PPIs. Generally, many of these methods that produce good results cannot be used without additional biological information such as protein domains, protein structural information, gene neighborhoods, gene expressions, and phylogenetic profiles. Therefore, there is a need for computational methods that can successfully predict interactions using only protein sequences. In this study, we present a novel sequence-based computational model. We applied a new technique called weighted skip-sequential conjoint triads in the proposed method. The results of this research were evaluated on generally used databases and demonstrated its success in this field.

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